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(54) Title: SYNTHETIC PEPTIDES AND USES THEREFORE

(57) Abstract: A synthetic polypeptide is disclosed, which comprises a plurality of different segments of at least one parent polypeptide, wherein the segments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide. Synthetic polynucleotides are also disclosed that code for the synthetic polypeptides of the invention as well as expression constructs comprising the synthetic polynucleotides. Also disclosed are methods for constructing the aforementioned molecules and immunopotentiating compositions and methods for treating and/or preventing a disease or condition.



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Synthetic Peptides And Uses Therefore.

FIELD OF THE INVENTION

THIS INVENTION relates generally to agents for modulating immune responses. More particularly, the present invention relates to a synthetic polypeptide comprising a plurality of different segments of a parent polypeptide, wherein the segments are linked to each other such that one or more functions of the parent polypeptide are impeded, abrogated or otherwise altered and such that the synthetic polypeptide, when introduced into a suitable host, can elicit an immune response against the parent polypeptide. The invention also relates to synthetic polynucleotides encoding the synthetic polypeptides and to synthetic constructs comprising these polynucleotides. The invention further relates to the use of the polypeptides and polynucleotides of the invention in compositions for modulating immune responses. The invention also extends to methods of using such compositions for prophylactic and/or therapeutic purposes.

Bibliographic details of various publications referred to in this specification are collected at the end of the description.

BACKGROUND OF THE INVENTION

The modern reductionist approach to vaccine and therapy development has been pursued for a number of decades and attempts to focus only on those parts of pathogens or of cancer proteins which are relevant to the immune system. To date the performance of this approach has been relatively poor considering the vigorous research carried out and the number of effective vaccines and therapies that it has produced. This approach is still being actively pursued, however, despite its poor performance because vaccines developed using this approach are often extremely safe and because only by completely understanding the immune system can new vaccine strategies be developed.

One area that has benefited greatly from research efforts is knowledge about how the adaptive immune system operates and more specifically how T and B cells learn to recognise specific parts of pathogens and cancers. T cells are mainly involved in cell-mediated immunity whereas B cells are involved in the generation of antibody-mediated immunity. The two most important types of T cells involved in adaptive cellular immunity

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are $\alpha\beta$ CD8⁺ cytotoxic T lymphocytes (CTL) and CD4⁺ T helper lymphocytes. CTL are important mediators of cellular immunity against many viruses, tumours, some bacteria and some parasites because they are able to kill infected cells directly and secrete various factors which can have powerful effects on the spread of infectious organisms. CTLs
5 recognise epitopes derived from foreign intracellular proteins, which are 8-10 amino acids long and which are presented by class I major histocompatibility complex (MHC) molecules (in humans called human lymphocyte antigens - HLAs) (Jardetzky *et al.*, 1991; Fremont *et al.*, 1992; Rotzschke *et al.*, 1990). T helper cells enhance and regulate CTL responses and are necessary for the establishment of long-lived memory CTL. They also
10 inhibit infectious organisms by secreting cytokines such as IFN- γ . T helper cells recognise epitopes derived mostly from extracellular proteins which are 12-25 amino acids long and which are presented by class II MHC molecules (Chicz *et al.*, 1993; Newcomb *et al.*, 1993). B cells, or more specifically the antibodies they secrete, are important mediators in the control and clearance of mostly extracellular organisms. Antibodies recognise mainly
15 conformational determinants on the surface of organisms, for example, although sometimes they may recognise short linear determinants.

Despite significant advances towards understanding how T and linear B cell epitopes are processed and presented to the immune system, the full potential of epitope-based vaccines has not been fully exploited. The main reason for this is the large number
20 of different T cell epitopes, which have to be included into such vaccines to cover the extreme HLA polymorphism in the human population. The human HLA diversity is one of the main reasons why whole pathogen vaccines frequently provide better population coverage than subunit or peptide-based vaccine strategies. There is a range of epitope-based strategies though which have tried to solve this problem, *e.g.*, peptide blends, peptide
25 conjugates and polyepitope vaccines (ie comprising strings of multiple epitopes) (Dyall *et al.*, 1995; Thomson *et al.*, 1996; Thomson *et al.*, 1998; Thomson *et al.*, 1998). These approaches however will always be sub optimal not only because of the slow pace of epitope characterisation but also, because it is virtually impossible for them to cover every existing HLA polymorphism in the population. A number of strategies have sought to
30 avoid both problems by not identifying epitopes and instead incorporating larger amounts of sequence information *e.g.*, approaches using whole genes or proteins and approaches that mix multiple protein or gene sequences together. The proteins used by these strategies

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however sometimes still function and therefore can compromise vaccine safety *e.g.*, whole cancer proteins. Alternative strategies have tried to improve the safety of vaccines by fragmenting the genes and expressing them either separately or as complex mixtures *e.g.*, library DNA immunisation or by ligating such fragments back together. These approaches
5 are still sub-optimal because they are too complex, generate poor levels of immunity, cannot guarantee that all proteins no longer function and/or that all fragments are present, which compromises substantially complete immunological coverage.

The lack of a safe and efficient vaccine strategy that can provide substantially complete immunological coverage is an important problem, especially when trying to
10 develop vaccines against rapidly mutating and persistent viruses such as HIV and hepatitis C virus, because partial population coverage could allow vaccine-resistant pathogens to re-emerge in the future. Human immunodeficiency virus (HIV) is an RNA lentivirus virus approximately 9 kb in length, which infects CD4⁺ T cells, causing T cell decline and AIDS typically 3-8 years after infection. It is currently the most serious human viral infection,
15 evidenced by the number of people currently infected with HIV or who have died from AIDS, estimated by the World Health Organisation (WHO) and UNAIDS in their AIDS epidemic update (December 1999) to be 33.6 and 16.3 million people, respectively. The spread of HIV is also now increasing fastest in areas of the world where over half of the human population reside, hence an effective vaccine is desperately needed to curb the
20 spread of this epidemic. Despite the urgency, an effective vaccine for HIV is still some way off because of delays in defining the correlates of immune protection, lack of a suitable animal model, existence of up to 8 different subtypes of HIV and a high HIV mutation rate.

A significant amount of research has been carried out to try and develop a vaccine
25 capable of generating neutralising antibody responses that can protect against field isolates of HIV. Despite these efforts, it is now clear that the variability, instability and inaccessibility of critical determinants on the HIV envelope protein will make it extremely difficult and perhaps impossible to develop such a vaccine (Kwong *et al.*, 1998). The limited ability of antibodies to block HIV infection is also supported by the observation
30 that development of AIDS correlates primarily with a reduction in CTL responsiveness to HIV and not to altered antibody levels (Ogg *et al.*, 1998). Hence CTL-mediated and not antibody-mediated responses appear to be critical for maintaining the asymptomatic state

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in vivo. There is also some evidence to suggest that pre-existing HIV-specific CTL responses can block the establishment of a latent HIV infection. This evidence comes from a number of cases where individuals have generated HIV-specific CTL responses without becoming infected and appear to be protected from establishing latent HIV infections despite repeated virus exposure (Rowland-Jones *et al.*, 1995; Parmiani 1998). Taken together, these observations suggest that a vaccine capable of generating a broad range of strong CTL responses may be able to stop individuals from becoming latently infected with HIV or at least allow infected individuals to remain asymptomatic for life. Virtually all of the candidate HIV vaccines developed to date have been derived from subtype B HIV proteins (western world subtype) whereas the majority of the HIV infections worldwide are caused by subtypes A/E or C (E and A are similar except in the envelop protein)(referred to as developing world subtypes). Hence existing candidate vaccines may not be suitable for the more common HIV subtypes. Recently, there has been some evidence that B subtype vaccines may be partially effective against other common HIV subtypes (Rowland-Jones *et al.*, 1998). Accordingly, the desirability of a vaccine still remains, whose effectiveness is substantially complete against all isolates of all strains of HIV.

SUMMARY OF THE INVENTION

The present invention is predicated in part on a novel strategy for enhancing the efficacy of an immunopotentiating composition. This strategy involves utilising the sequence information of a parent polypeptide to produce a synthetic polypeptide that
5 comprises a plurality of different segments of the parent polypeptide, which are linked sequentially together in a different arrangement relative to that of the parent polypeptide. As a result of this change in relationship, the sequence of the linked segments in the synthetic polypeptide is different to a sequence contained within the parent polypeptide. As more fully described hereinafter, the present strategy is used advantageously to cause
10 significant disruption to the structure and/or function of the parent polypeptide while minimising the destruction of potentially useful epitopes encoded by the parent polypeptide.

Thus, in one aspect of the present invention, there is provided a synthetic polypeptide comprising a plurality of different segments of at least one parent polypeptide,
15 wherein the segments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide.

In one embodiment, the synthetic polypeptide consists essentially of different segments of a single parent polypeptide.

In an alternate embodiment, the synthetic polypeptide consists essentially of
20 different segments of a plurality of different parent polypeptides.

Suitably, said segments in said synthetic polypeptide are linked sequentially in a different order or arrangement relative to that of corresponding segments in said at least one parent polypeptide.

Preferably, at least one of said segments comprises partial sequence identity or
25 homology to one or more other said segments. The sequence identity or homology is preferably contained at one or both ends of said at least one segment.

In another aspect, the invention resides in a synthetic polynucleotide encoding the synthetic polypeptide as broadly described above.

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According to yet another aspect, the invention contemplates a synthetic construct comprising a said polynucleotide as broadly described above that is operably linked to a regulatory polynucleotide.

In a further aspect of the invention, there is provided a method for producing a
5 synthetic polynucleotide as broadly described above, comprising:

- linking together in the same reading frame a plurality of nucleic acid sequences encoding different segments of at least one parent polypeptide to form a synthetic polynucleotide whose sequence encodes said segments linked together in a different relationship relative to their linkage in the at least one parent polypeptide.

10 Preferably, the method further comprises fragmenting the sequence of a respective parent polypeptide into fragments and linking said fragments together in a different relationship relative to their linkage in said parent polypeptide sequence. In a preferred embodiment of this type, the fragments are randomly linked together.

Suitably, the method further comprises reverse translating the sequence of a
15 respective parent polypeptide or a segment thereof to provide a nucleic acid sequence encoding said parent polypeptide or said segment. In a preferred embodiment of this type, an amino acid of said parent polypeptide sequence is reverse translated to provide a codon, which has higher translational efficiency than other synonymous codons in a cell of interest. Suitably, an amino acid of said parent polypeptide sequence is reverse translated
20 to provide a codon which, in the context of adjacent or local sequence elements, has a lower propensity of forming an undesirable sequence (*e.g.*, a palindromic sequence or a duplicated sequence) that is refractory to the execution of a task (*e.g.*, cloning or sequencing).

In another aspect, the invention encompasses a computer program product for
25 designing the sequence of a synthetic polypeptide as broadly described above, comprising:

- code that receives as input the sequence of at least one parent polypeptide;
- code that fragments the sequence of a respective parent polypeptide into fragments;

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- code that links together said fragments in a different relationship relative to their linkage in said parent polypeptide sequence; and
- a computer readable medium that stores the codes.

In yet another aspect, the invention provides a computer program product for
5 designing the sequence of a synthetic polynucleotide as broadly described above, comprising:

- code that receives as input the sequence of at least one parent polypeptide;
- code that fragments the sequence of a respective parent polypeptide into fragments;
- 10 - code that reverse translates the sequence of a respective fragment to provide a nucleic acid sequence encoding said fragment;
- code that links together in the same reading frame each said nucleic acid sequence to provide a polynucleotide sequence that codes for a polypeptide sequence in which said fragments are linked together in a different relationship relative to their
15 linkage in the at least one parent polypeptide sequence; and
- a computer readable medium that stores the codes.

In still yet another aspect, the invention provides a computer for designing the sequence of a synthetic polypeptide as broadly described above, wherein said computer comprises:

- 20 (a) a machine-readable data storage medium comprising a data storage material encoded with machine-readable data, wherein said machine-readable data comprise the sequence of at least one parent polypeptide;
- (b) a working memory for storing instructions for processing said machine-readable data;
- 25 (c) a central-processing unit coupled to said working memory and to said machine-readable data storage medium, for processing said machine readable data to provide said synthetic polypeptide sequence; and
- (d) an output hardware coupled to said central processing unit, for receiving said synthetic polypeptide sequence.

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In a preferred embodiment, the processing of said machine readable data comprises fragmenting the sequence of a respective parent polypeptide into fragments and linking together said fragments in a different relationship relative to their linkage in the sequence of said parent polypeptide.

5 In still yet another aspect, the invention resides in a computer for designing the sequence of a synthetic polynucleotide as broadly described above, wherein said computer comprises:

(a) a machine-readable data storage medium comprising a data storage material encoded with machine-readable data, wherein said machine-readable data comprise the
10 sequence of at least one parent polypeptide;

(b) a working memory for storing instructions for processing said machine-readable data;

(c) a central-processing unit coupled to said working memory and to said machine-readable data storage medium, for processing said machine readable data to provide said
15 synthetic polynucleotide sequence; and

(d) an output hardware coupled to said central processing unit, for receiving said synthetic polynucleotide sequence.

In a preferred embodiment, the processing of said machine readable data comprises fragmenting the sequence of a respective parent polypeptide into fragments,
20 reverse translating the sequence of a respective fragment to provide a nucleic acid sequence encoding said fragment and linking together in the same reading frame each said nucleic acid sequence to provide a polynucleotide sequence that codes for a polypeptide sequence in which said fragments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide sequence.

25 According to another aspect, the invention contemplates a composition, comprising an immunopotentiating agent selected from the group consisting of a synthetic polypeptide as broadly described above, a synthetic polynucleotide as broadly described above and a synthetic construct as broadly described above, together with a pharmaceutically acceptable carrier.

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The composition may optionally comprise an adjuvant.

In a further aspect, the invention encompasses a method for modulating an immune response, which response is preferably directed against a pathogen or a cancer, comprising administering to a patient in need of such treatment an effective amount of an immunopotentiating agent selected from the group consisting of a synthetic polypeptide as
5 broadly described above, a synthetic polynucleotide as broadly described above and a synthetic construct as broadly described above, or a composition as broadly described above.

According to still a further aspect of the invention, there is provided a method for
10 treatment and/or prophylaxis of a disease or condition, comprising administering to a patient in need of such treatment an effective amount of an immunopotentiating agent selected from the group consisting of a synthetic polypeptide as broadly described above, a synthetic polynucleotide as broadly described above and a synthetic construct as broadly described above, or a composition as broadly described above.

15 The invention also encompasses the use of the synthetic polypeptide, the synthetic polynucleotide and the synthetic construct as broadly described above in the study, and modulation of immune responses.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a diagrammatic representation showing the number of people living with AIDS in 1998 in various parts of the world and most prevalent HIV clades in these regions. Estimates generated by UNAIDS.

5 Figure 2 is a graphical representation showing trends in the incidence of the common HIV clades and estimates for the future. Graph from the International Aids Vaccine Initiative (IAVI).

Figure 3 is a diagrammatic representation showing overlapping segments of a parent polypeptide sequence for HIV gag [SEQ ID NO: 1] used for the construction of an
10 embodiment of an HIV Savine. Also shown are the alignments of common HIV clade consensus sequences for the HIV gag protein from the HIV Molecular Immunology Database 1997, Editors Bette Korber, John Moore, Cristian Brander, Richard Koup, Barton Haynes and Bruce Walker. Publisher, Los Alamos National Laboratory, Theoretical Biology and Biophysics, Los Alamos, New Mexico, Pub LAUR 98-485.

15 Figure 4 is a diagrammatic representation showing overlapping segments of a parent polypeptide sequence for HIV pol [SEQ ID NO: 2] used for the construction of an embodiment of an HIV Savine. Also shown are the alignments of common HIV clade consensus sequences for the HIV pol protein from the HIV Molecular Immunology Database 1997, Editors Bette Korber, John Moore, Cristian Brander, Richard Koup, Barton
20 Haynes and Bruce Walker. Publisher, Los Alamos National Laboratory, Theoretical Biology and Biophysics, Los Alamos, New Mexico, Pub LAUR98-485.

Figure 5 is a diagrammatic representation showing overlapping segments of a parent polypeptide sequence for HIV vif [SEQ ID NO: 3] used for the construction of an
25 embodiment of an HIV Savine. Also shown are the alignments of common HIV clade consensus sequences for the HIV vif protein from the HIV Molecular Immunology Database 1997, Editors Bette Korber, John Moore, Cristian Brander, Richard Koup, Barton Haynes and Bruce Walker. Publisher, Los Alamos National Laboratory, Theoretical Biology and Biophysics, Los Alamos, New Mexico, Pub LAUR98-485.

Figure 6 is a diagrammatic representation showing overlapping segments of a parent polypeptide sequence for HIV vpr [SEQ ID NO: 4] used for the construction of an embodiment of an HIV Savine. Also shown are the alignments of common HIV clade consensus sequences for the HIV vpr protein from the HIV Molecular Immunology Database 1997, Editors Bette Korber, John Moore, Cristian Brander, Richard Koup, Barton Haynes and Bruce Walker. Publisher, Los Alamos National Laboratory, Theoretical Biology and Biophysics, Los Alamos, New Mexico, Pub LAUR 98-485.

Figure 7 is a diagrammatic representation showing overlapping segments of a parent polypeptide sequence for HIV tat [SEQ ID NO: 5] used for the construction of an embodiment of an HIV Savine. Also shown are the alignments of common HIV clade consensus sequences for the HIV tat protein from the HIV Molecular Immunology Database 1997, Editors Bette Korber, John Moore, Cristian Brander, Richard Koup, Barton Haynes and Bruce Walker. Publisher, Los Alamos National Laboratory, Theoretical Biology and Biophysics, Los Alamos, New Mexico, Pub LAUR 98-485.

Figure 8 is a diagrammatic representation showing overlapping segments of a parent polypeptide sequence for HIV rev [SEQ ID NO: 6] used for the construction of an embodiment of an HIV Savine. Also shown are the alignments of common HIV clade consensus sequences for the HIV rev protein from the HIV Molecular Immunology Database 1997, Editors Bette Korber, John Moore, Cristian Brander, Richard Koup, Barton Haynes and Bruce Walker. Publisher, Los Alamos National Laboratory, Theoretical Biology and Biophysics, Los Alamos, New Mexico, Pub LAUR 98-485.

Figure 9 is a diagrammatic representation showing overlapping segments of a parent polypeptide sequence for HIV vpu [SEQ ID NO: 7] used for the construction of an embodiment of an HIV Savine. Also shown are the alignments of common HIV clade consensus sequences for the HIV vpu protein from the HIV Molecular Immunology Database 1997, Editors Bette Korber, John Moore, Cristian Brander, Richard Koup, Barton Haynes and Bruce Walker. Publisher, Los Alamos National Laboratory, Theoretical Biology and Biophysics, Los Alamos, New Mexico, Pub LAUR 98-485.

Figure 10 is a diagrammatic representation showing overlapping segments of a parent polypeptide sequence for HIV env [SEQ ID NO: 8] used for the construction of an embodiment of an HIV Savine. Also shown are the alignments of common HIV clade

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consensus sequences for the HIV env protein from the HIV Molecular Immunology Database 1997, Editors Bette Korber, John Moore, Cristian Brander, Richard Koup, Barton Haynes and Bruce Walker. Publisher, Los Alamos National Laboratory, Theoretical Biology and Biophysics, Los Alamos, New Mexico, Pub LAUR 98-485.

5 Figure 11 is a diagrammatic representation showing overlapping segments of a parent polypeptide sequence for HIV nef [SEQ ID NO: 9] used for the construction of an embodiment of an HIV Savine. Also shown are the alignments of common HIV clade consensus sequences for the HIV nef protein from the HIV Molecular Immunology Database 1997, Editors Bette Korber, John Moore, Cristian Brander, Richard Koup, Barton
10 Haynes and Bruce Walker. Publisher, Los Alamos National Laboratory, Theoretical Biology and Biophysics, Los Alamos, New Mexico, Pub LAUR 98-485.

Figure 12 is a diagrammatic representation depicting the systematic segmentation of the designed degenerate consensus sequences for each HIV protein and the reverse translation of each segment into a DNA sequence. Also shown is the number of segments
15 used during random rearrangement and amino acids that were removed. Amino acids surrounded by an open square were removed from the design, because degenerate codons to cater for the desired amino acid combination required too many degenerate bases to comply with the incorporation of degenerate sequence rules outlined in the description of the invention herein. Amino acids surrounded by an open circle were removed only in the
20 segment concerned mainly because they were coded for in an oligonucleotide overlap region. Amino acids marked with an asterisk were designed differently in one fragment compared to the corresponding overlap region (see tat gene)

Figure 13 is a diagrammatic representation showing the first and second most frequently used codons in mammals used to reverse translate HIV protein segments. Also
25 shown are all first and second most frequently used degenerate codons for two amino acids where only one base is varied. Codons used where more than one base was varied were worked out in each case by comparing all the codons for each amino acid. The IUPAC codes for degenerate bases are also shown.

Figure 14 illustrates the construction plan for the HIV Savine showing the
30 approximate sizes of the subcassettes, cassettes and full-length Savine cDNA and the restriction sites involved in joining them together. Also shown are the extra sequences

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added onto each subcassette during their design and a brief description of how the subcassettes, cassettes and full length cDNA were constructed and transferred into appropriate DNA plasmids. *Description of full length construction:* pA was cleaved with *XhoI/SaII* and cloned into *XhoI* arms of the B cassette; pAB was cleaved with *XhoI* and
 5 cloned into *XhoI* arms of the C cassette; full length construct is excisable with either *XbaI/BamHI* at the 5' end or *BglII* at the 3' end. *Options for excising cassettes:* A) *XbaI/BamHI* at the 5' end, *BglII/XhoI* at the 3' end; B) *XbaI/BamHI* at the 5' end, *BglII/SaII* at the 3' end; C) *XbaI/BamHI* at the 5' end, *BglII/SaII* at the 3' end. *Cleaving plasmid vectors:* pDNAVacc is cleavable with *XbaI/XhoI* (DNA vaccination); pBCB07 or
 10 pTK7.5 vectors are cleavable with *BamHI/SaII* (Recombinant Vaccinia); pAvipox vector pAF09 is cleavable with *BamHI/SaII* (Recombinant Avipox).

Figure 15 shows the full length DNA (17253 bp) and protein sequence (5742 aas) of the HIV Savine construct. Fragment boundaries are shown, together with the position of each fragment in each designed HIV protein, fragment number (in brackets), spacer residues (two alanine residues) and which fragment the spacer was for (open boxes and
 15 arrows). The location of residual restriction site joining sequences corresponding to subcassette or cassette boundaries (shaded boxes) are also shown, along with start and stop codons, Kozak sequence, the location of the murine influenza virus CTL epitope sequence (near the 3' end), important restriction sites at each end and the position of each degenerate
 20 amino acid (indicated by 'X').

Figure 16 depicts the layout and position of oligonucleotides in the designed DNA sequence for subcassette A1. The sequences which anneal to the short amplification oligonucleotides are indicated by hatched boxes and the position of oligonucleotide overlap regions are dark shaded.

25 Figure 17: Panel (a) depicts the stepwise asymmetric PCR of the two halves of subcassette A1 (lanes 2-5 and 7-9, respectively) and final splicing together by SOEing (lane 10). DNA standards in lane 1 are pUC18 digested with *Sau3AI*. Panel (b) shows the stepwise ligation-mediated joining and PCR amplification of each cassette as indicated. DNA standards in lane 1 are SPP1 cut with *EcoRI*.

30 Figure 18: Panel (a) shows summary of the construction of the DNA vaccine plasmids that express one HIV Savine cassette. Panel (b) shows a summary of the

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construction of the plasmids used for marker rescue recombination to generate Vaccinia viruses expressing one HIV Savine cassette. Panel (c) shows a summary of the construction of the DNA vaccine plasmids which each express a version of the full-length HIV Savine cDNA

5 Figure 19 shows restimulation of HIV specific polyclonal CTL responses from three HIV-infected patients by the HIV Savine constructs. PBMCs from three different patients were restimulated for 7 days by infection with Vaccinia virus pools expressing the HIV Savine cassettes: Pool 1 included VV-AC1 and VV-BC1; Pool 2 included VV-AC2, VV-BC2 and VV-CC2. The restimulated PBMCs were then mixed with autologous LCLs
10 (effector to target ratio of 50:1), which were either uninfected or infected with either Vaccinia viruses expressing the HIV proteins gag (VV-gag), env (VV-env) or pol (VV-pol), VV- HIV Savine pools 1 (light bars) or 2 (dark bars) or a control Vaccinia virus (VV-Lac) and the amount of ^{51}Cr released used to determine percent specific lysis. K562 cells were used to determine the level of NK cell-mediated killing in their stimulated culture.

15 Figure 20 is a diagrammatic representation showing CD4+ proliferation of PBMCs from HIV-1 infected patients restimulated with either Pool1 or Pool2 of the HIV-1 Savine. Briefly PBMCs were stained with CFSE and culture for 6 days with or without VVs encoding either pool1 or pool2 of the HIV-1 Savine. Restimulated Cells were then labelled with antibodies and analysed by FACS.

20 Figure 21 is a graphical representation showing the CTL response in mice vaccinated with the HIV Savine. C57BL6 mice were immunised with the HIV-1 Savine DNA vaccine comprising the six plasmids described in Figure 18a (100 μg total DNA was given as 50 $\mu\text{g}/\text{leg}$ i.m.). One week later Poxviruses (1×10^7 pfu) comprising Pool 1 of the HIV-1 Savine were used to boost the immune responses. Three weeks later splenocytes
25 from these mice were restimulated with VV-Pool 1 or VV-Pool 2 for 5 days and the resultant effectors used in a ^{51}Cr release cytotoxicity assay against targets infected with CTRVV, VV-pools or VV expressing the natural antigens from HIV-1.

Figure 22 shows immune responses of HIV Immune Macaques (vaccinated with recombinant FPV expressing gag-pol and challenged with HIV-1 2 years prior to
30 experiment). Monkeys 1 and 2 were immunised once at day 0 with VV Savine pool 1 (Three VVs which together express the entire HIV Savine). Monkey 3 was immunised

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twice with FPV-gag-pol *i.e.*, Day 0 is 3 weeks after first FPV-gag-pol immunisation. **A)** IFN- γ detection by ELISPOT of whole blood (0.5 mL, venous blood heparin-anticoagulated) stimulated with Aldrithiol-2 inactivated whole HIV-1 (20 hours, 20 μ g/mL). Plasma samples were then centrifuged (1000xg) and assayed in duplicate for
5 antigen-specific IFN using capture ELISA. **B)** Flow cytometric detection of HIV-1 specific CD69+/CD8+ T cells. Freshly isolated PBMCs were stimulated with inactivated HIV-1 as above for 16 hours, washed and labelled with the antibodies. Cells were then analysed using a FACScalibur™ flow cytometer and data. analysed using Cell-Quest software. **C)** Flow cytometric detection of HIV-1 specific CD69+/CD4+ T cells carried out as in B).

10 Figure 23 shows a diagram of a system used to carry out the instructions encoded by the storage medium of Figures 28 and 29.

Figure 24 depicts a flow diagram showing an embodiment of a method for designing synthetic polynucleotide and synthetic polypeptides of the invention.

15 Figure 25 shows an algorithm, which *inter alia* utilises the steps of the method shown in Figure 24.

Figure 26 shows an example of applying the algorithm of Figure 25 to an input consensus polyprotein sequence of Hepatitis C 1a to execute the segmentation of the polyprotein sequence, the rearrangement of the segments, the linkage of the rearranged segments and the outputting of synthetic polynucleotide and polypeptide sequences for the
20 preparation of Savines for treating and/or preventing Hepatitis C infection.

Figure 27 illustrates an example of applying the algorithm of Figure 25 to input consensus melanocyte differentiation antigens (gp100, MART, TRP-1, Tyros, Trp-2, MC1R, MUC1F and MUC1R) and to consensus melanoma specific antigens (BAGE, GAGE-1, gp100In4, MAGE-1, MAGE-3, PRAME, TRP2IN2, NYNSO1a, NYNSO1b and
25 LAGE1) to facilitate segmentation of those sequences, to rearrange the segments, to link the rearranged segments and to synthetic polynucleotide and polypeptide sequences for the preparation of Savines for treating and/or preventing melanoma.

Figure 28 shows a cross section of a magnetic storage medium.

Figure 29 shows a cross section of an optically readable data storage medium.

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Figure 30 shows six HIV Savine cassette sequences (A1 [SEQ ID NO: 393], A2 [SEQ ID NO: 399], B1[SEQ ID NO: 395], B2 [SEQ ID NO: 401], C1 [SEQ ID NO: 397] and C2 [SEQ ID NO: 403]). A1, B1 and C1 can be joined together using, for example, convenient restriction enzyme sites provided at the ends of each cassette to construct an
5 embodiment of a full length HIV Savine [SEQ ID NO: 405]. A2, B2 and C2 can also be joined together to provide another embodiment of a full length HIV Savine with 350 aa mutations common in major HIV clades. The cassettes A/B/C can be joined into single constructs using specific restriction enzyme sites incorporated after the start codon or before the stop codon in the cassettes

BRIEF DESCRIPTION OF THE SEQUENCES: SUMMARY TABLE**TABLE A**

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 1	GAG consensus polypeptide	499 aa
SEQ ID NO: 2	POL consensus polypeptide	995 aa
SEQ ID NO: 3	VIF consensus polypeptide	192 aa
SEQ ID NO: 4	VPR consensus polypeptide	96 aa
SEQ ID NO: 5	TAT consensus polypeptide	102 aa
SEQ ID NO: 6	REV consensus polypeptide	123 aa
SEQ ID NO: 7	VPU consensus polypeptide	81 aa
SEQ ID NO: 8	ENV consensus polypeptide	651 aa
SEQ ID NO: 9	NEF consensus polypeptide	206 aa
SEQ ID NO: 10	GAG segment 1	90 nts
SEQ ID NO: 11	Polypeptide encoded by SEQ ID NO: 10	30 aa
SEQ ID NO: 12	GAG segment 2	90 nts
SEQ ID NO: 13	Polypeptide encoded by SEQ ID NO: 12	30 aa
SEQ ID NO: 14	GAG segment 3	90 nts
SEQ ID NO: 15	Polypeptide encoded by SEQ ID NO: 14	30 aa
SEQ ID NO: 16	GAG segment 4	90 nts
SEQ ID NO: 17	Polypeptide encoded by SEQ ID NO: 16	30 aa
SEQ ID NO: 18	GAG segment 5	90 nts
SEQ ID NO: 19	Polypeptide encoded by SEQ ID NO: 18	30 aa
SEQ ID NO: 20	GAG segment 6	90 nts
SEQ ID NO: 21	Polypeptide encoded by SEQ ID NO: 20	30 aa
SEQ ID NO: 22	GAG segment 7	90 nts

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 23	Polypeptide encoded by SEQ ID NO: 22	30 aa
SEQ ID NO: 24	GAG segment 8	90 nts
SEQ ID NO: 25	Polypeptide encoded by SEQ ID NO: 24	30 aa
SEQ ID NO: 26	GAG segment 9	90 nts
SEQ ID NO: 27	Polypeptide encoded by SEQ ID NO: 26	30 aa
SEQ ID NO: 28	GAG segment 10	90 nts
SEQ ID NO: 29	Polypeptide encoded by SEQ ID NO: 28	30 aa
SEQ ID NO: 30	GAG segment 11	90 nts
SEQ ID NO: 31	Polypeptide encoded by SEQ ID NO: 30	30 aa
SEQ ID NO: 32	GAG segment 12	90 nts
SEQ ID NO: 33	Polypeptide encoded by SEQ ID NO: 32	30 aa
SEQ ID NO: 34	GAG segment 13	90 nts
SEQ ID NO: 35	Polypeptide encoded by SEQ ID NO: 34	30 aa
SEQ ID NO: 36	GAG segment 14	90 nts
SEQ ID NO: 37	Polypeptide encoded by SEQ ID NO: 36	30 aa
SEQ ID NO: 38	GAG segment 15	90 nts
SEQ ID NO: 39	Polypeptide encoded by SEQ ID NO: 38	30 aa
SEQ ID NO: 40	GAG segment 16	90 nts
SEQ ID NO: 41	Polypeptide encoded by SEQ ID NO: 40	30 aa
SEQ ID NO: 42	GAG segment 17	90 nts
SEQ ID NO: 43	Polypeptide encoded by SEQ ID NO: 42	30 aa
SEQ ID NO: 44	GAG segment 18	90 nts
SEQ ID NO: 45	Polypeptide encoded by SEQ ID NO: 44	30 aa
SEQ ID NO: 46	GAG segment 19	90 nts

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 47	Polypeptide encoded by SEQ ID NO: 46	30 aa
SEQ ID NO: 48	GAG segment 20	90 nts
SEQ ID NO: 49	Polypeptide encoded by SEQ ID NO: 48	30 aa
SEQ ID NO: 50	GAG segment 21	90 nts
SEQ ID NO: 51	Polypeptide encoded by SEQ ID NO: 50	30 aa
SEQ ID NO: 52	GAG segment 22	90 nts
SEQ ID NO: 53	Polypeptide encoded by SEQ ID NO: 52	30 aa
SEQ ID NO: 54	GAG segment 23	90 nts
SEQ ID NO: 55	Polypeptide encoded by SEQ ID NO: 54	30 aa
SEQ ID NO: 56	GAG segment 24	90 nts
SEQ ID NO: 57	Polypeptide encoded by SEQ ID NO: 56	30 aa
SEQ ID NO: 58	GAG segment 25	90 nts
SEQ ID NO: 59	Polypeptide encoded by SEQ ID NO: 58	30 aa
SEQ ID NO: 60	GAG segment 26	90 nts
SEQ ID NO: 61	Polypeptide encoded by SEQ ID NO: 60	30 aa
SEQ ID NO: 62	GAG segment 27	90 nts
SEQ ID NO: 63	Polypeptide encoded by SEQ ID NO: 62	30 aa
SEQ ID NO: 64	GAG segment 28	90 nts
SEQ ID NO: 65	Polypeptide encoded by SEQ ID NO: 64	30 aa
SEQ ID NO: 66	GAG segment 29	90 nts
SEQ ID NO: 67	Polypeptide encoded by SEQ ID NO: 66	30 aa
SEQ ID NO: 68	GAG segment 30	90 nts
SEQ ID NO: 69	Polypeptide encoded by SEQ ID NO: 68	30 aa
SEQ ID NO: 70	GAG segment 31	90 nts

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 71	Polypeptide encoded by SEQ ID NO: 70	30 aa
SEQ ID NO: 72	GAG segment 32	90 nts
SEQ ID NO: 73	Polypeptide encoded by SEQ ID NO: 72	30 aa
SEQ ID NO: 74	GAG segment 33	57 nts
SEQ ID NO: 75	Polypeptide encoded by SEQ ID NO: 74	19 aa
SEQ ID NO: 76	POL segment 1	90 nts
SEQ ID NO: 77	Polypeptide encoded by SEQ ID NO: 76	30 aa
SEQ ID NO: 78	POL segment 2	90 nts
SEQ ID NO: 79	Polypeptide encoded by SEQ ID NO: 78	30 aa
SEQ ID NO: 80	POL segment 3	90 nts
SEQ ID NO: 81	Polypeptide encoded by SEQ ID NO: 80	30 aa
SEQ ID NO: 82	POL segment 4	90 nts
SEQ ID NO: 83	Polypeptide encoded by SEQ ID NO: 82	30 aa
SEQ ID NO: 84	POL segment 5	90 nts
SEQ ID NO: 85	Polypeptide encoded by SEQ ID NO: 84	30 aa
SEQ ID NO: 86	POL segment 6	90 nts
SEQ ID NO: 87	Polypeptide encoded by SEQ ID NO: 86	30 aa
SEQ ID NO: 88	POL segment 7	90 nts
SEQ ID NO: 89	Polypeptide encoded by SEQ ID NO: 88	30 aa
SEQ ID NO: 90	POL segment 8	90 nts
SEQ ID NO: 91	Polypeptide encoded by SEQ ID NO: 90	30 aa
SEQ ID NO: 92	POL segment 9	90 nts
SEQ ID NO: 93	Polypeptide encoded by SEQ ID NO: 92	30 aa
SEQ ID NO: 94	POL segment 10	90 nts

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<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 95	Polypeptide encoded by SEQ ID NO: 94	30 aa
SEQ ID NO: 96	POL segment 11	90 nts
SEQ ID NO: 97	Polypeptide encoded by SEQ ID NO: 96	30 aa
SEQ ID NO: 98	POL segment 12	90 nts
SEQ ID NO: 99	Polypeptide encoded by SEQ ID NO: 98	30 aa
SEQ ID NO: 100	POL segment 13	90 nts
SEQ ID NO: 101	Polypeptide encoded by SEQ ID NO: 100	30 aa
SEQ ID NO: 102	POL segment 14	90 nts
SEQ ID NO: 103	Polypeptide encoded by SEQ ID NO: 102	30 aa
SEQ ID NO: 104	POL segment 15	90 nts
SEQ ID NO: 105	Polypeptide encoded by SEQ ID NO: 104	30 aa
SEQ ID NO: 106	POL segment 16	90 nts
SEQ ID NO: 107	Polypeptide encoded by SEQ ID NO: 106	30 aa
SEQ ID NO: 108	POL segment 17	90 nts
SEQ ID NO: 109	Polypeptide encoded by SEQ ID NO: 108	30 aa
SEQ ID NO: 110	POL segment 18	90 nts
SEQ ID NO: 111	Polypeptide encoded by SEQ ID NO: 110	30 aa
SEQ ID NO: 112	POL segment 19	90 nts
SEQ ID NO: 113	Polypeptide encoded by SEQ ID NO: 112	30 aa
SEQ ID NO: 114	POL segment 20	90 nts
SEQ ID NO: 115	Polypeptide encoded by SEQ ID NO: 114	30 aa
SEQ ID NO: 116	POL segment 21	90 nts
SEQ ID NO: 117	Polypeptide encoded by SEQ ID NO: 116	30 aa
SEQ ID NO: 118	POL segment 22	90 nts

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<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 119	Polypeptide encoded by SEQ ID NO: 118	30 aa
SEQ ID NO: 120	POL segment 23	90 nts
SEQ ID NO: 121	Polypeptide encoded by SEQ ID NO: 120	30 aa
SEQ ID NO: 122	POL segment 24	90 nts
SEQ ID NO: 123	Polypeptide encoded by SEQ ID NO: 122	30 aa
SEQ ID NO: 124	POL segment 25	90 nts
SEQ ID NO: 125	Polypeptide encoded by SEQ ID NO: 124	30 aa
SEQ ID NO: 126	POL segment 26	90 nts
SEQ ID NO: 127	Polypeptide encoded by SEQ ID NO: 126	30 aa
SEQ ID NO: 128	POL segment 27	90 nts
SEQ ID NO: 129	Polypeptide encoded by SEQ ID NO: 128	30 aa
SEQ ID NO: 130	POL segment 28	90 nts
SEQ ID NO: 131	Polypeptide encoded by SEQ ID NO: 130	30 aa
SEQ ID NO: 132	POL segment 29	90 nts
SEQ ID NO: 133	Polypeptide encoded by SEQ ID NO: 132	30 aa
SEQ ID NO: 134	POL segment 30	90 nts
SEQ ID NO: 135	Polypeptide encoded by SEQ ID NO: 134	30 aa
SEQ ID NO: 136	POL segment 31	90 nts
SEQ ID NO: 137	Polypeptide encoded by SEQ ID NO: 136	30 aa
SEQ ID NO: 138	POL segment 32	90 nts
SEQ ID NO: 139	Polypeptide encoded by SEQ ID NO: 138	30 aa
SEQ ID NO: 140	POL segment 33	90 nts
SEQ ID NO: 141	Polypeptide encoded by SEQ ID NO: 140	30 aa
SEQ ID NO: 142	POL segment 34	90 nts

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 143	Polypeptide encoded by SEQ ID NO: 142	30 aa
SEQ ID NO: 144	POL segment 35	90 nts
SEQ ID NO: 145	Polypeptide encoded by SEQ ID NO: 144	30 aa
SEQ ID NO: 146	POL segment 36	90 nts
SEQ ID NO: 147	Polypeptide encoded by SEQ ID NO: 146	30 aa
SEQ ID NO: 148	POL segment 37	90 nts
SEQ ID NO: 149	Polypeptide encoded by SEQ ID NO: 148	30 aa
SEQ ID NO: 150	POL segment 38	90 nts
SEQ ID NO: 151	Polypeptide encoded by SEQ ID NO: 150	30 aa
SEQ ID NO: 152	POL segment 39	90 nts
SEQ ID NO: 153	Polypeptide encoded by SEQ ID NO: 152	30 aa
SEQ ID NO: 154	POL segment 40	90 nts
SEQ ID NO: 155	Polypeptide encoded by SEQ ID NO: 154	30 aa
SEQ ID NO: 156	POL segment 41	90 nts
SEQ ID NO: 157	Polypeptide encoded by SEQ ID NO: 156	30 aa
SEQ ID NO: 158	POL segment 42	90 nts
SEQ ID NO: 159	Polypeptide encoded by SEQ ID NO: 158	30 aa
SEQ ID NO: 160	POL segment 43	90 nts
SEQ ID NO: 161	Polypeptide encoded by SEQ ID NO: 160	30 aa
SEQ ID NO: 162	POL segment 44	90 nts
SEQ ID NO: 163	Polypeptide encoded by SEQ ID NO: 162	30 aa
SEQ ID NO: 164	POL segment 45	90 nts
SEQ ID NO: 165	Polypeptide encoded by SEQ ID NO: 164	30 aa
SEQ ID NO: 166	POL segment 46	90 nts

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 167	Polypeptide encoded by SEQ ID NO: 166	30 aa
SEQ ID NO: 168	POL segment 47	90 nts
SEQ ID NO: 169	Polypeptide encoded by SEQ ID NO: 168	30 aa
SEQ ID NO: 170	POL segment 48	90 nts
SEQ ID NO: 171	Polypeptide encoded by SEQ ID NO: 170	30 aa
SEQ ID NO: 172	POL segment 49	90 nts
SEQ ID NO: 173	Polypeptide encoded by SEQ ID NO: 172	30 aa
SEQ ID NO: 174	POL segment 50	90 nts
SEQ ID NO: 175	Polypeptide encoded by SEQ ID NO: 174	30 aa
SEQ ID NO: 176	POL segment 51	90 nts
SEQ ID NO: 177	Polypeptide encoded by SEQ ID NO: 176	30 aa
SEQ ID NO: 178	POL segment 52	90 nts
SEQ ID NO: 179	Polypeptide encoded by SEQ ID NO: 178	30 aa
SEQ ID NO: 180	POL segment 53	90 nts
SEQ ID NO: 181	Polypeptide encoded by SEQ ID NO: 180	30 aa
SEQ ID NO: 182	POL segment 54	90 nts
SEQ ID NO: 183	Polypeptide encoded by SEQ ID NO: 182	30 aa
SEQ ID NO: 184	POL segment 55	90 nts
SEQ ID NO: 185	Polypeptide encoded by SEQ ID NO: 184	30 aa
SEQ ID NO: 186	POL segment 56	90 nts
SEQ ID NO: 187	Polypeptide encoded by SEQ ID NO: 186	30 aa
SEQ ID NO: 188	POL segment 57	90 nts
SEQ ID NO: 189	Polypeptide encoded by SEQ ID NO: 188	30 aa
SEQ ID NO: 190	POL segment 58	90 nts

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 191	Polypeptide encoded by SEQ ID NO: 190	30 aa
SEQ ID NO: 192	POL segment 59	90 nts
SEQ ID NO: 193	Polypeptide encoded by SEQ ID NO: 192	30 aa
SEQ ID NO: 194	POL segment 60	90 nts
SEQ ID NO: 195	Polypeptide encoded by SEQ ID NO: 194	30 aa
SEQ ID NO: 196	POL segment 61	90 nts
SEQ ID NO: 197	Polypeptide encoded by SEQ ID NO: 196	30 aa
SEQ ID NO: 198	POL segment 62	90 nts
SEQ ID NO: 199	Polypeptide encoded by SEQ ID NO: 198	30 aa
SEQ ID NO: 200	POL segment 63	90 nts
SEQ ID NO: 201	Polypeptide encoded by SEQ ID NO: 200	30 aa
SEQ ID NO: 202	POL segment 64	90 nts
SEQ ID NO: 203	Polypeptide encoded by SEQ ID NO: 202	30 aa
SEQ ID NO: 204	POL segment 65	90 nts
SEQ ID NO: 205	Polypeptide encoded by SEQ ID NO: 204	30 aa
SEQ ID NO: 206	POL segment 66	60 nts
SEQ ID NO: 207	Polypeptide encoded by SEQ ID NO: 206	20 aa
SEQ ID NO: 208	VIF segment 1	90 nts
SEQ ID NO: 209	Polypeptide encoded by SEQ ID NO: 208	30 aa
SEQ ID NO: 210	VIF segment 2	90 nts
SEQ ID NO: 211	Polypeptide encoded by SEQ ID NO: 210	30 aa
SEQ ID NO: 212	VIF segment 3	90 nts
SEQ ID NO: 213	Polypeptide encoded by SEQ ID NO: 212	30 aa
SEQ ID NO: 214	VIF segment 4	90 nts

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 215	Polypeptide encoded by SEQ ID NO: 214	30 aa
SEQ ID NO: 216	VIF segment 5	90 nts
SEQ ID NO: 217	Polypeptide encoded by SEQ ID NO: 216	30 aa
SEQ ID NO: 218	VIF segment 6	90 nts
SEQ ID NO: 219	Polypeptide encoded by SEQ ID NO: 218	30 aa
SEQ ID NO: 220	VIF segment 7	90 nts
SEQ ID NO: 221	Polypeptide encoded by SEQ ID NO: 220	30 aa
SEQ ID NO: 222	VIF segment 8	90 nts
SEQ ID NO: 223	Polypeptide encoded by SEQ ID NO: 222	30 aa
SEQ ID NO: 224	VIF segment 9	90 nts
SEQ ID NO: 225	Polypeptide encoded by SEQ ID NO: 224	30 aa
SEQ ID NO: 226	VIF segment 10	90 nts
SEQ ID NO: 227	Polypeptide encoded by SEQ ID NO: 226	30 aa
SEQ ID NO: 228	VIF segment 11	90 nts
SEQ ID NO: 229	Polypeptide encoded by SEQ ID NO: 228	30 aa
SEQ ID NO: 230	VIF segment 12	81 nts
SEQ ID NO: 231	Polypeptide encoded by SEQ ID NO: 230	27 aa
SEQ ID NO: 232	VPR segment 1	90 nts
SEQ ID NO: 233	Polypeptide encoded by SEQ ID NO: 232	30 aa
SEQ ID NO: 234	VPR segment 2	90 nts
SEQ ID NO: 235	Polypeptide encoded by SEQ ID NO: 234	30 aa
SEQ ID NO: 236	VPR segment 3	90 nts
SEQ ID NO: 237	Polypeptide encoded by SEQ ID NO: 236	30 aa
SEQ ID NO: 238	VPR segment 4	90 nts

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<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 239	Polypeptide encoded by SEQ ID NO: 238	30 aa
SEQ ID NO: 240	VPR segment 5	90 nts
SEQ ID NO: 241	Polypeptide encoded by SEQ ID NO: 240	30 aa
SEQ ID NO: 242	VPR segment 6	63 nts
SEQ ID NO: 243	Polypeptide encoded by SEQ ID NO: 242	21 aa
SEQ ID NO: 244	TAT segment 1	90 nts
SEQ ID NO: 245	Polypeptide encoded by SEQ ID NO: 244	30 aa
SEQ ID NO: 246	TAT segment 2	90 nts
SEQ ID NO: 247	Polypeptide encoded by SEQ ID NO: 246	30 aa
SEQ ID NO: 248	TAT segment 3	90 nts
SEQ ID NO: 249	Polypeptide encoded by SEQ ID NO: 248	30 aa
SEQ ID NO: 250	TAT segment 4	90 nts
SEQ ID NO: 251	Polypeptide encoded by SEQ ID NO: 250	30 aa
SEQ ID NO: 252	TAT segment 5	90 nts
SEQ ID NO: 253	Polypeptide encoded by SEQ ID NO: 252	30 aa
SEQ ID NO: 254	TAT segment 6	81 nts
SEQ ID NO: 255	Polypeptide encoded by SEQ ID NO: 254	27 aa
SEQ ID NO: 256	REV segment 1	90 nts
SEQ ID NO: 257	Polypeptide encoded by SEQ ID NO: 256	30 aa
SEQ ID NO: 258	REV segment 2	90 nts
SEQ ID NO: 259	Polypeptide encoded by SEQ ID NO: 258	30 aa
SEQ ID NO: 260	REV segment 3	90 nts
SEQ ID NO: 261	Polypeptide encoded by SEQ ID NO: 260	30 aa
SEQ ID NO: 262	REV segment 4	90 nts

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<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 263	Polypeptide encoded by SEQ ID NO: 262	30 aa
SEQ ID NO: 264	REV segment 5	90 nts
SEQ ID NO: 265	Polypeptide encoded by SEQ ID NO: 264	30 aa
SEQ ID NO: 266	REV segment 6	90 nts
SEQ ID NO: 267	Polypeptide encoded by SEQ ID NO: 266	30 aa
SEQ ID NO: 268	REV segment 7	90 nts
SEQ ID NO: 269	Polypeptide encoded by SEQ ID NO: 268	30 aa
SEQ ID NO: 270	REV segment 8	54 nts
SEQ ID NO: 271	Polypeptide encoded by SEQ ID NO: 270	18 aa
SEQ ID NO: 272	VPU segment 1	90 nts
SEQ ID NO: 273	Polypeptide encoded by SEQ ID NO: 272	30 aa
SEQ ID NO: 274	VPU segment 2	90 nts
SEQ ID NO: 275	Polypeptide encoded by SEQ ID NO: 274	30 aa
SEQ ID NO: 276	VPU segment 3	90 nts
SEQ ID NO: 277	Polypeptide encoded by SEQ ID NO: 276	30 aa
SEQ ID NO: 278	VPU segment 4	90 nts
SEQ ID NO: 279	Polypeptide encoded by SEQ ID NO: 278	30 aa
SEQ ID NO: 280	VPU segment 5	63 nts
SEQ ID NO: 281	Polypeptide encoded by SEQ ID NO: 280	21 aa
SEQ ID NO: 282	ENV segment 1	90 nts
SEQ ID NO: 283	Polypeptide encoded by SEQ ID NO: 282	30 aa
SEQ ID NO: 284	ENV segment 2	90 nts
SEQ ID NO: 285	Polypeptide encoded by SEQ ID NO: 284	30 aa
SEQ ID NO: 286	ENV segment 3	90 nts

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 287	Polypeptide encoded by SEQ ID NO: 286	30 aa
SEQ ID NO: 288	ENV segment 4	90 nts
SEQ ID NO: 289	Polypeptide encoded by SEQ ID NO: 288	30 aa
SEQ ID NO: 290	ENV segment 5	90 nts
SEQ ID NO: 291	Polypeptide encoded by SEQ ID NO: 290	30 aa
SEQ ID NO: 292	ENV segment 6	90 nts
SEQ ID NO: 293	Polypeptide encoded by SEQ ID NO: 292	30 aa
SEQ ID NO: 294	ENV segment 7	90 nts
SEQ ID NO: 295	Polypeptide encoded by SEQ ID NO: 294	30 aa
SEQ ID NO: 296	ENV segment 8	90 nts
SEQ ID NO: 297	Polypeptide encoded by SEQ ID NO: 296	30 aa
SEQ ID NO: 298	ENV segment 9	57 nts
SEQ ID NO: 299	Polypeptide encoded by SEQ ID NO: 298	19 aa
SEQ ID NO: 300	GAP A segment 1	90 nts
SEQ ID NO: 301	Polypeptide encoded by SEQ ID NO: 300	30 aa
SEQ ID NO: 302	GAP A segment 2	90 nts
SEQ ID NO: 303	Polypeptide encoded by SEQ ID NO: 302	30 aa
SEQ ID NO: 304	GAP A segment 3	90 nts
SEQ ID NO: 305	Polypeptide encoded by SEQ ID NO: 304	30 aa
SEQ ID NO: 306	GAP A segment 4	90 nts
SEQ ID NO: 307	Polypeptide encoded by SEQ ID NO: 306	30 aa
SEQ ID NO: 308	GAP A segment 5	90 nts
SEQ ID NO: 309	Polypeptide encoded by SEQ ID NO: 308	30 aa
SEQ ID NO: 310	GAP A segment 6	90 nts

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<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 311	Polypeptide encoded by SEQ ID NO: 310	30 aa
SEQ ID NO: 312	GAP A segment 7	75 nts
SEQ ID NO: 313	Polypeptide encoded by SEQ ID NO: 312	25 nts
SEQ ID NO: 314	GAP B segment 1	90 nts
SEQ ID NO: 315	Polypeptide encoded by SEQ ID NO: 314	30 aa
SEQ ID NO: 316	GAP B segment 2	90 nts
SEQ ID NO: 317	Polypeptide encoded by SEQ ID NO: 316	30 aa
SEQ ID NO: 318	GAP B segment 3	90 nts
SEQ ID NO: 319	Polypeptide encoded by SEQ ID NO: 318	30 aa
SEQ ID NO: 320	GAP B segment 4	90 nts
SEQ ID NO: 321	Polypeptide encoded by SEQ ID NO: 320	30 aa
SEQ ID NO: 322	GAP B segment 5	90 nts
SEQ ID NO: 323	Polypeptide encoded by SEQ ID NO: 322	30 aa
SEQ ID NO: 324	GAP B segment 6	90 nts
SEQ ID NO: 325	Polypeptide encoded by SEQ ID NO: 324	30 aa
SEQ ID NO: 326	GAP B segment 7	90 nts
SEQ ID NO: 327	Polypeptide encoded by SEQ ID NO: 326	30 aa
SEQ ID NO: 328	GAP B segment 8	90 nts
SEQ ID NO: 329	Polypeptide encoded by SEQ ID NO: 328	30 aa
SEQ ID NO: 330	GAP B segment 9	90 nts
SEQ ID NO: 331	Polypeptide encoded by SEQ ID NO: 330	30 aa
SEQ ID NO: 332	GAP B segment 10	90 nts
SEQ ID NO: 333	Polypeptide encoded by SEQ ID NO: 332	30 aa
SEQ ID NO: 334	GAP B segment 11	90 nts

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<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 335	Polypeptide encoded by SEQ ID NO: 334	30 aa
SEQ ID NO: 336	GAP B segment 12	90 nts
SEQ ID NO: 337	Polypeptide encoded by SEQ ID NO: 336	30 aa
SEQ ID NO: 338	GAP B segment 13	90 nts
SEQ ID NO: 339	Polypeptide encoded by SEQ ID NO: 338	30 aa
SEQ ID NO: 340	GAP B segment 14	90 nts
SEQ ID NO: 341	Polypeptide encoded by SEQ ID NO: 340	30 aa
SEQ ID NO: 342	GAP B segment 15	90 nts
SEQ ID NO: 343	Polypeptide encoded by SEQ ID NO: 342	30 aa
SEQ ID NO: 344	GAP B segment 16	90 nts
SEQ ID NO: 345	Polypeptide encoded by SEQ ID NO: 344	30 aa
SEQ ID NO: 346	GAP B segment 17	90 nts
SEQ ID NO: 347	Polypeptide encoded by SEQ ID NO: 346	30 aa
SEQ ID NO: 348	GAP B segment 18	90 nts
SEQ ID NO: 349	Polypeptide encoded by SEQ ID NO: 348	30 aa
SEQ ID NO: 350	GAP B segment 19	90 nts
SEQ ID NO: 351	Polypeptide encoded by SEQ ID NO: 350	30 aa
SEQ ID NO: 352	GAP B segment 20	90 nts
SEQ ID NO: 353	Polypeptide encoded by SEQ ID NO: 352	30 aa
SEQ ID NO: 354	GAP B segment 21	90 nts
SEQ ID NO: 355	Polypeptide encoded by SEQ ID NO: 354	30 aa
SEQ ID NO: 356	GAP B segment 22	90 nts
SEQ ID NO: 357	Polypeptide encoded by SEQ ID NO: 356	30 aa
SEQ ID NO: 358	GAP B segment 23	90 nts

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 359	Polypeptide encoded by SEQ ID NO: 358	30 aa
SEQ ID NO: 360	GAP B segment 24	90 nts
SEQ ID NO: 361	Polypeptide encoded by SEQ ID NO: 360	30 aa
SEQ ID NO: 362	GAP B segment 25	90 nts
SEQ ID NO: 363	Polypeptide encoded by SEQ ID NO: 362	30 aa
SEQ ID NO: 364	GAP B segment 26	66 nts
SEQ ID NO: 365	Polypeptide encoded by SEQ ID NO: 364	22 aa
SEQ ID NO: 366	NEF segment 1	90 nts
SEQ ID NO: 367	Polypeptide encoded by SEQ ID NO: 366	30 aa
SEQ ID NO: 368	NEF segment 2	90 nts
SEQ ID NO: 369	Polypeptide encoded by SEQ ID NO: 368	30 aa
SEQ ID NO: 370	NEF segment 3	90 nts
SEQ ID NO: 371	Polypeptide encoded by SEQ ID NO: 370	30 aa
SEQ ID NO: 372	NEF segment 4	90 nts
SEQ ID NO: 373	Polypeptide encoded by SEQ ID NO: 372	30 aa
SEQ ID NO: 374	NEF segment 5	90 nts
SEQ ID NO: 375	Polypeptide encoded by SEQ ID NO: 374	30 aa
SEQ ID NO: 376	NEF segment 6	90 nts
SEQ ID NO: 377	Polypeptide encoded by SEQ ID NO: 376	30 aa
SEQ ID NO: 378	NEF segment 7	90 nts
SEQ ID NO: 379	Polypeptide encoded by SEQ ID NO: 378	30 aa
SEQ ID NO: 380	NEF segment 8	90 nts
SEQ ID NO: 381	Polypeptide encoded by SEQ ID NO: 380	30 aa
SEQ ID NO: 382	NEF segment 9	90 nts

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 383	Polypeptide encoded by SEQ ID NO: 382	30 aa
SEQ ID NO: 384	NEF segment 10	90 nts
SEQ ID NO: 385	Polypeptide encoded by SEQ ID NO: 384	30 aa
SEQ ID NO: 386	NEF segment 11	90 nts
SEQ ID NO: 387	Polypeptide encoded by SEQ ID NO: 386	30 aa
SEQ ID NO: 388	NEF segment 12	90 nts
SEQ ID NO: 389	Polypeptide encoded by SEQ ID NO: 388	30 aa
SEQ ID NO: 390	NEF segment 13	78 nts
SEQ ID NO: 391	Polypeptide encoded by SEQ ID NO: 390	26 aa
SEQ ID NO: 392	HIV Cassette A1	5703 nts
SEQ ID NO: 393	Polypeptide encoded by SEQ ID NO: 392	1896 aa
SEQ ID NO: 394	HIV Cassette B1	5685 nts
SEQ ID NO: 395	Polypeptide encoded by SEQ ID NO: 394	1890 aa
SEQ ID NO: 396	HIV Cassette C1	5925 nts
SEQ ID NO: 397	Polypeptide encoded by SEQ ID NO: 396	1967 aa
SEQ ID NO: 398	HIV Cassette A2	5703 nts
SEQ ID NO: 399	Polypeptide encoded by SEQ ID NO: 398	1896 aa
SEQ ID NO: 400	HIV Cassette B2	5685 nts
SEQ ID NO: 401	Polypeptide encoded by SEQ ID NO: 400	1890 aa
SEQ ID NO: 402	HIV Cassette C2	5925 nts
SEQ ID NO: 403	Polypeptide encoded by SEQ ID NO: 402	1967 aa
SEQ ID NO: 404	HIV complete Savine	17244 nts
SEQ ID NO: 405	Polypeptide encoded by SEQ ID NO: 404	5747 aa
SEQ ID NO: 406	HepC1a consensus polyprotein sequence	3011 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 407	HepC1a segment 1	90 nts
SEQ ID NO: 408	Polypeptide encoded by SEQ ID NO: 407	30 aa
SEQ ID NO: 409	HepC1a segment 2	90 nts
SEQ ID NO: 410	Polypeptide encoded by SEQ ID NO: 409	30 aa
SEQ ID NO: 411	HepC1a segment 3	90 nts
SEQ ID NO: 412	Polypeptide encoded by SEQ ID NO: 411	30 aa
SEQ ID NO: 413	HepC1a segment 4	90 nts
SEQ ID NO: 414	Polypeptide encoded by SEQ ID NO: 413	30 aa
SEQ ID NO: 415	HepC1a segment 5	90 nts
SEQ ID NO: 416	Polypeptide encoded by SEQ ID NO: 415	30 aa
SEQ ID NO: 417	HepC1a segment 6	90 nts
SEQ ID NO: 418	Polypeptide encoded by SEQ ID NO: 417	30 aa
SEQ ID NO: 419	HepC1a segment 7	90 nts
SEQ ID NO: 420	Polypeptide encoded by SEQ ID NO: 419	30 aa
SEQ ID NO: 421	HepC1a segment 8	90 nts
SEQ ID NO: 422	Polypeptide encoded by SEQ ID NO: 421	30 aa
SEQ ID NO: 423	HepC1a segment 9	90 nts
SEQ ID NO: 424	Polypeptide encoded by SEQ ID NO: 423	30 aa
SEQ ID NO: 425	HepC1a segment 10	90 nts
SEQ ID NO: 426	Polypeptide encoded by SEQ ID NO: 425	30 aa
SEQ ID NO: 427	HepC1a segment 11	90 nts
SEQ ID NO: 428	Polypeptide encoded by SEQ ID NO: 427	30 aa
SEQ ID NO: 429	HepC1a segment 12	90 nts
SEQ ID NO: 430	Polypeptide encoded by SEQ ID NO: 429	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 431	HepC1a segment 13	90 nts
SEQ ID NO: 432	Polypeptide encoded by SEQ ID NO: 431	30 aa
SEQ ID NO: 433	HepC1a segment 14	90 nts
SEQ ID NO: 434	Polypeptide encoded by SEQ ID NO: 433	30 aa
SEQ ID NO: 435	HepC1a segment 15	90 nts
SEQ ID NO: 436	Polypeptide encoded by SEQ ID NO: 435	30 aa
SEQ ID NO: 437	HepC1a segment 16	90 nts
SEQ ID NO: 438	Polypeptide encoded by SEQ ID NO: 437	30 aa
SEQ ID NO: 439	HepC1a segment 17	90 nts
SEQ ID NO: 440	Polypeptide encoded by SEQ ID NO: 439	30 aa
SEQ ID NO: 441	HepC1a segment 18	90 nts
SEQ ID NO: 442	Polypeptide encoded by SEQ ID NO: 441	30 aa
SEQ ID NO: 443	HepC1a segment 19	90 nts
SEQ ID NO: 444	Polypeptide encoded by SEQ ID NO: 443	30 aa
SEQ ID NO: 445	HepC1a segment 20	90 nts
SEQ ID NO: 446	Polypeptide encoded by SEQ ID NO: 445	30 aa
SEQ ID NO: 447	HepC1a segment 21	90 nts
SEQ ID NO: 448	Polypeptide encoded by SEQ ID NO: 447	30 aa
SEQ ID NO: 449	HepC1a segment 22	90 nts
SEQ ID NO: 450	Polypeptide encoded by SEQ ID NO: 449	30 aa
SEQ ID NO: 451	HepC1a segment 23	90 nts
SEQ ID NO: 452	Polypeptide encoded by SEQ ID NO: 451	30 aa
SEQ ID NO: 453	HepC1a segment 24	90 nts
SEQ ID NO: 454	Polypeptide encoded by SEQ ID NO: 453	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 455	HepC1a segment 25	90 nts
SEQ ID NO: 456	Polypeptide encoded by SEQ ID NO: 455	30 aa
SEQ ID NO: 457	HepC1a segment 26	90 nts
SEQ ID NO: 458	Polypeptide encoded by SEQ ID NO: 457	30 aa
SEQ ID NO: 459	HepC1a segment 27	90 nts
SEQ ID NO: 460	Polypeptide encoded by SEQ ID NO: 459	30 aa
SEQ ID NO: 461	HepC1a segment 28	90 nts
SEQ ID NO: 462	Polypeptide encoded by SEQ ID NO: 461	30 aa
SEQ ID NO: 463	HepC1a segment 29	90 nts
SEQ ID NO: 464	Polypeptide encoded by SEQ ID NO: 463	30 aa
SEQ ID NO: 465	HepC1a segment 30	90 nts
SEQ ID NO: 466	Polypeptide encoded by SEQ ID NO: 465	30 aa
SEQ ID NO: 467	HepC1a segment 31	90 nts
SEQ ID NO: 468	Polypeptide encoded by SEQ ID NO: 467	30 aa
SEQ ID NO: 469	HepC1a segment 32	90 nts
SEQ ID NO: 470	Polypeptide encoded by SEQ ID NO: 469	30 aa
SEQ ID NO: 471	HepC1a segment 33	90 nts
SEQ ID NO: 472	Polypeptide encoded by SEQ ID NO: 471	30 aa
SEQ ID NO: 473	HepC1a segment 34	90 nts
SEQ ID NO: 474	Polypeptide encoded by SEQ ID NO: 473	30 aa
SEQ ID NO: 475	HepC1a segment 35	90 nts
SEQ ID NO: 476	Polypeptide encoded by SEQ ID NO: 475	30 aa
SEQ ID NO: 477	HepC1a segment 36	90 nts
SEQ ID NO: 478	Polypeptide encoded by SEQ ID NO: 477	30 aa

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<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 479	HepC1a segment 37	90 nts
SEQ ID NO: 480	Polypeptide encoded by SEQ ID NO: 479	30 aa
SEQ ID NO: 481	HepC1a segment 38	90 nts
SEQ ID NO: 482	Polypeptide encoded by SEQ ID NO: 481	30 aa
SEQ ID NO: 483	HepC1a segment 39	90 nts
SEQ ID NO: 484	Polypeptide encoded by SEQ ID NO: 483	30 aa
SEQ ID NO: 485	HepC1a segment 40	90 nts
SEQ ID NO: 486	Polypeptide encoded by SEQ ID NO: 485	30 aa
SEQ ID NO: 487	HepC1a segment 41	90 nts
SEQ ID NO: 488	Polypeptide encoded by SEQ ID NO: 487	30 aa
SEQ ID NO: 489	HepC1a segment 42	90 nts
SEQ ID NO: 490	Polypeptide encoded by SEQ ID NO: 489	30 aa
SEQ ID NO: 491	HepC1a segment 43	90 nts
SEQ ID NO: 492	Polypeptide encoded by SEQ ID NO: 491	30 aa
SEQ ID NO: 493	HepC1a segment 44	90 nts
SEQ ID NO: 494	Polypeptide encoded by SEQ ID NO: 493	30 aa
SEQ ID NO: 495	HepC1a segment 45	90 nts
SEQ ID NO: 496	Polypeptide encoded by SEQ ID NO: 495	30 aa
SEQ ID NO: 497	HepC1a segment 46	90 nts
SEQ ID NO: 498	Polypeptide encoded by SEQ ID NO: 497	30 aa
SEQ ID NO: 499	HepC1a segment 47	90 nts
SEQ ID NO: 500	Polypeptide encoded by SEQ ID NO: 499	30 aa
SEQ ID NO: 501	HepC1a segment 48	90 nts
SEQ ID NO: 502	Polypeptide encoded by SEQ ID NO: 501	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 503	HepC1a segment 49	90 nts
SEQ ID NO: 504	Polypeptide encoded by SEQ ID NO: 503	30 aa
SEQ ID NO: 505	HepC1a segment 50	90 nts
SEQ ID NO: 506	Polypeptide encoded by SEQ ID NO: 505	30 aa
SEQ ID NO: 507	HepC1a segment 51	90 nts
SEQ ID NO: 508	Polypeptide encoded by SEQ ID NO: 507	30 aa
SEQ ID NO: 509	HepC1a segment 52	90 nts
SEQ ID NO: 510	Polypeptide encoded by SEQ ID NO: 509	30 aa
SEQ ID NO: 511	HepC1a segment 53	90 nts
SEQ ID NO: 512	Polypeptide encoded by SEQ ID NO: 511	30 aa
SEQ ID NO: 513	HepC1a segment 54	90 nts
SEQ ID NO: 514	Polypeptide encoded by SEQ ID NO: 513	30 aa
SEQ ID NO: 515	HepC1a segment 55	90 nts
SEQ ID NO: 516	Polypeptide encoded by SEQ ID NO: 515	30 aa
SEQ ID NO: 517	HepC1a segment 56	90 nts
SEQ ID NO: 518	Polypeptide encoded by SEQ ID NO: 517	30 aa
SEQ ID NO: 519	HepC1a segment 57	90 nts
SEQ ID NO: 520	Polypeptide encoded by SEQ ID NO: 519	30 aa
SEQ ID NO: 521	HepC1a segment 58	90 nts
SEQ ID NO: 522	Polypeptide encoded by SEQ ID NO: 521	30 aa
SEQ ID NO: 523	HepC1a segment 59	90 nts
SEQ ID NO: 524	Polypeptide encoded by SEQ ID NO: 523	30 aa
SEQ ID NO: 525	HepC1a segment 60	90 nts
SEQ ID NO: 526	Polypeptide encoded by SEQ ID NO: 525	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 527	HepC1a segment 61	90 nts
SEQ ID NO: 528	Polypeptide encoded by SEQ ID NO: 527	30 aa
SEQ ID NO: 529	HepC1a segment 62	90 nts
SEQ ID NO: 530	Polypeptide encoded by SEQ ID NO: 529	30 aa
SEQ ID NO: 531	HepC1a segment 63	90 nts
SEQ ID NO: 532	Polypeptide encoded by SEQ ID NO: 531	30 aa
SEQ ID NO: 533	HepC1a segment 64	90 nts
SEQ ID NO: 534	Polypeptide encoded by SEQ ID NO: 533	30 aa
SEQ ID NO: 535	HepC1a segment 65	90 nts
SEQ ID NO: 536	Polypeptide encoded by SEQ ID NO: 535	30 aa
SEQ ID NO: 537	HepC1a segment 66	90 nts
SEQ ID NO: 538	Polypeptide encoded by SEQ ID NO: 537	30 aa
SEQ ID NO: 539	HepC1a segment 67	90 nts
SEQ ID NO: 540	Polypeptide encoded by SEQ ID NO: 539	30 aa
SEQ ID NO: 541	HepC1a segment 68	90 nts
SEQ ID NO: 542	Polypeptide encoded by SEQ ID NO: 541	30 aa
SEQ ID NO: 543	HepC1a segment 69	90 nts
SEQ ID NO: 544	Polypeptide encoded by SEQ ID NO: 543	30 aa
SEQ ID NO: 545	HepC1a segment 70	90 nts
SEQ ID NO: 546	Polypeptide encoded by SEQ ID NO: 545	30 aa
SEQ ID NO: 547	HepC1a segment 71	90 nts
SEQ ID NO: 548	Polypeptide encoded by SEQ ID NO: 547	30 aa
SEQ ID NO: 549	HepC1a segment 72	90 nts
SEQ ID NO: 550	Polypeptide encoded by SEQ ID NO: 549	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 551	HepC1a segment 73	90 nts
SEQ ID NO: 552	Polypeptide encoded by SEQ ID NO: 551	30 aa
SEQ ID NO: 553	HepC1a segment 74	90 nts
SEQ ID NO: 554	Polypeptide encoded by SEQ ID NO: 553	30 aa
SEQ ID NO: 555	HepC1a segment 75	90 nts
SEQ ID NO: 556	Polypeptide encoded by SEQ ID NO: 555	30 aa
SEQ ID NO: 557	HepC1a segment 76	90 nts
SEQ ID NO: 558	Polypeptide encoded by SEQ ID NO: 557	30 aa
SEQ ID NO: 559	HepC1a segment 77	90 nts
SEQ ID NO: 560	Polypeptide encoded by SEQ ID NO: 559	30 aa
SEQ ID NO: 561	HepC1a segment 78	90 nts
SEQ ID NO: 562	Polypeptide encoded by SEQ ID NO: 561	30 aa
SEQ ID NO: 563	HepC1a segment 79	90 nts
SEQ ID NO: 564	Polypeptide encoded by SEQ ID NO: 563	30 aa
SEQ ID NO: 565	HepC1a segment 80	90 nts
SEQ ID NO: 566	Polypeptide encoded by SEQ ID NO: 565	30 aa
SEQ ID NO: 567	HepC1a segment 81	90 nts
SEQ ID NO: 568	Polypeptide encoded by SEQ ID NO: 567	30 aa
SEQ ID NO: 569	HepC1a segment 82	90 nts
SEQ ID NO: 570	Polypeptide encoded by SEQ ID NO: 569	30 aa
SEQ ID NO: 571	HepC1a segment 83	90 nts
SEQ ID NO: 572	Polypeptide encoded by SEQ ID NO: 571	30 aa
SEQ ID NO: 573	HepC1a segment 84	90 nts
SEQ ID NO: 574	Polypeptide encoded by SEQ ID NO: 573	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 575	HepC1a segment 85	90 nts
SEQ ID NO: 576	Polypeptide encoded by SEQ ID NO: 575	30 aa
SEQ ID NO: 577	HepC1a segment 86	90 nts
SEQ ID NO: 578	Polypeptide encoded by SEQ ID NO: 577	30 aa
SEQ ID NO: 579	HepC1a segment 87	90 nts
SEQ ID NO: 580	Polypeptide encoded by SEQ ID NO: 579	30 aa
SEQ ID NO: 581	HepC1a segment 88	90 nts
SEQ ID NO: 582	Polypeptide encoded by SEQ ID NO: 581	30 aa
SEQ ID NO: 583	HepC1a segment 89	90 nts
SEQ ID NO: 584	Polypeptide encoded by SEQ ID NO: 583	30 aa
SEQ ID NO: 585	HepC1a segment 90	90 nts
SEQ ID NO: 586	Polypeptide encoded by SEQ ID NO: 585	30 aa
SEQ ID NO: 587	HepC1a segment 91	90 nts
SEQ ID NO: 588	Polypeptide encoded by SEQ ID NO: 587	30 aa
SEQ ID NO: 589	HepC1a segment 92	90 nts
SEQ ID NO: 590	Polypeptide encoded by SEQ ID NO: 589	30 aa
SEQ ID NO: 591	HepC1a segment 93	90 nts
SEQ ID NO: 592	Polypeptide encoded by SEQ ID NO: 591	30 aa
SEQ ID NO: 593	HepC1a segment 94	90 nts
SEQ ID NO: 594	Polypeptide encoded by SEQ ID NO: 593	30 aa
SEQ ID NO: 595	HepC1a segment 95	90 nts
SEQ ID NO: 596	Polypeptide encoded by SEQ ID NO: 595	30 aa
SEQ ID NO: 597	HepC1a segment 96	90 nts
SEQ ID NO: 598	Polypeptide encoded by SEQ ID NO: 597	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 599	HepC1a segment 97	90 nts
SEQ ID NO: 600	Polypeptide encoded by SEQ ID NO: 599	30 aa
SEQ ID NO: 601	HepC1a segment 98	90 nts
SEQ ID NO: 602	Polypeptide encoded by SEQ ID NO: 601	30 aa
SEQ ID NO: 603	HepC1a segment 99	90 nts
SEQ ID NO: 604	Polypeptide encoded by SEQ ID NO: 603	30 aa
SEQ ID NO: 605	HepC1a segment 100	90 nts
SEQ ID NO: 606	Polypeptide encoded by SEQ ID NO: 605	30 aa
SEQ ID NO: 607	HepC1a segment 101	90 nts
SEQ ID NO: 608	Polypeptide encoded by SEQ ID NO: 607	30 aa
SEQ ID NO: 609	HepC1a segment 102	90 nts
SEQ ID NO: 610	Polypeptide encoded by SEQ ID NO: 609	30 aa
SEQ ID NO: 611	HepC1a segment 103	90 nts
SEQ ID NO: 612	Polypeptide encoded by SEQ ID NO: 611	30 aa
SEQ ID NO: 613	HepC1a segment 104	90 nts
SEQ ID NO: 614	Polypeptide encoded by SEQ ID NO: 613	30 aa
SEQ ID NO: 615	HepC1a segment 105	90 nts
SEQ ID NO: 616	Polypeptide encoded by SEQ ID NO: 615	30 aa
SEQ ID NO: 617	HepC1a segment 106	90 nts
SEQ ID NO: 618	Polypeptide encoded by SEQ ID NO: 617	30 aa
SEQ ID NO: 619	HepC1a segment 107	90 nts
SEQ ID NO: 620	Polypeptide encoded by SEQ ID NO: 619	30 aa
SEQ ID NO: 621	HepC1a segment 108	90 nts
SEQ ID NO: 622	Polypeptide encoded by SEQ ID NO: 621	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 623	HepC1a segment 109	90 nts
SEQ ID NO: 624	Polypeptide encoded by SEQ ID NO: 623	30 aa
SEQ ID NO: 625	HepC1a segment 110	90 nts
SEQ ID NO: 626	Polypeptide encoded by SEQ ID NO: 625	30 aa
SEQ ID NO: 627	HepC1a segment 111	90 nts
SEQ ID NO: 628	Polypeptide encoded by SEQ ID NO: 627	30 aa
SEQ ID NO: 629	HepC1a segment 112	90 nts
SEQ ID NO: 630	Polypeptide encoded by SEQ ID NO: 629	30 aa
SEQ ID NO: 631	HepC1a segment 113	90 nts
SEQ ID NO: 632	Polypeptide encoded by SEQ ID NO: 631	30 aa
SEQ ID NO: 633	HepC1a segment 114	90 nts
SEQ ID NO: 634	Polypeptide encoded by SEQ ID NO: 633	30 aa
SEQ ID NO: 635	HepC1a segment 115	90 nts
SEQ ID NO: 636	Polypeptide encoded by SEQ ID NO: 635	30 aa
SEQ ID NO: 637	HepC1a segment 116	90 nts
SEQ ID NO: 638	Polypeptide encoded by SEQ ID NO: 637	30 aa
SEQ ID NO: 639	HepC1a segment 117	90 nts
SEQ ID NO: 640	Polypeptide encoded by SEQ ID NO: 639	30 aa
SEQ ID NO: 641	HepC1a segment 118	90 nts
SEQ ID NO: 642	Polypeptide encoded by SEQ ID NO: 641	30 aa
SEQ ID NO: 643	HepC1a segment 119	90 nts
SEQ ID NO: 644	Polypeptide encoded by SEQ ID NO: 643	30 aa
SEQ ID NO: 645	HepC1a segment 120	90 nts
SEQ ID NO: 646	Polypeptide encoded by SEQ ID NO: 645	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 647	HepC1a segment 121	90 nts
SEQ ID NO: 648	Polypeptide encoded by SEQ ID NO: 647	30 aa
SEQ ID NO: 649	HepC1a segment 122	90 nts
SEQ ID NO: 650	Polypeptide encoded by SEQ ID NO: 649	30 aa
SEQ ID NO: 651	HepC1a segment 123	90 nts
SEQ ID NO: 652	Polypeptide encoded by SEQ ID NO: 651	30 aa
SEQ ID NO: 653	HepC1a segment 124	90 nts
SEQ ID NO: 654	Polypeptide encoded by SEQ ID NO: 653	30 aa
SEQ ID NO: 655	HepC1a segment 125	90 nts
SEQ ID NO: 656	Polypeptide encoded by SEQ ID NO: 655	30 aa
SEQ ID NO: 657	HepC1a segment 126	90 nts
SEQ ID NO: 658	Polypeptide encoded by SEQ ID NO: 657	30 aa
SEQ ID NO: 659	HepC1a segment 127	90 nts
SEQ ID NO: 660	Polypeptide encoded by SEQ ID NO: 659	30 aa
SEQ ID NO: 661	HepC1a segment 128	90 nts
SEQ ID NO: 662	Polypeptide encoded by SEQ ID NO: 661	30 aa
SEQ ID NO: 663	HepC1a segment 129	90 nts
SEQ ID NO: 664	Polypeptide encoded by SEQ ID NO: 663	30 aa
SEQ ID NO: 665	HepC1a segment 130	90 nts
SEQ ID NO: 666	Polypeptide encoded by SEQ ID NO: 665	30 aa
SEQ ID NO: 667	HepC1a segment 131	90 nts
SEQ ID NO: 668	Polypeptide encoded by SEQ ID NO: 667	30 aa
SEQ ID NO: 669	HepC1a segment 132	90 nts
SEQ ID NO: 670	Polypeptide encoded by SEQ ID NO: 669	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 671	HepC1a segment 133	90 nts
SEQ ID NO: 672	Polypeptide encoded by SEQ ID NO: 671	30 aa
SEQ ID NO: 673	HepC1a segment 134	90 nts
SEQ ID NO: 674	Polypeptide encoded by SEQ ID NO: 673	30 aa
SEQ ID NO: 675	HepC1a segment 135	90 nts
SEQ ID NO: 676	Polypeptide encoded by SEQ ID NO: 675	30 aa
SEQ ID NO: 677	HepC1a segment 136	90 nts
SEQ ID NO: 678	Polypeptide encoded by SEQ ID NO: 677	30 aa
SEQ ID NO: 679	HepC1a segment 137	90 nts
SEQ ID NO: 680	Polypeptide encoded by SEQ ID NO: 679	30 aa
SEQ ID NO: 681	HepC1a segment 138	90 nts
SEQ ID NO: 682	Polypeptide encoded by SEQ ID NO: 681	30 aa
SEQ ID NO: 683	HepC1a segment 139	90 nts
SEQ ID NO: 684	Polypeptide encoded by SEQ ID NO: 683	30 aa
SEQ ID NO: 685	HepC1a segment 140	90 nts
SEQ ID NO: 686	Polypeptide encoded by SEQ ID NO: 685	30 aa
SEQ ID NO: 687	HepC1a segment 141	90 nts
SEQ ID NO: 688	Polypeptide encoded by SEQ ID NO: 687	30 aa
SEQ ID NO: 689	HepC1a segment 142	90 nts
SEQ ID NO: 690	Polypeptide encoded by SEQ ID NO: 689	30 aa
SEQ ID NO: 691	HepC1a segment 143	90 nts
SEQ ID NO: 692	Polypeptide encoded by SEQ ID NO: 691	30 aa
SEQ ID NO: 693	HepC1a segment 144	90 nts
SEQ ID NO: 694	Polypeptide encoded by SEQ ID NO: 693	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 695	HepC1a segment 145	90 nts
SEQ ID NO: 696	Polypeptide encoded by SEQ ID NO: 695	30 aa
SEQ ID NO: 697	HepC1a segment 146	90 nts
SEQ ID NO: 698	Polypeptide encoded by SEQ ID NO: 697	30 aa
SEQ ID NO: 699	HepC1a segment 147	90 nts
SEQ ID NO: 700	Polypeptide encoded by SEQ ID NO: 699	30 aa
SEQ ID NO: 701	HepC1a segment 148	90 nts
SEQ ID NO: 702	Polypeptide encoded by SEQ ID NO: 701	30 aa
SEQ ID NO: 703	HepC1a segment 149	90 nts
SEQ ID NO: 704	Polypeptide encoded by SEQ ID NO: 703	30 aa
SEQ ID NO: 705	HepC1a segment 150	90 nts
SEQ ID NO: 706	Polypeptide encoded by SEQ ID NO: 705	30 aa
SEQ ID NO: 707	HepC1a segment 151	90 nts
SEQ ID NO: 708	Polypeptide encoded by SEQ ID NO: 707	30 aa
SEQ ID NO: 709	HepC1a segment 152	90 nts
SEQ ID NO: 710	Polypeptide encoded by SEQ ID NO: 709	30 aa
SEQ ID NO: 711	HepC1a segment 153	90 nts
SEQ ID NO: 712	Polypeptide encoded by SEQ ID NO: 711	30 aa
SEQ ID NO: 713	HepC1a segment 154	90 nts
SEQ ID NO: 714	Polypeptide encoded by SEQ ID NO: 713	30 aa
SEQ ID NO: 715	HepC1a segment 155	90 nts
SEQ ID NO: 716	Polypeptide encoded by SEQ ID NO: 715	30 aa
SEQ ID NO: 717	HepC1a segment 156	90 nts
SEQ ID NO: 718	Polypeptide encoded by SEQ ID NO: 717	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 719	HepC1a segment 157	90 nts
SEQ ID NO: 720	Polypeptide encoded by SEQ ID NO: 719	30 aa
SEQ ID NO: 721	HepC1a segment 158	90 nts
SEQ ID NO: 722	Polypeptide encoded by SEQ ID NO: 721	30 aa
SEQ ID NO: 723	HepC1a segment 159	90 nts
SEQ ID NO: 724	Polypeptide encoded by SEQ ID NO: 723	30 aa
SEQ ID NO: 725	HepC1a segment 160	90 nts
SEQ ID NO: 726	Polypeptide encoded by SEQ ID NO: 725	30 aa
SEQ ID NO: 727	HepC1a segment 161	90 nts
SEQ ID NO: 728	Polypeptide encoded by SEQ ID NO: 727	30 aa
SEQ ID NO: 729	HepC1a segment 162	90 nts
SEQ ID NO: 730	Polypeptide encoded by SEQ ID NO: 729	30 aa
SEQ ID NO: 731	HepC1a segment 163	90 nts
SEQ ID NO: 732	Polypeptide encoded by SEQ ID NO: 731	30 aa
SEQ ID NO: 733	HepC1a segment 164	90 nts
SEQ ID NO: 734	Polypeptide encoded by SEQ ID NO: 733	30 aa
SEQ ID NO: 735	HepC1a segment 165	90 nts
SEQ ID NO: 736	Polypeptide encoded by SEQ ID NO: 735	30 aa
SEQ ID NO: 737	HepC1a segment 166	90 nts
SEQ ID NO: 738	Polypeptide encoded by SEQ ID NO: 737	30 aa
SEQ ID NO: 739	HepC1a segment 167	90 nts
SEQ ID NO: 740	Polypeptide encoded by SEQ ID NO: 739	30 aa
SEQ ID NO: 741	HepC1a segment 168	90 nts
SEQ ID NO: 742	Polypeptide encoded by SEQ ID NO: 741	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 743	HepC1a segment 169	90 nts
SEQ ID NO: 744	Polypeptide encoded by SEQ ID NO: 743	30 aa
SEQ ID NO: 745	HepC1a segment 170	90 nts
SEQ ID NO: 746	Polypeptide encoded by SEQ ID NO: 745	30 aa
SEQ ID NO: 747	HepC1a segment 171	90 nts
SEQ ID NO: 748	Polypeptide encoded by SEQ ID NO: 747	30 aa
SEQ ID NO: 749	HepC1a segment 172	90 nts
SEQ ID NO: 750	Polypeptide encoded by SEQ ID NO: 749	30 aa
SEQ ID NO: 751	HepC1a segment 173	90 nts
SEQ ID NO: 752	Polypeptide encoded by SEQ ID NO: 751	30 aa
SEQ ID NO: 753	HepC1a segment 174	90 nts
SEQ ID NO: 754	Polypeptide encoded by SEQ ID NO: 753	30 aa
SEQ ID NO: 755	HepC1a segment 175	90 nts
SEQ ID NO: 756	Polypeptide encoded by SEQ ID NO: 755	30 aa
SEQ ID NO: 757	HepC1a segment 176	90 nts
SEQ ID NO: 758	Polypeptide encoded by SEQ ID NO: 757	30 aa
SEQ ID NO: 759	HepC1a segment 177	90 nts
SEQ ID NO: 760	Polypeptide encoded by SEQ ID NO: 759	30 aa
SEQ ID NO: 761	HepC1a segment 178	90 nts
SEQ ID NO: 762	Polypeptide encoded by SEQ ID NO: 761	30 aa
SEQ ID NO: 763	HepC1a segment 179	90 nts
SEQ ID NO: 764	Polypeptide encoded by SEQ ID NO: 763	30 aa
SEQ ID NO: 765	HepC1a segment 180	90 nts
SEQ ID NO: 766	Polypeptide encoded by SEQ ID NO: 765	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 767	HepC1a segment 181	90 nts
SEQ ID NO: 768	Polypeptide encoded by SEQ ID NO: 767	30 aa
SEQ ID NO: 769	HepC1a segment 182	90 nts
SEQ ID NO: 770	Polypeptide encoded by SEQ ID NO: 769	30 aa
SEQ ID NO: 771	HepC1a segment 183	90 nts
SEQ ID NO: 772	Polypeptide encoded by SEQ ID NO: 771	30 aa
SEQ ID NO: 773	HepC1a segment 184	90 nts
SEQ ID NO: 774	Polypeptide encoded by SEQ ID NO: 773	30 aa
SEQ ID NO: 775	HepC1a segment 185	90 nts
SEQ ID NO: 776	Polypeptide encoded by SEQ ID NO: 775	30 aa
SEQ ID NO: 777	HepC1a segment 186	90 nts
SEQ ID NO: 778	Polypeptide encoded by SEQ ID NO: 777	30 aa
SEQ ID NO: 779	HepC1a segment 187	90 nts
SEQ ID NO: 780	Polypeptide encoded by SEQ ID NO: 779	30 aa
SEQ ID NO: 781	HepC1a segment 188	90 nts
SEQ ID NO: 782	Polypeptide encoded by SEQ ID NO: 781	30 aa
SEQ ID NO: 783	HepC1a segment 189	90 nts
SEQ ID NO: 784	Polypeptide encoded by SEQ ID NO: 783	30 aa
SEQ ID NO: 785	HepC1a segment 190	90 nts
SEQ ID NO: 786	Polypeptide encoded by SEQ ID NO: 785	30 aa
SEQ ID NO: 787	HepC1a segment 191	90 nts
SEQ ID NO: 788	Polypeptide encoded by SEQ ID NO: 787	30 aa
SEQ ID NO: 789	HepC1a segment 192	90 nts
SEQ ID NO: 790	Polypeptide encoded by SEQ ID NO: 789	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 791	HepC1a segment 193	90 nts
SEQ ID NO: 792	Polypeptide encoded by SEQ ID NO: 791	30 aa
SEQ ID NO: 793	HepC1a segment 194	90 nts
SEQ ID NO: 794	Polypeptide encoded by SEQ ID NO: 793	30 aa
SEQ ID NO: 795	HepC1a segment 195	90 nts
SEQ ID NO: 796	Polypeptide encoded by SEQ ID NO: 795	30 aa
SEQ ID NO: 797	HepC1a segment 196	90 nts
SEQ ID NO: 798	Polypeptide encoded by SEQ ID NO: 797	30 aa
SEQ ID NO: 799	HepC1a segment 197	90 nts
SEQ ID NO: 800	Polypeptide encoded by SEQ ID NO: 799	30 aa
SEQ ID NO: 801	HepC1a segment 198	90 nts
SEQ ID NO: 802	Polypeptide encoded by SEQ ID NO: 801	30 aa
SEQ ID NO: 803	HepC1a segment 199	90 nts
SEQ ID NO: 804	Polypeptide encoded by SEQ ID NO: 803	30 aa
SEQ ID NO: 805	HepC1a segment 200	90 nts
SEQ ID NO: 806	Polypeptide encoded by SEQ ID NO: 805	30 aa
SEQ ID NO: 807	HepC1a segment 201	45 nts
SEQ ID NO: 808	Polypeptide encoded by SEQ ID NO: 807	15 aa
SEQ ID NO: 809	HepC1a scrambled	17955 nts
SEQ ID NO: 810	Polypeptide encoded by SEQ ID NO: 809	5985 aa
SEQ ID NO: 811	HepC Cassette A	6065 nts
SEQ ID NO: 812	Polypeptide encoded by SEQ ID NO: 811	2011 aa
SEQ ID NO: 813	HepC Cassette B	6069 nts
SEQ ID NO: 814	Polypeptide encoded by SEQ ID NO: 813	2010 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 815	HepC Cassette C	6030 nts
SEQ ID NO: 816	Polypeptide encoded by SEQ ID NO: 815	1997 aa
SEQ ID NO: 817	gp100 consensus polypeptide	661 aa
SEQ ID NO: 818	MART consensus polypeptide	118 aa
SEQ ID NO: 819	TRP-1 consensus polypeptide	248 aa
SEQ ID NO: 820	Tyros consensus polypeptide	529 aa
SEQ ID NO: 821	TRP2 consensus polypeptide	519 aa
SEQ ID NO: 822	MC1R consensus polypeptide	317 aa
SEQ ID NO: 823	MUC1F consensus polypeptide	125 aa
SEQ ID NO: 824	MUC1R consensus polypeptide	312 aa
SEQ ID NO: 825	BAGE consensus polypeptide	43 aa
SEQ ID NO: 826	GAGE-1 consensus polypeptide	138 aa
SEQ ID NO: 827	gp100ln4 consensus polypeptide	51 aa
SEQ ID NO: 828	MAGE-1 consensus polypeptide	309 aa
SEQ ID NO: 829	MAGE-3 consensus polypeptide	314 aa
SEQ ID NO: 830	PRAME consensus polypeptide	509 aa
SEQ ID NO: 831	TRP2IN2 consensus polypeptide	54 aa
SEQ ID NO: 832	NYNSO1a consensus polypeptide	180 aa
SEQ ID NO: 833	NYNSO1b consensus polypeptide	58 aa
SEQ ID NO: 834	LAGE1 consensus polypeptide	180 aa
SEQ ID NO: 835	gp100 segment 1	90 nts
SEQ ID NO: 836	Polypeptide encoded by SEQ ID NO: 835	30 aa
SEQ ID NO: 837	gp100 segment 2	90 nts
SEQ ID NO: 838	Polypeptide encoded by SEQ ID NO: 837	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 839	gp100 segment 3	90 nts
SEQ ID NO: 840	Polypeptide encoded by SEQ ID NO: 839	30 aa
SEQ ID NO: 841	gp100 segment 4	90 nts
SEQ ID NO: 842	Polypeptide encoded by SEQ ID NO: 841	30 aa
SEQ ID NO: 843	gp100 segment 5	90 nts
SEQ ID NO: 844	Polypeptide encoded by SEQ ID NO: 843	30 aa
SEQ ID NO: 845	gp100 segment 6	90 nts
SEQ ID NO: 846	Polypeptide encoded by SEQ ID NO: 845	30 aa
SEQ ID NO: 847	gp100 segment 7	90 nts
SEQ ID NO: 848	Polypeptide encoded by SEQ ID NO: 847	30 aa
SEQ ID NO: 849	gp100 segment 8	90 nts
SEQ ID NO: 850	Polypeptide encoded by SEQ ID NO: 849	30 aa
SEQ ID NO: 851	gp100 segment 9	90 nts
SEQ ID NO: 852	Polypeptide encoded by SEQ ID NO: 851	30 aa
SEQ ID NO: 853	gp100 segment 10	90 nts
SEQ ID NO: 854	Polypeptide encoded by SEQ ID NO: 853	30 aa
SEQ ID NO: 855	gp100 segment 11	90 nts
SEQ ID NO: 856	Polypeptide encoded by SEQ ID NO: 855	30 aa
SEQ ID NO: 857	gp100 segment 12	90 nts
SEQ ID NO: 858	Polypeptide encoded by SEQ ID NO: 857	30 aa
SEQ ID NO: 859	gp100 segment 13	90 nts
SEQ ID NO: 860	Polypeptide encoded by SEQ ID NO: 859	30 aa
SEQ ID NO: 861	gp100 segment 14	90 nts
SEQ ID NO: 862	Polypeptide encoded by SEQ ID NO: 861	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 863	gp100 segment 15	90 nts
SEQ ID NO: 864	Polypeptide encoded by SEQ ID NO: 863	30 aa
SEQ ID NO: 865	gp100 segment 16	90 nts
SEQ ID NO: 866	Polypeptide encoded by SEQ ID NO: 865	30 aa
SEQ ID NO: 867	gp100 segment 17	90 nts
SEQ ID NO: 868	Polypeptide encoded by SEQ ID NO: 867	30 aa
SEQ ID NO: 869	gp100 segment 18	90 nts
SEQ ID NO: 870	Polypeptide encoded by SEQ ID NO: 869	30 aa
SEQ ID NO: 871	gp100 segment 19	90 nts
SEQ ID NO: 872	Polypeptide encoded by SEQ ID NO: 871	30 aa
SEQ ID NO: 873	gp100 segment 20	90 nts
SEQ ID NO: 874	Polypeptide encoded by SEQ ID NO: 873	30 aa
SEQ ID NO: 875	gp100 segment 21	90 nts
SEQ ID NO: 876	Polypeptide encoded by SEQ ID NO: 875	30 aa
SEQ ID NO: 877	gp100 segment 22	90 nts
SEQ ID NO: 878	Polypeptide encoded by SEQ ID NO: 877	30 aa
SEQ ID NO: 879	gp100 segment 23	90 nts
SEQ ID NO: 880	Polypeptide encoded by SEQ ID NO: 879	30 aa
SEQ ID NO: 881	gp100 segment 24	90 nts
SEQ ID NO: 882	Polypeptide encoded by SEQ ID NO: 881	30 aa
SEQ ID NO: 883	gp100 segment 25	90 nts
SEQ ID NO: 884	Polypeptide encoded by SEQ ID NO: 883	30 aa
SEQ ID NO: 885	gp100 segment 26	90 nts
SEQ ID NO: 886	Polypeptide encoded by SEQ ID NO: 885	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 887	gp100 segment 27	90 nts
SEQ ID NO: 888	Polypeptide encoded by SEQ ID NO: 887	30 aa
SEQ ID NO: 889	gp100 segment 28	90 nts
SEQ ID NO: 890	Polypeptide encoded by SEQ ID NO: 889	30 aa
SEQ ID NO: 891	gp100 segment 29	90 nts
SEQ ID NO: 892	Polypeptide encoded by SEQ ID NO: 891	30 aa
SEQ ID NO: 893	gp100 segment 30	90 nts
SEQ ID NO: 894	Polypeptide encoded by SEQ ID NO: 893	30 aa
SEQ ID NO: 895	gp100 segment 31	90 nts
SEQ ID NO: 896	Polypeptide encoded by SEQ ID NO: 895	30 aa
SEQ ID NO: 897	gp100 segment 32	90 nts
SEQ ID NO: 898	Polypeptide encoded by SEQ ID NO: 897	30 aa
SEQ ID NO: 899	gp100 segment 33	90 nts
SEQ ID NO: 900	Polypeptide encoded by SEQ ID NO: 899	30 aa
SEQ ID NO: 901	gp100 segment 34	90 nts
SEQ ID NO: 902	Polypeptide encoded by SEQ ID NO: 901	30 aa
SEQ ID NO: 903	gp100 segment 35	90 nts
SEQ ID NO: 904	Polypeptide encoded by SEQ ID NO: 903	30 aa
SEQ ID NO: 905	gp100 segment 36	90 nts
SEQ ID NO: 906	Polypeptide encoded by SEQ ID NO: 905	30 aa
SEQ ID NO: 907	gp100 segment 37	90 nts
SEQ ID NO: 908	Polypeptide encoded by SEQ ID NO: 907	30 aa
SEQ ID NO: 909	gp100 segment 38	90 nts
SEQ ID NO: 910	Polypeptide encoded by SEQ ID NO: 909	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 911	gp100 segment 39	90 nts
SEQ ID NO: 912	Polypeptide encoded by SEQ ID NO: 911	30 aa
SEQ ID NO: 913	gp100 segment 40	90 nts
SEQ ID NO: 914	Polypeptide encoded by SEQ ID NO: 913	30 aa
SEQ ID NO: 915	gp100 segment 41	90 nts
SEQ ID NO: 916	Polypeptide encoded by SEQ ID NO: 915	30 aa
SEQ ID NO: 917	gp100 segment 42	90 nts
SEQ ID NO: 918	Polypeptide encoded by SEQ ID NO: 917	30 aa
SEQ ID NO: 919	gp100 segment 43	90 nts
SEQ ID NO: 920	Polypeptide encoded by SEQ ID NO: 919	30 aa
SEQ ID NO: 921	gp100 segment 44	60nts
SEQ ID NO: 922	Polypeptide encoded by SEQ ID NO: 921	20 aa
SEQ ID NO: 923	MART segment 1	90 nts
SEQ ID NO: 924	Polypeptide encoded by SEQ ID NO: 923	30 aa
SEQ ID NO: 925	MART segment 2	90 nts
SEQ ID NO: 926	Polypeptide encoded by SEQ ID NO: 925	30 aa
SEQ ID NO: 927	MART segment 3	90 nts
SEQ ID NO: 928	Polypeptide encoded by SEQ ID NO: 927	30 aa
SEQ ID NO: 929	MART segment 4	90 nts
SEQ ID NO: 930	Polypeptide encoded by SEQ ID NO: 929	30 aa
SEQ ID NO: 931	MART segment 5	90 nts
SEQ ID NO: 932	Polypeptide encoded by SEQ ID NO: 931	30 aa
SEQ ID NO: 933	MART segment 6	90 nts
SEQ ID NO: 934	Polypeptide encoded by SEQ ID NO: 933	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 935	MART segment 7	90 nts
SEQ ID NO: 936	Polypeptide encoded by SEQ ID NO: 935	30 aa
SEQ ID NO: 937	MART segment 8	51 nts
SEQ ID NO: 938	Polypeptide encoded by SEQ ID NO: 937	17 aa
SEQ ID NO: 939	trp-1 segment 1	90 nts
SEQ ID NO: 940	Polypeptide encoded by SEQ ID NO: 939	30 aa
SEQ ID NO: 941	trp-1 segment 2	90 nts
SEQ ID NO: 942	Polypeptide encoded by SEQ ID NO: 941	30 aa
SEQ ID NO: 943	trp-1 segment 3	90 nts
SEQ ID NO: 944	Polypeptide encoded by SEQ ID NO: 943	30 aa
SEQ ID NO: 945	trp-1 segment 4	90 nts
SEQ ID NO: 946	Polypeptide encoded by SEQ ID NO: 945	30 aa
SEQ ID NO: 947	trp-1 segment 5	90 nts
SEQ ID NO: 948	Polypeptide encoded by SEQ ID NO: 947	30 aa
SEQ ID NO: 949	trp-1 segment 6	90 nts
SEQ ID NO: 950	Polypeptide encoded by SEQ ID NO: 949	30 aa
SEQ ID NO: 951	trp-1 segment 7	90 nts
SEQ ID NO: 952	Polypeptide encoded by SEQ ID NO: 951	30 aa
SEQ ID NO: 953	trp-1 segment 8	90 nts
SEQ ID NO: 954	Polypeptide encoded by SEQ ID NO: 953	30 aa
SEQ ID NO: 955	trp-1 segment 9	90 nts
SEQ ID NO: 956	Polypeptide encoded by SEQ ID NO: 955	30 aa
SEQ ID NO: 957	trp-1 segment 10	90 nts
SEQ ID NO: 958	Polypeptide encoded by SEQ ID NO: 957	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 959	trp-1 segment 11	90 nts
SEQ ID NO: 960	Polypeptide encoded by SEQ ID NO: 959	30 aa
SEQ ID NO: 961	trp-1 segment 12	90 nts
SEQ ID NO: 962	Polypeptide encoded by SEQ ID NO: 961	30 aa
SEQ ID NO: 963	trp-1 segment 13	90 nts
SEQ ID NO: 964	Polypeptide encoded by SEQ ID NO: 963	30 aa
SEQ ID NO: 965	trp-1 segment 14	90 nts
SEQ ID NO: 966	Polypeptide encoded by SEQ ID NO: 965	30 aa
SEQ ID NO: 967	trp-1 segment 15	90 nts
SEQ ID NO: 968	Polypeptide encoded by SEQ ID NO: 967	30 aa
SEQ ID NO: 969	trp-1 segment 16	81 nts
SEQ ID NO: 970	Polypeptide encoded by SEQ ID NO: 969	27 aa
SEQ ID NO: 971	tyros segment 1	90 nts
SEQ ID NO: 972	Polypeptide encoded by SEQ ID NO: 971	30 aa
SEQ ID NO: 973	tyros segment 2	90 nts
SEQ ID NO: 974	Polypeptide encoded by SEQ ID NO: 973	30 aa
SEQ ID NO: 975	tyros segment 3	90 nts
SEQ ID NO: 976	Polypeptide encoded by SEQ ID NO: 975	30 aa
SEQ ID NO: 977	tyros segment 4	90 nts
SEQ ID NO: 978	Polypeptide encoded by SEQ ID NO: 977	30 aa
SEQ ID NO: 979	tyros segment 5	90 nts
SEQ ID NO: 980	Polypeptide encoded by SEQ ID NO: 979	30 aa
SEQ ID NO: 981	tyros segment 6	90 nts
SEQ ID NO: 982	Polypeptide encoded by SEQ ID NO: 981	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 983	tyros segment 7	90 nts
SEQ ID NO: 984	Polypeptide encoded by SEQ ID NO: 983	30 aa
SEQ ID NO: 985	tyros segment 8	90 nts
SEQ ID NO: 986	Polypeptide encoded by SEQ ID NO: 985	30 aa
SEQ ID NO: 987	tyros segment 9	90 nts
SEQ ID NO: 988	Polypeptide encoded by SEQ ID NO: 987	30 aa
SEQ ID NO: 989	tyros segment 10	90 nts
SEQ ID NO: 990	Polypeptide encoded by SEQ ID NO: 989	30 aa
SEQ ID NO: 991	tyros segment 11	90 nts
SEQ ID NO: 992	Polypeptide encoded by SEQ ID NO: 991	30 aa
SEQ ID NO: 993	tyros segment 12	90 nts
SEQ ID NO: 994	Polypeptide encoded by SEQ ID NO: 993	30 aa
SEQ ID NO: 995	tyros segment 13	90 nts
SEQ ID NO: 996	Polypeptide encoded by SEQ ID NO: 995	30 aa
SEQ ID NO: 997	tyros segment 14	90 nts
SEQ ID NO: 998	Polypeptide encoded by SEQ ID NO: 997	30 aa
SEQ ID NO: 999	tyros segment 15	90 nts
SEQ ID NO: 1000	Polypeptide encoded by SEQ ID NO: 999	30 aa
SEQ ID NO: 1001	tyros segment 16	90 nts
SEQ ID NO: 1002	Polypeptide encoded by SEQ ID NO: 1001	30 aa
SEQ ID NO: 1003	tyros segment 17	90 nts
SEQ ID NO: 1004	Polypeptide encoded by SEQ ID NO: 1003	30 aa
SEQ ID NO: 1005	tyros segment 18	90 nts
SEQ ID NO: 1006	Polypeptide encoded by SEQ ID NO: 1005	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 1007	tyros segment 19	90 nts
SEQ ID NO: 1008	Polypeptide encoded by SEQ ID NO: 1007	30 aa
SEQ ID NO: 1009	tyros segment 20	90 nts
SEQ ID NO: 1010	Polypeptide encoded by SEQ ID NO: 1009	30 aa
SEQ ID NO: 1011	tyros segment 21	90 nts
SEQ ID NO: 1012	Polypeptide encoded by SEQ ID NO: 1011	30 aa
SEQ ID NO: 1013	tyros segment 22	90 nts
SEQ ID NO: 1014	Polypeptide encoded by SEQ ID NO: 1013	30 aa
SEQ ID NO: 1015	tyros segment 23	90 nts
SEQ ID NO: 1016	Polypeptide encoded by SEQ ID NO: 1015	30 aa
SEQ ID NO: 1017	tyros segment 24	90 nts
SEQ ID NO: 1018	Polypeptide encoded by SEQ ID NO: 1017	30 aa
SEQ ID NO: 1019	tyros segment 25	90 nts
SEQ ID NO: 1020	Polypeptide encoded by SEQ ID NO: 1019	30 aa
SEQ ID NO: 1021	tyros segment 26	90 nts
SEQ ID NO: 1022	Polypeptide encoded by SEQ ID NO: 1021	30 aa
SEQ ID NO: 1023	tyros segment 27	90 nts
SEQ ID NO: 1024	Polypeptide encoded by SEQ ID NO: 1023	30 aa
SEQ ID NO: 1025	tyros segment 28	90 nts
SEQ ID NO: 1026	Polypeptide encoded by SEQ ID NO: 1025	30 aa
SEQ ID NO: 1027	tyros segment 29	90 nts
SEQ ID NO: 1028	Polypeptide encoded by SEQ ID NO: 1027	30 aa
SEQ ID NO: 1029	tyros segment 30	90 nts
SEQ ID NO: 1030	Polypeptide encoded by SEQ ID NO: 1029	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 1031	tyros segment 31	90 nts
SEQ ID NO: 1032	Polypeptide encoded by SEQ ID NO: 1031	30 aa
SEQ ID NO: 1033	tyros segment 32	90 nts
SEQ ID NO: 1034	Polypeptide encoded by SEQ ID NO: 1033	30 aa
SEQ ID NO: 1035	tyros segment 33	90 nts
SEQ ID NO: 1036	Polypeptide encoded by SEQ ID NO: 1035	30 aa
SEQ ID NO: 1037	tyros segment 34	90 nts
SEQ ID NO: 1038	Polypeptide encoded by SEQ ID NO: 1037	30 aa
SEQ ID NO: 1039	tyros segment 35	69 nts
SEQ ID NO: 1040	Polypeptide encoded by SEQ ID NO: 1039	23 aa
SEQ ID NO: 1041	trp2 segment 1	90 nts
SEQ ID NO: 1042	Polypeptide encoded by SEQ ID NO: 1041	30 aa
SEQ ID NO: 1043	trp2 segment 2	90 nts
SEQ ID NO: 1044	Polypeptide encoded by SEQ ID NO: 1043	30 aa
SEQ ID NO: 1045	trp2 segment 3	90 nts
SEQ ID NO: 1046	Polypeptide encoded by SEQ ID NO: 1045	30 aa
SEQ ID NO: 1047	trp2 segment 4	90 nts
SEQ ID NO: 1048	Polypeptide encoded by SEQ ID NO: 1047	30 aa
SEQ ID NO: 1049	trp2 segment 5	90 nts
SEQ ID NO: 1050	Polypeptide encoded by SEQ ID NO: 1049	30 aa
SEQ ID NO: 1051	trp2 segment 6	90 nts
SEQ ID NO: 1052	Polypeptide encoded by SEQ ID NO: 1051	30 aa
SEQ ID NO: 1053	trp2 segment 7	90 nts
SEQ ID NO: 1054	Polypeptide encoded by SEQ ID NO: 1053	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 1055	trp2 segment 8	90 nts
SEQ ID NO: 1056	Polypeptide encoded by SEQ ID NO: 1055	30 aa
SEQ ID NO: 1057	trp2 segment 9	90 nts
SEQ ID NO: 1058	Polypeptide encoded by SEQ ID NO: 1057	30 aa
SEQ ID NO: 1059	trp2 segment 10	90 nts
SEQ ID NO: 1060	Polypeptide encoded by SEQ ID NO: 1059	30 aa
SEQ ID NO: 1061	trp2 segment 11	90 nts
SEQ ID NO: 1062	Polypeptide encoded by SEQ ID NO: 1061	30 aa
SEQ ID NO: 1063	trp2 segment 12	90 nts
SEQ ID NO: 1064	Polypeptide encoded by SEQ ID NO: 1063	30 aa
SEQ ID NO: 1065	trp2 segment 13	90 nts
SEQ ID NO: 1066	Polypeptide encoded by SEQ ID NO: 1065	30 aa
SEQ ID NO: 1067	trp2 segment 14	90 nts
SEQ ID NO: 1068	Polypeptide encoded by SEQ ID NO: 1067	30 aa
SEQ ID NO: 1069	trp2 segment 15	90 nts
SEQ ID NO: 1070	Polypeptide encoded by SEQ ID NO: 1069	30 aa
SEQ ID NO: 1071	trp2 segment 16	90 nts
SEQ ID NO: 1072	Polypeptide encoded by SEQ ID NO: 1071	30 aa
SEQ ID NO: 1073	trp2 segment 17	90 nts
SEQ ID NO: 1074	Polypeptide encoded by SEQ ID NO: 1073	30 aa
SEQ ID NO: 1075	trp2 segment 18	90 nts
SEQ ID NO: 1076	Polypeptide encoded by SEQ ID NO: 1075	30 aa
SEQ ID NO: 1077	trp2 segment 19	90 nts
SEQ ID NO: 1078	Polypeptide encoded by SEQ ID NO: 1077	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 1079	trp2 segment 20	90 nts
SEQ ID NO: 1080	Polypeptide encoded by SEQ ID NO: 1079	30 aa
SEQ ID NO: 1081	trp2 segment 21	90 nts
SEQ ID NO: 1082	Polypeptide encoded by SEQ ID NO: 1081	30 aa
SEQ ID NO: 1083	trp2 segment 22	90 nts
SEQ ID NO: 1084	Polypeptide encoded by SEQ ID NO: 1083	30 aa
SEQ ID NO: 1085	trp2 segment 23	90 nts
SEQ ID NO: 1086	Polypeptide encoded by SEQ ID NO: 1085	30 aa
SEQ ID NO: 1087	trp2 segment 24	90 nts
SEQ ID NO: 1088	Polypeptide encoded by SEQ ID NO: 1087	30 aa
SEQ ID NO: 1089	trp2 segment 25	90 nts
SEQ ID NO: 1090	Polypeptide encoded by SEQ ID NO: 1089	30 aa
SEQ ID NO: 1091	trp2 segment 26	90 nts
SEQ ID NO: 1092	Polypeptide encoded by SEQ ID NO: 1091	30 aa
SEQ ID NO: 1093	trp2 segment 27	90 nts
SEQ ID NO: 1094	Polypeptide encoded by SEQ ID NO: 1093	30 aa
SEQ ID NO: 1095	trp2 segment 28	90 nts
SEQ ID NO: 1096	Polypeptide encoded by SEQ ID NO: 1095	30 aa
SEQ ID NO: 1097	trp2 segment 29	90 nts
SEQ ID NO: 1098	Polypeptide encoded by SEQ ID NO: 1097	30 aa
SEQ ID NO: 1099	trp2 segment 30	90 nts
SEQ ID NO: 1100	Polypeptide encoded by SEQ ID NO: 1099	30 aa
SEQ ID NO: 1101	trp2 segment 31	90 nts
SEQ ID NO: 1102	Polypeptide encoded by SEQ ID NO: 1101	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 1103	trp2 segment 32	90 nts
SEQ ID NO: 1104	Polypeptide encoded by SEQ ID NO: 1103	30 aa
SEQ ID NO: 1105	trp2 segment 33	90 nts
SEQ ID NO: 1106	Polypeptide encoded by SEQ ID NO: 1105	30 aa
SEQ ID NO: 1107	trp2 segment 34	84 nts
SEQ ID NO: 1108	Polypeptide encoded by SEQ ID NO: 1107	28 aa
SEQ ID NO: 1109	MC1R segment 1	90 nts
SEQ ID NO: 1110	Polypeptide encoded by SEQ ID NO: 1109	30 aa
SEQ ID NO: 1111	MC1R segment 2	90 nts
SEQ ID NO: 1112	Polypeptide encoded by SEQ ID NO: 1111	30 aa
SEQ ID NO: 1113	MC1R segment 3	90 nts
SEQ ID NO: 1114	Polypeptide encoded by SEQ ID NO: 1113	30 aa
SEQ ID NO: 1115	MC1R segment 4	90 nts
SEQ ID NO: 1116	Polypeptide encoded by SEQ ID NO: 1115	30 aa
SEQ ID NO: 1117	MC1R segment 5	90 nts
SEQ ID NO: 1118	Polypeptide encoded by SEQ ID NO: 1117	30 aa
SEQ ID NO: 1119	MC1R segment 6	90 nts
SEQ ID NO: 1120	Polypeptide encoded by SEQ ID NO: 1119	30 aa
SEQ ID NO: 1121	MC1R segment 7	90 nts
SEQ ID NO: 1122	Polypeptide encoded by SEQ ID NO: 1121	30 aa
SEQ ID NO: 1123	MC1R segment 8	90 nts
SEQ ID NO: 1124	Polypeptide encoded by SEQ ID NO: 1123	30 aa
SEQ ID NO: 1125	MC1R segment 9	90 nts
SEQ ID NO: 1126	Polypeptide encoded by SEQ ID NO: 1125	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 1127	MC1R segment 10	90 nts
SEQ ID NO: 1128	Polypeptide encoded by SEQ ID NO: 1127	30 aa
SEQ ID NO: 1129	MC1R segment 11	90 nts
SEQ ID NO: 1130	Polypeptide encoded by SEQ ID NO: 1129	30 aa
SEQ ID NO: 1131	MC1R segment 12	90 nts
SEQ ID NO: 1132	Polypeptide encoded by SEQ ID NO: 1131	30 aa
SEQ ID NO: 1133	MC1R segment 13	90 nts
SEQ ID NO: 1134	Polypeptide encoded by SEQ ID NO: 1133	30 aa
SEQ ID NO: 1135	MC1R segment 14	90 nts
SEQ ID NO: 1136	Polypeptide encoded by SEQ ID NO: 1135	30 aa
SEQ ID NO: 1137	MC1R segment 15	90 nts
SEQ ID NO: 1138	Polypeptide encoded by SEQ ID NO: 1137	30 aa
SEQ ID NO: 1139	MC1R segment 16	90 nts
SEQ ID NO: 1140	Polypeptide encoded by SEQ ID NO: 1139	30 aa
SEQ ID NO: 1141	MC1R segment 17	90 nts
SEQ ID NO: 1142	Polypeptide encoded by SEQ ID NO: 1141	30 aa
SEQ ID NO: 1143	MC1R segment 18	90 nts
SEQ ID NO: 1144	Polypeptide encoded by SEQ ID NO: 1143	30 aa
SEQ ID NO: 1145	MC1R segment 19	90 nts
SEQ ID NO: 1146	Polypeptide encoded by SEQ ID NO: 1145	30 aa
SEQ ID NO: 1147	MC1R segment 20	90 nts
SEQ ID NO: 1148	Polypeptide encoded by SEQ ID NO: 1147	30 aa
SEQ ID NO: 1149	MC1R segment 21	63 nts
SEQ ID NO: 1150	Polypeptide encoded by SEQ ID NO: 1149	21 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 1151	MUC1F segment 1	90 nts
SEQ ID NO: 1152	Polypeptide encoded by SEQ ID NO: 1151	30 aa
SEQ ID NO: 1153	MUC1F segment 2	90 nts
SEQ ID NO: 1154	Polypeptide encoded by SEQ ID NO: 1153	30 aa
SEQ ID NO: 1155	MUC1F segment 3	90 nts
SEQ ID NO: 1156	Polypeptide encoded by SEQ ID NO: 1155	30 aa
SEQ ID NO: 1157	MUC1F segment 4	90 nts
SEQ ID NO: 1158	Polypeptide encoded by SEQ ID NO: 1157	30 aa
SEQ ID NO: 1159	MUC1F segment 5	90 nts
SEQ ID NO: 1160	Polypeptide encoded by SEQ ID NO: 1159	30 aa
SEQ ID NO: 1161	MUC1F segment 6	90 nts
SEQ ID NO: 1162	Polypeptide encoded by SEQ ID NO: 1161	30 aa
SEQ ID NO: 1163	MUC1F segment 7	90 nts
SEQ ID NO: 1164	Polypeptide encoded by SEQ ID NO: 1163	30 aa
SEQ ID NO: 1165	MUC1F segment 8	72 nts
SEQ ID NO: 1166	Polypeptide encoded by SEQ ID NO: 1165	24 aa
SEQ ID NO: 1167	MUC1R segment 1	90 nts
SEQ ID NO: 1168	Polypeptide encoded by SEQ ID NO: 1167	30 aa
SEQ ID NO: 1169	MUC1R segment 2	90 nts
SEQ ID NO: 1170	Polypeptide encoded by SEQ ID NO: 1169	30 aa
SEQ ID NO: 1171	MUC1R segment 3	90 nts
SEQ ID NO: 1172	Polypeptide encoded by SEQ ID NO: 1171	30 aa
SEQ ID NO: 1173	MUC1R segment 4	90 nts
SEQ ID NO: 1174	Polypeptide encoded by SEQ ID NO: 1173	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 1175	MUC1R segment 5	90 nts
SEQ ID NO: 1176	Polypeptide encoded by SEQ ID NO: 1175	30 aa
SEQ ID NO: 1177	MUC1R segment 6	90 nts
SEQ ID NO: 1178	Polypeptide encoded by SEQ ID NO: 1177	30 aa
SEQ ID NO: 1179	MUC1R segment 7	90 nts
SEQ ID NO: 1180	Polypeptide encoded by SEQ ID NO: 1179	30 aa
SEQ ID NO: 1181	MUC1R segment 8	90 nts
SEQ ID NO: 1182	Polypeptide encoded by SEQ ID NO: 1181	30 aa
SEQ ID NO: 1183	MUC1R segment 9	90 nts
SEQ ID NO: 1184	Polypeptide encoded by SEQ ID NO: 1183	30 aa
SEQ ID NO: 1185	MUC1R segment 10	90 nts
SEQ ID NO: 1186	Polypeptide encoded by SEQ ID NO: 1185	30 aa
SEQ ID NO: 1187	MUC1R segment 11	90 nts
SEQ ID NO: 1188	Polypeptide encoded by SEQ ID NO: 1187	30 aa
SEQ ID NO: 1189	MUC1R segment 12	90 nts
SEQ ID NO: 1190	Polypeptide encoded by SEQ ID NO: 1189	30 aa
SEQ ID NO: 1191	MUC1R segment 13	90 nts
SEQ ID NO: 1192	Polypeptide encoded by SEQ ID NO: 1191	30 aa
SEQ ID NO: 1193	MUC1R segment 14	90 nts
SEQ ID NO: 1194	Polypeptide encoded by SEQ ID NO: 1193	30 aa
SEQ ID NO: 1195	MUC1R segment 15	90 nts
SEQ ID NO: 1196	Polypeptide encoded by SEQ ID NO: 1195	30 aa
SEQ ID NO: 1197	MUC1R segment 16	90 nts
SEQ ID NO: 1198	Polypeptide encoded by SEQ ID NO: 1197	30 aa

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<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 1199	MUC1R segment 17	90 nts
SEQ ID NO: 1200	Polypeptide encoded by SEQ ID NO: 1199	30 aa
SEQ ID NO: 1201	MUC1R segment 18	90 nts
SEQ ID NO: 1202	Polypeptide encoded by SEQ ID NO: 1201	30 aa
SEQ ID NO: 1203	MUC1R segment 19	90 nts
SEQ ID NO: 1204	Polypeptide encoded by SEQ ID NO: 1203	30 aa
SEQ ID NO: 1205	MUC1R segment 20	90 nts
SEQ ID NO: 1206	Polypeptide encoded by SEQ ID NO: 1205	30 aa
SEQ ID NO: 1207	MUC1R segment 21	48 nts
SEQ ID NO: 1208	Polypeptide encoded by SEQ ID NO: 1207	16 aa
SEQ ID NO: 1209	Differentiation Savine	16638 nts
SEQ ID NO: 1210	Polypeptide encoded by SEQ ID NO: 1209	5546 aa
SEQ ID NO: 1211	BAGE segment 1	90 nts
SEQ ID NO: 1212	Polypeptide encoded by SEQ ID NO: 1211	30 aa
SEQ ID NO: 1213	BAGE segment 2	90 nts
SEQ ID NO: 1214	Polypeptide encoded by SEQ ID NO: 1213	30 aa
SEQ ID NO: 1215	BAGE segment 3	51 nts
SEQ ID NO: 1216	Polypeptide encoded by SEQ ID NO: 1215	17 aa
SEQ ID NO: 1217	GAGE-1 segment 1	90 nts
SEQ ID NO: 1218	Polypeptide encoded by SEQ ID NO: 1217	30 aa
SEQ ID NO: 1219	GAGE-1 segment 2	90 nts
SEQ ID NO: 1220	Polypeptide encoded by SEQ ID NO: 1219	30 aa
SEQ ID NO: 1221	GAGE-1 segment 3	90 nts
SEQ ID NO: 1222	Polypeptide encoded by SEQ ID NO: 1221	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 1223	GAGE-1 segment 4	90 nts
SEQ ID NO: 1224	Polypeptide encoded by SEQ ID NO: 1223	30 aa
SEQ ID NO: 1225	GAGE-1 segment 5	90 nts
SEQ ID NO: 1226	Polypeptide encoded by SEQ ID NO: 1225	30 aa
SEQ ID NO: 1227	GAGE-1 segment 6	90 nts
SEQ ID NO: 1228	Polypeptide encoded by SEQ ID NO: 1227	30 aa
SEQ ID NO: 1229	GAGE-1 segment 7	90 nts
SEQ ID NO: 1230	Polypeptide encoded by SEQ ID NO: 1229	30 aa
SEQ ID NO: 1231	GAGE-1 segment 8	90 nts
SEQ ID NO: 1232	Polypeptide encoded by SEQ ID NO: 1231	30 aa
SEQ ID NO: 1233	GAGE-1 segment 9	66 nts
SEQ ID NO: 1234	Polypeptide encoded by SEQ ID NO: 1233	22 aa
SEQ ID NO: 1235	gp100ln4 segment 1	90 nts
SEQ ID NO: 1236	Polypeptide encoded by SEQ ID NO: 1235	30 aa
SEQ ID NO: 1237	gp100ln4 segment 2	90 nts
SEQ ID NO: 1238	Polypeptide encoded by SEQ ID NO: 1237	30 aa
SEQ ID NO: 1239	gp100ln4 segment 3	75 nts
SEQ ID NO: 1240	Polypeptide encoded by SEQ ID NO: 1239	25 aa
SEQ ID NO: 1241	MAGE-1 segment 1	90 nts
SEQ ID NO: 1242	Polypeptide encoded by SEQ ID NO: 1241	30 aa
SEQ ID NO: 1243	MAGE-1 segment 2	90 nts
SEQ ID NO: 1244	Polypeptide encoded by SEQ ID NO: 1243	30 aa
SEQ ID NO: 1245	MAGE-1 segment 3	90 nts
SEQ ID NO: 1246	Polypeptide encoded by SEQ ID NO: 1245	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 1247	MAGE-1 segment 4	90 nts
SEQ ID NO: 1248	Polypeptide encoded by SEQ ID NO: 1247	30 aa
SEQ ID NO: 1249	MAGE-1 segment 5	90 nts
SEQ ID NO: 1250	Polypeptide encoded by SEQ ID NO: 1249	30 aa
SEQ ID NO: 1251	MAGE-1 segment 6	90 nts
SEQ ID NO: 1252	Polypeptide encoded by SEQ ID NO: 1251	30 aa
SEQ ID NO: 1253	MAGE-1 segment 7	90 nts
SEQ ID NO: 1254	Polypeptide encoded by SEQ ID NO: 1253	30 aa
SEQ ID NO: 1255	MAGE-1 segment 8	90 nts
SEQ ID NO: 1256	Polypeptide encoded by SEQ ID NO: 1255	30 aa
SEQ ID NO: 1257	MAGE-1 segment 9	90 nts
SEQ ID NO: 1258	Polypeptide encoded by SEQ ID NO: 1257	30 aa
SEQ ID NO: 1259	MAGE-1 segment 10	90 nts
SEQ ID NO: 1260	Polypeptide encoded by SEQ ID NO: 1259	30 aa
SEQ ID NO: 1261	MAGE-1 segment 11	90 nts
SEQ ID NO: 1262	Polypeptide encoded by SEQ ID NO: 1261	30 aa
SEQ ID NO: 1263	MAGE-1 segment 12	90 nts
SEQ ID NO: 1264	Polypeptide encoded by SEQ ID NO: 1263	30 aa
SEQ ID NO: 1265	MAGE-1 segment 13	90 nts
SEQ ID NO: 1266	Polypeptide encoded by SEQ ID NO: 1265	30 aa
SEQ ID NO: 1267	MAGE-1 segment 14	90 nts
SEQ ID NO: 1268	Polypeptide encoded by SEQ ID NO: 1267	30 aa
SEQ ID NO: 1269	MAGE-1 segment 15	90 nts
SEQ ID NO: 1270	Polypeptide encoded by SEQ ID NO: 1269	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 1271	MAGE-1 segment 16	90 nts
SEQ ID NO: 1272	Polypeptide encoded by SEQ ID NO: 1271	30 aa
SEQ ID NO: 1273	MAGE-1 segment 17	90 nts
SEQ ID NO: 1274	Polypeptide encoded by SEQ ID NO: 1273	30 aa
SEQ ID NO: 1275	MAGE-1 segment 18	90 nts
SEQ ID NO: 1276	Polypeptide encoded by SEQ ID NO: 1275	30 aa
SEQ ID NO: 1277	MAGE-1 segment 19	90 nts
SEQ ID NO: 1278	Polypeptide encoded by SEQ ID NO: 1277	30 aa
SEQ ID NO: 1279	MAGE-1 segment 20	84 nts
SEQ ID NO: 1280	Polypeptide encoded by SEQ ID NO: 1279	28 aa
SEQ ID NO: 1281	MAGE-3 segment 1	90 nts
SEQ ID NO: 1282	Polypeptide encoded by SEQ ID NO: 1281	30 aa
SEQ ID NO: 1283	MAGE-3 segment 2	90 nts
SEQ ID NO: 1284	Polypeptide encoded by SEQ ID NO: 1283	30 aa
SEQ ID NO: 1285	MAGE-3 segment 3	90 nts
SEQ ID NO: 1286	Polypeptide encoded by SEQ ID NO: 1285	30 aa
SEQ ID NO: 1287	MAGE-3 segment 4	90 nts
SEQ ID NO: 1288	Polypeptide encoded by SEQ ID NO: 1287	30 aa
SEQ ID NO: 1289	MAGE-3 segment 5	90 nts
SEQ ID NO: 1290	Polypeptide encoded by SEQ ID NO: 1289	30 aa
SEQ ID NO: 1291	MAGE-3 segment 6	90 nts
SEQ ID NO: 1292	Polypeptide encoded by SEQ ID NO: 1291	30 aa
SEQ ID NO: 1293	MAGE-3 segment 7	90 nts
SEQ ID NO: 1294	Polypeptide encoded by SEQ ID NO: 1293	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 1295	MAGE-3 segment 8	90 nts
SEQ ID NO: 1296	Polypeptide encoded by SEQ ID NO: 1295	30 aa
SEQ ID NO: 1297	MAGE-3 segment 9	90 nts
SEQ ID NO: 1298	Polypeptide encoded by SEQ ID NO: 1297	30 aa
SEQ ID NO: 1299	MAGE-3 segment 10	90 nts
SEQ ID NO: 1300	Polypeptide encoded by SEQ ID NO: 1299	30 aa
SEQ ID NO: 1301	MAGE-3 segment 11	90 nts
SEQ ID NO: 1302	Polypeptide encoded by SEQ ID NO: 1301	30 aa
SEQ ID NO: 1303	MAGE-3 segment 12	90 nts
SEQ ID NO: 1304	Polypeptide encoded by SEQ ID NO: 1303	30 aa
SEQ ID NO: 1305	MAGE-3 segment 13	90 nts
SEQ ID NO: 1306	Polypeptide encoded by SEQ ID NO: 1305	30 aa
SEQ ID NO: 1307	MAGE-3 segment 14	90 nts
SEQ ID NO: 1308	Polypeptide encoded by SEQ ID NO: 1307	30 aa
SEQ ID NO: 1309	MAGE-3 segment 15	90 nts
SEQ ID NO: 1310	Polypeptide encoded by SEQ ID NO: 1309	30 aa
SEQ ID NO: 1311	MAGE-3 segment 16	90 nts
SEQ ID NO: 1312	Polypeptide encoded by SEQ ID NO: 1311	30 aa
SEQ ID NO: 1313	MAGE-3 segment 17	90 nts
SEQ ID NO: 1314	Polypeptide encoded by SEQ ID NO: 1313	30 aa
SEQ ID NO: 1315	MAGE-3 segment 18	90 nts
SEQ ID NO: 1316	Polypeptide encoded by SEQ ID NO: 1315	30 aa
SEQ ID NO: 1317	MAGE-3 segment 19	90 nts
SEQ ID NO: 1318	Polypeptide encoded by SEQ ID NO: 1317	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 1319	MAGE-3 segment 20	90 nts
SEQ ID NO: 1320	Polypeptide encoded by SEQ ID NO: 1319	30 aa
SEQ ID NO: 1321	MAGE-3 segment 21	54 nts
SEQ ID NO: 1322	Polypeptide encoded by SEQ ID NO: 1321	18 aa
SEQ ID NO: 1323	PRAME segment 1	90 nts
SEQ ID NO: 1324	Polypeptide encoded by SEQ ID NO: 1323	30 aa
SEQ ID NO: 1325	PRAME segment 2	90 nts
SEQ ID NO: 1326	Polypeptide encoded by SEQ ID NO: 1325	30 aa
SEQ ID NO: 1327	PRAME segment 3	90 nts
SEQ ID NO: 1328	Polypeptide encoded by SEQ ID NO: 1327	30 aa
SEQ ID NO: 1329	PRAME segment 4	90 nts
SEQ ID NO: 1330	Polypeptide encoded by SEQ ID NO: 1329	30 aa
SEQ ID NO: 1331	PRAME segment 5	90 nts
SEQ ID NO: 1332	Polypeptide encoded by SEQ ID NO: 1331	30 aa
SEQ ID NO: 1333	PRAME segment 6	90 nts
SEQ ID NO: 1334	Polypeptide encoded by SEQ ID NO: 1333	30 aa
SEQ ID NO: 1335	PRAME segment 7	90 nts
SEQ ID NO: 1336	Polypeptide encoded by SEQ ID NO: 1335	30 aa
SEQ ID NO: 1337	PRAME segment 8	90 nts
SEQ ID NO: 1338	Polypeptide encoded by SEQ ID NO: 1337	30 aa
SEQ ID NO: 1339	PRAME segment 9	90 nts
SEQ ID NO: 1340	Polypeptide encoded by SEQ ID NO: 1339	30 aa
SEQ ID NO: 1341	PRAME segment 10	90 nts
SEQ ID NO: 1342	Polypeptide encoded by SEQ ID NO: 1341	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 1343	PRAME segment 11	90 nts
SEQ ID NO: 1344	Polypeptide encoded by SEQ ID NO: 1343	30 aa
SEQ ID NO: 1345	PRAME segment 12	90 nts
SEQ ID NO: 1346	Polypeptide encoded by SEQ ID NO: 1345	30 aa
SEQ ID NO: 1347	PRAME segment 13	90 nts
SEQ ID NO: 1348	Polypeptide encoded by SEQ ID NO: 1347	30 aa
SEQ ID NO: 1349	PRAME segment 14	90 nts
SEQ ID NO: 1350	Polypeptide encoded by SEQ ID NO: 1349	30 aa
SEQ ID NO: 1351	PRAME segment 15	90 nts
SEQ ID NO: 1352	Polypeptide encoded by SEQ ID NO: 1351	30 aa
SEQ ID NO: 1353	PRAME segment 16	90 nts
SEQ ID NO: 1354	Polypeptide encoded by SEQ ID NO: 1353	30 aa
SEQ ID NO: 1355	PRAME segment 17	90 nts
SEQ ID NO: 1356	Polypeptide encoded by SEQ ID NO: 1355	30 aa
SEQ ID NO: 1357	PRAME segment 18	90 nts
SEQ ID NO: 1358	Polypeptide encoded by SEQ ID NO: 1357	30 aa
SEQ ID NO: 1359	PRAME segment 19	90 nts
SEQ ID NO: 1360	Polypeptide encoded by SEQ ID NO: 1359	30 aa
SEQ ID NO: 1361	PRAME segment 20	90 nts
SEQ ID NO: 1362	Polypeptide encoded by SEQ ID NO: 1361	30 aa
SEQ ID NO: 1363	PRAME segment 21	90 nts
SEQ ID NO: 1364	Polypeptide encoded by SEQ ID NO: 1363	30 aa
SEQ ID NO: 1365	PRAME segment 22	90 nts
SEQ ID NO: 1366	Polypeptide encoded by SEQ ID NO: 1365	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 1367	PRAME segment 23	90 nts
SEQ ID NO: 1368	Polypeptide encoded by SEQ ID NO: 1367	30 aa
SEQ ID NO: 1369	PRAME segment 24	90 nts
SEQ ID NO: 1370	Polypeptide encoded by SEQ ID NO: 1369	30 aa
SEQ ID NO: 1371	PRAME segment 25	90 nts
SEQ ID NO: 1372	Polypeptide encoded by SEQ ID NO: 1371	30 aa
SEQ ID NO: 1373	PRAME segment 26	90 nts
SEQ ID NO: 1374	Polypeptide encoded by SEQ ID NO: 1373	30 aa
SEQ ID NO: 1375	PRAME segment 27	90 nts
SEQ ID NO: 1376	Polypeptide encoded by SEQ ID NO: 1375	30 aa
SEQ ID NO: 1377	PRAME segment 28	90 nts
SEQ ID NO: 1378	Polypeptide encoded by SEQ ID NO: 1377	30 aa
SEQ ID NO: 1379	PRAME segment 29	90 nts
SEQ ID NO: 1380	Polypeptide encoded by SEQ ID NO: 1379	30 aa
SEQ ID NO: 1381	PRAME segment 30	90 nts
SEQ ID NO: 1382	Polypeptide encoded by SEQ ID NO: 1381	30 aa
SEQ ID NO: 1383	PRAME segment 31	90 nts
SEQ ID NO: 1384	Polypeptide encoded by SEQ ID NO: 1383	30 aa
SEQ ID NO: 1385	PRAME segment 32	90 nts
SEQ ID NO: 1386	Polypeptide encoded by SEQ ID NO: 1385	30 aa
SEQ ID NO: 1387	PRAME segment 33	90 nts
SEQ ID NO: 1388	Polypeptide encoded by SEQ ID NO: 1387	30 aa
SEQ ID NO: 1389	PRAME segment 34	54 nts
SEQ ID NO: 1390	Polypeptide encoded by SEQ ID NO: 1389	18 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 1391	TRP2IN2 segment 1	90 nts
SEQ ID NO: 1392	Polypeptide encoded by SEQ ID NO: 1391	30 aa
SEQ ID NO: 1393	TRP2IN2 segment 2	90 nts
SEQ ID NO: 1394	Polypeptide encoded by SEQ ID NO: 1393	30 aa
SEQ ID NO: 1395	TRP2IN2 segment 3	84 nts
SEQ ID NO: 1396	Polypeptide encoded by SEQ ID NO: 1395	28 aa
SEQ ID NO: 1397	NYNSO1a segment 1	90 nts
SEQ ID NO: 1398	Polypeptide encoded by SEQ ID NO: 1397	30 aa
SEQ ID NO: 1399	NYNSO1a segment 2	90 nts
SEQ ID NO: 1400	Polypeptide encoded by SEQ ID NO: 1399	30 aa
SEQ ID NO: 1401	NYNSO1a segment 3	90 nts
SEQ ID NO: 1402	Polypeptide encoded by SEQ ID NO: 1401	30 aa
SEQ ID NO: 1403	NYNSO1a segment 4	90 nts
SEQ ID NO: 1404	Polypeptide encoded by SEQ ID NO: 1403	30 aa
SEQ ID NO: 1405	NYNSO1a segment 5	90 nts
SEQ ID NO: 1406	Polypeptide encoded by SEQ ID NO: 1405	30 aa
SEQ ID NO: 1407	NYNSO1a segment 6	90 nts
SEQ ID NO: 1408	Polypeptide encoded by SEQ ID NO: 1407	30 aa
SEQ ID NO: 1409	NYNSO1a segment 7	90 nts
SEQ ID NO: 1410	Polypeptide encoded by SEQ ID NO: 1409	30 aa
SEQ ID NO: 1411	NYNSO1a segment 8	90 nts
SEQ ID NO: 1412	Polypeptide encoded by SEQ ID NO: 1411	30 aa
SEQ ID NO: 1413	NYNSO1a segment 9	90 nts
SEQ ID NO: 1414	Polypeptide encoded by SEQ ID NO: 1413	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 1415	NYNSO1a segment 10	90 nts
SEQ ID NO: 1416	Polypeptide encoded by SEQ ID NO: 1415	30 aa
SEQ ID NO: 1417	NYNSO1a segment 11	90 nts
SEQ ID NO: 1418	Polypeptide encoded by SEQ ID NO: 1417	30 aa
SEQ ID NO: 1419	NYNSO1a segment 12	57 nts
SEQ ID NO: 1420	Polypeptide encoded by SEQ ID NO: 1419	19 aa
SEQ ID NO: 1421	NYNSO1b segment 1	90 nts
SEQ ID NO: 1422	Polypeptide encoded by SEQ ID NO: 1421	30 aa
SEQ ID NO: 1423	NYNSO1b segment 2	90 nts
SEQ ID NO: 1424	Polypeptide encoded by SEQ ID NO: 1423	30 aa
SEQ ID NO: 1425	NYNSO1b segment 3	90 nts
SEQ ID NO: 1426	Polypeptide encoded by SEQ ID NO: 1425	30 aa
SEQ ID NO: 1427	NYNSO1b segment 4	51 nts
SEQ ID NO: 1428	Polypeptide encoded by SEQ ID NO: 1427	
SEQ ID NO: 1429	LAGE1 segment 1	90 nts
SEQ ID NO: 1430	Polypeptide encoded by SEQ ID NO: 1429	30 aa
SEQ ID NO: 1431	LAGE1 segment 2	90 nts
SEQ ID NO: 1432	Polypeptide encoded by SEQ ID NO: 1431	30 aa
SEQ ID NO: 1433	LAGE1 segment 3	90 nts
SEQ ID NO: 1434	Polypeptide encoded by SEQ ID NO: 1433	30 aa
SEQ ID NO: 1435	LAGE1 segment 4	90 nts
SEQ ID NO: 1436	Polypeptide encoded by SEQ ID NO: 1435	30 aa
SEQ ID NO: 1437	LAGE1 segment 5	90 nts
SEQ ID NO: 1438	Polypeptide encoded by SEQ ID NO: 1437	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 1439	LAGE1 segment 6	90 nts
SEQ ID NO: 1440	Polypeptide encoded by SEQ ID NO: 1439	30 aa
SEQ ID NO: 1441	LAGE1 segment 7	90 nts
SEQ ID NO: 1442	Polypeptide encoded by SEQ ID NO: 1441	30 aa
SEQ ID NO: 1443	LAGE1 segment 8	90 nts
SEQ ID NO: 1444	Polypeptide encoded by SEQ ID NO: 1443	30 aa
SEQ ID NO: 1445	LAGE1 segment 9	90 nts
SEQ ID NO: 1446	Polypeptide encoded by SEQ ID NO: 1445	30 aa
SEQ ID NO: 1447	LAGE1 segment 10	90 nts
SEQ ID NO: 1448	Polypeptide encoded by SEQ ID NO: 1447	30 aa
SEQ ID NO: 1449	LAGE1 segment 11	90 nts
SEQ ID NO: 1450	Polypeptide encoded by SEQ ID NO: 1449	30 aa
SEQ ID NO: 1451	LAGE1 segment 12	57 nts
SEQ ID NO: 1452	Polypeptide encoded by SEQ ID NO: 1451	19 aa
SEQ ID NO: 1453	Melanoma cancer specific Savine	10623 nts
SEQ ID NO: 1454	Polypeptide encoded by SEQ ID NO: 1453	3541 aa
SEQ ID NO: 1455	Figure 16 A1S1 99mer	99 nts
SEQ ID NO: 1456	Figure 16 A1S2 100mer	100 nts
SEQ ID NO: 1457	Figure 16 A1S3 100mer	100 nts
SEQ ID NO: 1458	Figure 16 A1S4 100mer	100 nts
SEQ ID NO: 1459	Figure 16 A1S5 100mer	100 nts
SEQ ID NO: 1460	Figure 16 A1S6 99mer	99 nts
SEQ ID NO: 1461	Figure 16 A1S7 97mer	99 nts
SEQ ID NO: 1462	Figure 16 A1S8 100mer	100 nts

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SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 1463	Figure 16 A1S9 100mer	100 nts
SEQ ID NO: 1464	Figure 16 A1S10 75mer	76 nts
SEQ ID NO: 1465	Figure 16 A1F 20mer	20 nts
SEQ ID NO: 1466	Figure 16 A1R 20mer	20 nts
SEQ ID NO: 1467	Amino acid sequence of immunostimulatory domain of an invasin protein from <i>Yersinia</i> spp.	16 aa

DETAILED DESCRIPTION OF THE INVENTION

1. Definitions

The articles “a” and “an” are used herein to refer to one or to more than one (*i.e.*, to at least one) of the grammatical object of the article. By way of example, “an element”
5 means one element or more than one element.

As used herein, the term “*about*” refers to a quantity, level, value, dimension, size, or amount that varies by as much as 30%, preferably by as much as 20%, and more preferably by as much as 10% to a reference quantity, level, value, dimension, size, or amount.

10 By “*antigen-binding molecule*” is meant a molecule that has binding affinity for a target antigen. It will be understood that this term extends to immunoglobulins, immunoglobulin fragments and non-immunoglobulin derived protein frameworks that exhibit antigen-binding activity.

The term “*clade*” as used herein refers to a hypothetical species of an organism
15 and its descendants or a monophyletic group of organisms. Clades carry a definition, based on ancestry, and a diagnosis, based on synapomorphies. It should be noted that diagnoses of clades could change while definitions do not.

Throughout this specification, unless the context requires otherwise, the words “*comprise*”, “*comprises*” and “*comprising*” will be understood to imply the inclusion of a
20 stated step or element or group of steps or elements but not the exclusion of any other step or element or group of steps or elements.

By “*expression vector*” is meant any autonomous genetic element capable of directing the synthesis of a protein encoded by the vector. Such expression vectors are known by practitioners in the art.

25 As used herein, the term “*function*” refers to a biological, enzymatic, or therapeutic function.

“Homology” refers to the percentage number of amino acids that are identical or constitute conservative substitutions as defined in Table B *infra*. Homology may be determined using sequence comparison programs such as GAP (Deveraux *et al.* 1984, *Nucleic Acids Research* **12**, 387-395). In this way, sequences of a similar or substantially
5 different length to those cited herein might be compared by insertion of gaps into the alignment, such gaps being determined, for example, by the comparison algorithm used by GAP.

To enhance an immune response (“*immunoenhancement*”), as is well-known in the art, means to increase an animal’s capacity to respond to foreign or disease-specific
10 antigens (*e.g.*, cancer antigens) *i.e.*, those cells primed to attack such antigens are increased in number, activity, and ability to detect and destroy the those antigens. Strength of immune response is measured by standard tests including: direct measurement of peripheral blood lymphocytes by means known to the art; natural killer cell cytotoxicity assays (see, *e.g.*, Provinciali M. *et al* (1992, *J. Immunol. Meth.* **155**: 19-24), cell
15 proliferation assays (see, *e.g.*, Vollenweider, I. and Groseurth, P. J. (1992, *J. Immunol. Meth.* **149**: 133-135), immunoassays of immune cells and subsets (see, *e.g.*, Loeffler, D. A., *et al.* (1992, *Cytom.* **13**: 169-174); Rivoltini, L., *et al.* (1992, *Can. Immunol. Immunother.* **34**: 241-251); or skin tests for cell-mediated immunity (see, *e.g.*, Chang, A. E. *et al* (1993, *Cancer Res.* **53**: 1043-1050). Any statistically significant increase in
20 strength of immune response as measured by the foregoing tests is considered “*enhanced immune response*” “*immunoenhancement*” or “*immunopotential*” as used herein. Enhanced immune response is also indicated by physical manifestations such as fever and inflammation, as well as healing of systemic and local infections, and reduction of symptoms in disease, *i.e.*, decrease in tumour size, alleviation of symptoms of a disease or
25 condition including, but not restricted to, leprosy, tuberculosis, malaria, naphthous ulcers, herpetic and papillomatous warts, gingivitis, arteriosclerosis, the concomitants of AIDS such as Kaposi’s sarcoma, bronchial infections, and the like. Such physical manifestations also define “*enhanced immune response*” “*immunoenhancement*” or “*immunopotential*” as used herein.

30 Reference herein to “*immuno-interactive*” includes reference to any interaction, reaction, or other form of association between molecules and in particular where one of the molecules is, or mimics, a component of the immune system.

By “*isolated*” is meant material that is substantially or essentially free from components that normally accompany it in its native state.

By “*modulating*” is meant increasing or decreasing, either directly or indirectly, an immune response against a target antigen of a member selected from the group
5 consisting of a cancer and an organism, preferably a pathogenic organism.

By “*natural gene*” is meant a gene that naturally encodes a protein.

The term “*natural polypeptide*” as used herein refers to a polypeptide that exists in nature.

By “*obtained from*” is meant that a sample such as, for example, a polynucleotide
10 extract or polypeptide extract is isolated from, or derived from, a particular source of the host. For example, the extract can be obtained from a tissue or a biological fluid isolated directly from the host.

The term “*oligonucleotide*” as used herein refers to a polymer composed of a multiplicity of nucleotide residues (deoxyribonucleotides or ribonucleotides, or related
15 structural variants or synthetic analogues thereof) linked via phosphodiester bonds (or related structural variants or synthetic analogues thereof). Thus, while the term “oligonucleotide” typically refers to a nucleotide polymer in which the nucleotide residues and linkages between them are naturally occurring, it will be understood that the term also includes within its scope various analogues including, but not restricted to, peptide nucleic
20 acids (PNAs), phosphoramidates, phosphorothioates, methyl phosphonates, 2-O-methyl ribonucleic acids, and the like. The exact size of the molecule can vary depending on the particular application. An oligonucleotide is typically rather short in length, generally from about 10 to 30 nucleotide residues, but the term can refer to molecules of any length, although the term “polynucleotide” or “nucleic acid” is typically used for large
25 oligonucleotides.

By “*operably linked*” is meant that transcriptional and translational regulatory polynucleotides are positioned relative to a polypeptide-encoding polynucleotide in such a manner that the polynucleotide is transcribed and the polypeptide is translated.

The term "*parent polypeptide*" as used herein typically refers to a polypeptide encoded by a natural gene. However, it is possible that the parent polypeptide corresponds to a protein that is not naturally-occurring but has been engineered using recombinant techniques. In this instance, a polynucleotide encoding the parent polypeptide may
5 comprise different but synonymous codons relative to a natural gene encoding the same polypeptide. Alternatively, the parent polypeptide may not correspond to a natural polypeptide sequence. For example, the parent polypeptide may comprise one or more consensus sequences common to a plurality of polypeptides.

The term "*patient*" refers to patients of human or other mammal and includes any
10 individual it is desired to examine or treat using the methods of the invention. However, it will be understood that "*patient*" does not imply that symptoms are present. Suitable mammals that fall within the scope of the invention include, but are not restricted to, primates, livestock animals (*e.g.*, sheep, cows, horses, donkeys, pigs), laboratory test animals (*e.g.*, rabbits, mice, rats, guinea pigs, hamsters), companion animals (*e.g.*, cats,
15 dogs) and captive wild animals (*e.g.*, foxes, deer, dingoes).

By "*pharmaceutically-acceptable carrier*" is meant a solid or liquid filler, diluent or encapsulating substance that can be safely used in topical or systemic administration to a mammal.

"*Polypeptide*", "*peptide*" and "*protein*" are used interchangeably herein to refer to
20 a polymer of amino acid residues and to variants and synthetic analogues of the same. Thus, these terms apply to amino acid polymers in which one or more amino acid residues is a synthetic non-naturally occurring amino acid, such as a chemical analogue of a corresponding naturally occurring amino acid, as well as to naturally-occurring amino acid polymers.

25 The term "*polynucleotide*" or "*nucleic acid*" as used herein designates mRNA, RNA, cRNA, cDNA or DNA. The term typically refers to oligonucleotides greater than 30 nucleotide residues in length.

By "*primer*" is meant an oligonucleotide which, when paired with a strand of DNA, is capable of initiating the synthesis of a primer extension product in the presence of
30 a suitable polymerising agent. The primer is preferably single-stranded for maximum

efficiency in amplification but can alternatively be double-stranded. A primer must be sufficiently long to prime the synthesis of extension products in the presence of the polymerisation agent. The length of the primer depends on many factors, including application, temperature to be employed, template reaction conditions, other reagents, and source of primers. For example, depending on the complexity of the target sequence, the oligonucleotide primer typically contains 15 to 35 or more nucleotide residues, although it can contain fewer nucleotide residues. Primers can be large polynucleotides, such as from about 35 nucleotides to several kilobases or more. Primers can be selected to be “substantially complementary” to the sequence on the template to which it is designed to hybridise and serve as a site for the initiation of synthesis. By “substantially complementary”, it is meant that the primer is sufficiently complementary to hybridise with a target polynucleotide. Preferably, the primer contains no mismatches with the template to which it is designed to hybridise but this is not essential. For example, non-complementary nucleotide residues can be attached to the 5' end of the primer, with the remainder of the primer sequence being complementary to the template. Alternatively, non-complementary nucleotide residues or a stretch of non-complementary nucleotide residues can be interspersed into a primer, provided that the primer sequence has sufficient complementarity with the sequence of the template to hybridise therewith and thereby form a template for synthesis of the extension product of the primer.

“Probe” refers to a molecule that binds to a specific sequence or sub-sequence or other moiety of another molecule. Unless otherwise indicated, the term “probe” typically refers to a polynucleotide probe that binds to another polynucleotide, often called the “target polynucleotide”, through complementary base pairing. Probes can bind target polynucleotides lacking complete sequence complementarity with the probe, depending on the stringency of the hybridisation conditions. Probes can be labelled directly or indirectly.

By “recombinant polypeptide” is meant a polypeptide made using recombinant techniques, *i.e.*, through the expression of a recombinant or synthetic polynucleotide.

Terms used to describe sequence relationships between two or more polynucleotides or polypeptides include “reference sequence”, “comparison window”, “sequence identity”, “percentage of sequence identity” and “substantial identity”. A “reference sequence” is at least 12 but frequently 15 to 18 and often at least 25 monomer

units, inclusive of nucleotides and amino acid residues, in length. Because two polynucleotides may each comprise (1) a sequence (*i.e.*, only a portion of the complete polynucleotide sequence) that is similar between the two polynucleotides, and (2) a sequence that is divergent between the two polynucleotides, sequence comparisons between two (or more) polynucleotides are typically performed by comparing sequences of the two polynucleotides over a "comparison window" to identify and compare local regions of sequence similarity. A "*comparison window*" refers to a conceptual segment of at least 50 contiguous positions, usually about 50 to about 100, more usually about 100 to about 150 in which a sequence is compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. The comparison window may comprise additions or deletions (*i.e.*, gaps) of about 20% or less as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Optimal alignment of sequences for aligning a comparison window may be conducted by computerised implementations of algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetics Computer Group, 575 Science Drive Madison, WI, USA) or by inspection and the best alignment (*i.e.*, resulting in the highest percentage homology over the comparison window) generated by any of the various methods selected. Reference also may be made to the BLAST family of programs as for example disclosed by Altschul *et al.*, 1997, *Nucl. Acids Res.* **25**:3389. A detailed discussion of sequence analysis can be found in Unit 19.3 of Ausubel *et al.*, "Current Protocols in Molecular Biology", John Wiley & Sons Inc, 1994-1998, Chapter 15.

The term "*sequence identity*" as used herein refers to the extent that sequences are identical on a nucleotide-by-nucleotide basis or an amino acid-by-amino acid basis over a window of comparison. Thus, a "*percentage of sequence identity*" is calculated by comparing two optimally aligned sequences over the window of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, I) or the identical amino acid residue (*e.g.*, Ala, Pro, Ser, Thr, Gly, Val, Leu, Ile, Phe, Tyr, Trp, Lys, Arg, His, Asp, Glu, Asn, Gln, Cys and Met) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of sequence identity. For the purposes of the present

invention, “*sequence identity*” will be understood to mean the “match percentage” calculated by the DNASIS computer program (Version 2.5 for windows; available from Hitachi Software engineering Co., Ltd., South San Francisco, California, USA) using standard defaults as used in the reference manual accompanying the software.

5 The term “*synthetic polynucleotide*” as used herein refers to a polynucleotide formed *in vitro* by the manipulation of a polynucleotide into a form not normally found in nature. For example, the synthetic polynucleotide can be in the form of an expression vector. Generally, such expression vectors include transcriptional and translational regulatory polynucleotide operably linked to the polynucleotide.

10 The term “*synonymous codon*” as used herein refers to a codon having a different nucleotide sequence than another codon but encoding the same amino acid as that other codon.

By “*translational efficiency*” is meant the efficiency of a cell’s protein synthesis machinery to incorporate the amino acid encoded by a codon into a nascent polypeptide chain. This efficiency can be evidenced, for example, by the rate at which the cell is able to synthesise the polypeptide from an RNA template comprising the codon, or by the amount of the polypeptide synthesised from such a template.

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By “*vector*” is meant a polynucleotide molecule, preferably a DNA molecule derived, for example, from a plasmid, bacteriophage, yeast or virus, into which a polynucleotide can be inserted or cloned. A vector preferably contains one or more unique restriction sites and can be capable of autonomous replication in a defined host cell including a target cell or tissue or a progenitor cell or tissue thereof, or be integrable with the genome of the defined host such that the cloned sequence is reproducible. Accordingly, the vector can be an autonomously replicating vector, *i.e.*, a vector that exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, *e.g.*, a linear or closed circular plasmid, an extrachromosomal element, a minichromosome, or an artificial chromosome. The vector can contain any means for assuring self-replication. Alternatively, the vector can be one which, when introduced into the host cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. A vector system can comprise a single vector or plasmid, two or more vectors or plasmids, which together contain the total DNA to be introduced

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into the genome of the host cell, or a transposon. The choice of the vector will typically depend on the compatibility of the vector with the host cell into which the vector is to be introduced. In the present case, the vector is preferably a viral or viral-derived vector, which is operably functional in animal and preferably mammalian cells. Such vector may
5 be derived from a poxvirus, an adenovirus or yeast. The vector can also include a selection marker such as an antibiotic resistance gene that can be used for selection of suitable transformants. Examples of such resistance genes are known to those of skill in the art and include the *nptII* gene that confers resistance to the antibiotics kanamycin and G418 (Geneticin®) and the *hph* gene which confers resistance to the antibiotic hygromycin B.

2. *Synthetic polypeptides*

The inventors have surprisingly discovered that the structure of a parent polypeptide can be disrupted sufficiently to impede, abrogate or otherwise alter at least one function of the parent polypeptide, while simultaneously minimising the destruction of potentially useful epitopes that are present in the parent polypeptide, by fusing, coupling or otherwise linking together different segments of the parent polypeptide in a different relationship relative to their linkage in the parent polypeptide. As a result of this change in relationship, the sequence of the linked segments in the resulting synthetic polypeptide is different to a sequence contained within the parent polypeptide. The synthetic polypeptides of the invention are useful as immunopotentiating agents, and are referred to elsewhere in the specification as scrambled antigen vaccines, super attenuated vaccines or "*Savines*".

Thus, the invention broadly resides in a synthetic polypeptide comprising a plurality of different segments of at least one parent polypeptide, wherein said segments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide.

It is preferable but not essential that the segments in said synthetic polypeptide are linked sequentially in a different order or arrangement relative to that of corresponding segments in said at least one parent polypeptide. For example, in the case of a parent polypeptide that comprises three contiguous or overlapping segments A-B-C-D, these segments may be linked in 23 other possible orders to form a synthetic polypeptide. These orders may be selected from the group consisting of: A-B-D-C, A-C-B-D, A-C-D-B, A-D-B-C, A-D-C-B, B-A-C-D, B-A-D-C, B-C-A-D, B-C-D-A, B-D-A-C, B-D-C-A, C-A-B-D, C-A-D-B, C-B-A-D, C-B-D-A, C-D-A-B, C-D-B-A, D-A-B-C, D-A-C-B, D-B-A-C, D-B-C-A, D-C-A-B, and D-C-B-A. Although the rearrangement of the segments is preferably random, it is especially preferable to exclude or otherwise minimise rearrangements that result in complete or partial reassembly of the parent sequence (*e.g.*, ADBC, BACD, DABC). It will be appreciated, however, that the probability of such complete or partial reassembly diminishes as the number of segments for rearrangement increases.

The order of the segments is suitably shuffled, reordered or otherwise rearranged relative to the order in which they exist in the parent polypeptide so that the structure of the polypeptide is disrupted sufficiently to impede, abrogate or otherwise alter at least one

function associated with the parent polypeptide. Preferably, the segments of the parent polypeptide are randomly rearranged in the synthetic polypeptide.

The parent polypeptide is suitably a polypeptide that is associated with a disease or condition. For example, the parent polypeptide may be a polypeptide expressed by a pathogenic organism or a cancer. Alternatively, the parent polypeptide can be a self peptide related to an autoimmune disease including, but are not limited to, diseases such as diabetes (*e.g.*, juvenile diabetes), multiple sclerosis, rheumatoid arthritis, myasthenia gravis, atopic dermatitis, and psoriasis and ankylosing spondylitis. Accordingly, the synthetic molecules of the present invention may also have utility for the induction of tolerance in a subject afflicted with an autoimmune disease or condition or with an allergy or other condition to which tolerance is desired. For example tolerance may be induced by contacting an immature dendritic cell of the individual to be treated with a synthetic polypeptide of the invention or by expressing in an immature dendritic cell a synthetic polynucleotide of the invention. Tolerance may also be induced against antigens causing allergic responses (*e.g.*, asthma, hay fever). In this case, the parent polypeptide is suitably an allergenic protein including, but not restricted to, house-dust-mite allergenic proteins as for example described by Thomas and Smith (1998, *Allergy*, **53**(9): 821-832).

The pathogenic organism includes, but is not restricted to, yeast, a virus, a bacterium, and a parasite. Any natural host of the pathogenic organism is contemplated by the present invention and includes, but is not limited to, mammals, avians and fish. In a preferred embodiment, the pathogenic organism is a virus, which may be an RNA virus or a DNA virus. Preferably, the RNA virus is Human Immunodeficiency Virus (HIV), Poliovirus, and Influenza virus, Rous sarcoma virus, or a Flavivirus such as Japanese encephalitis virus. In a preferred embodiment, the RNA virus is a Hepatitis virus including, but not limited to, Hepatitis strains A, B and C. Suitably, the DNA virus is a Herpesvirus including, but not limited to, Herpes simplex virus, Epstein-Barr virus, Cytomegalovirus and Parvovirus. In a preferred embodiment, the virus is HIV and the parent polypeptide is suitably selected from env, gag, pol, vif, vpr, tat, rev, vpu and nef, or combination thereof. In an alternate preferred embodiment, the virus is Hepatitis C1a virus and the parent polypeptide is the Hepatitis C1a virus polyprotein.

In another embodiment, the pathogenic organism is a bacterium, which includes, but is not restricted to, *Neisseria* species, *Meningococcal* species, *Haemophilus* species, *Salmonella* species, *Streptococcal* species, *Legionella* species and *Mycobacterium* species.

In yet another embodiment, the pathogenic organism is a parasite, which includes,
5 but is not restricted to, *Plasmodium* species, *Schistosoma* species, *Leishmania* species, *Trypanosoma* species, *Toxoplasma* species and *Giardia* species.

Any cancer or tumour is contemplated by the present invention. For example, the cancer or tumour includes, but is not restricted to, melanoma, lung cancer, breast cancer, cervical cancer, prostate cancer, colon cancer, pancreatic cancer, stomach cancer, bladder
10 cancer, kidney cancer, post transplant lymphoproliferative disease (PTLD), Hodgkin's Lymphoma and the like. Preferably, the cancer or tumour relates to melanoma. In a preferred embodiment of this type, the parent polypeptide is a melanocyte differentiation antigen which is suitably selected from gp100, MART, TRP-1, Tyros, TRP2, MC1R, MUC1F, MUC1R or a combination thereof. In an alternate preferred embodiment of this
15 type, the parent polypeptide is a melanoma-specific antigen which is suitably selected from BAGE, GAGE-1, gp100In4, MAGE-1, MAGE-3, PRAME, TRP2IN2, NYNSO1a, NYNSO1b, LAGE1 or a combination thereof.

In a preferred embodiment, the segments are selected on the basis of size. A segment according to the invention may be of any suitable size that can be utilised to elicit
20 an immune response against an antigen encoded by the parent polypeptide. A number of factors can influence the choice of segment size. For example, the size of a segment should be preferably chosen such that it includes, or corresponds to the size of, T cell epitopes and their processing requirement. Practitioners in the art will recognise that class I-restricted T cell epitopes can be between 8 and 10 amino acids in length and if placed next to unnatural
25 flanking residues, such epitopes can generally require 2 to 3 natural flanking amino acids to ensure that they are efficiently processed and presented. Class II-restricted T cell epitopes can range between 12 and 25 amino acids in length and may not require natural flanking residues for efficient proteolytic processing although it is believed that natural flanking residues may play a role. Another important feature of class II-restricted epitopes
30 is that they generally contain a core of 9-10 amino acids in the middle which bind specifically to class II MHC molecules with flanking sequences either side of this core

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stabilising binding by associating with conserved structures on either side of class II MHC antigens in a sequence independent manner (Brown *et al.*, 1993). Thus the functional region of class II-restricted epitopes is typically less than 15 amino acids long. The size of linear B cell epitopes and the factors effecting their processing, like class II-restricted epitopes, are quite variable although such epitopes are frequently smaller in size than 15 amino acids. From the foregoing, it is preferable, but not essential, that the size of the segment is at least 4 amino acids, preferably at least 7 amino acids, more preferably at least 12 amino acids, more preferably at least 20 amino acids and more preferably at least 30 amino acids. Suitably, the size of the segment is less than 2000 amino acids, more preferably less than 1000 amino acids, more preferably less than 500 amino acids, more preferably less than 200 amino acids, more preferably less than 100 amino acids, more preferably less than 80 amino acids and even more preferably less than 60 amino acids and still even more preferably less than 40 amino acids. In this regard, it is preferable that the size of the segments is as small as possible so that the synthetic polypeptide adopts a functionally different structure relative to the structure of the parent polypeptide. It is also preferable that the size of the segments is large enough to minimise loss of T cell epitopes. In an especially preferred embodiment, the size of the segment is about 30 amino acids.

An optional spacer may be utilised to space adjacent segments relative to each other. Accordingly, an optional spacer may be interposed between some or all of the segments. The spacer suitably alters proteolytic processing and/or presentation of adjacent segment(s). In a preferred embodiment of this type, the spacer promotes or otherwise enhances proteolytic processing and/or presentation of adjacent segment(s). Preferably, the spacer comprises at least one amino acid. The at least one amino acid is suitably a neutral amino acid. The neutral amino acid is preferably alanine. Alternatively, the at least one amino acid is cysteine.

In a preferred embodiment, segments are selected such that they have partial sequence identity or homology with one or more other segments. Suitably, at one or both ends of a respective segment there is comprised at least 4 contiguous amino acids, preferably at least 7 contiguous amino acids, more preferably at least 10 contiguous amino acids, more preferably at least 15 contiguous amino acids and even more preferably at least 20 contiguous amino acids that are identical to, or homologous with, an amino acid sequence contained within one or more other of said segments. Preferably, at the or each

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end of a respective segment there is comprised less than 500 contiguous amino acids, more preferably less than 200 contiguous amino acids, more preferably less than 100 contiguous amino acids, more preferably less than 50 contiguous amino acids, more preferably less than 40 contiguous amino acids, and even more preferably less than 30 contiguous amino acids that are identical to, or homologous with, an amino acid sequence contained within one or more other of said segments. Such sequence overlap (also referred to elsewhere in the specification as "*overlapping fragments*" or "*overlapping segments*") is preferable to ensure potential epitopes at segment boundaries are not lost and to ensure that epitopes at or near segment boundaries are processed efficiently if placed beside or near amino acids that inhibit processing. Preferably, the segment size is about twice the size of the overlap.

In a preferred embodiment, when segments have partial sequence homology therebetween, the homologous sequences suitably comprise conserved and/or non-conserved amino acid differences. Exemplary conservative substitutions are listed in the following table.

15 **TABLE B**

<i>Original Residue</i>	<i>Exemplary Substitutions</i>
Ala	Ser
Arg	Lys
Asn	Gln, His
Asp	Glu
Cys	Ser
Gln	Asn
Glu	Asp
Gly	Pro
His	Asn, Gln
Ile	Leu, Val
Leu	Ile, Val

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<i>Original Residue</i>	<i>Exemplary Substitutions</i>
Lys	Arg, Gln, Glu
Met	Leu, Ile,
Phe	Met, Leu, Tyr
Ser	Thr
Thr	Ser
Trp	Tyr
Tyr	Trp, Phe
Val	Ile, Leu

Conserved or non-conserved differences may correspond to polymorphisms in corresponding parent polypeptides. Polymorphic polypeptides are expressed by various pathogenic organisms and cancers. For example, the polymorphic polypeptides may be
5 expressed by different viral strains or clades or by cancers in different individuals.

Sequence overlap between respective segments is preferable to minimise destruction of any epitope sequences that may result from any shuffling or rearrangement of the segments relative to their existing order in the parent polypeptide. If overlapping segments as described above are employed to form a synthetic polypeptide, it may not be
10 necessary to change the order in which those segments are linked together relative to the order in which corresponding segments are normally present in the parent polypeptide. In this regard, such overlapping segments when linked together in the synthetic polypeptide can adopt a different structure relative to the structure of the parent polypeptide, wherein the different structure does not provide for one or more functions associated with the
15 parent polypeptide. For example, in the case of four segments A-B-C-D each spanning 30 contiguous amino acids of the parent polypeptide and having a 10-amino acid overlapping sequence with one or more adjacent segments, the synthetic polypeptide will have duplicated 10-amino acid sequences bridging segments A-B, B-C and C-D. The presence of these duplicated sequences may be sufficient to render a different structure and to
20 abrogate or alter function relative to the parent polypeptide.

In a preferred embodiment, segment size is about 30 amino acids and sequence overlap at one or both ends of a respective segment is about 15 amino acids. However, it will be understood that other suitable segment sizes and sequence overlap sizes are contemplated by the present invention, which can be readily ascertained by persons of skill in the art.

It is preferable but not necessary to utilise all the segments of the parent polypeptide in the construction of the synthetic polypeptide. Suitably, at least 30%, preferably at least 40%, more preferably at least 50%, even more preferably at least 60%, even more preferably at least 70%, even more preferably at least 80% and still even more preferably at least 90% of the parent polypeptide sequence is used in the construction of the synthetic polypeptide. However, it will be understood that the more sequence information from a parent polypeptide that is utilised to construct the synthetic polypeptide, the greater the population coverage will be of the synthetic polypeptide as an immunogen. Preferably, no sequence information from the parent polypeptide is excluded (*e.g.*, because of an apparent lack of immunological epitopes).

Persons of skill in the art will appreciate that when preparing a synthetic polypeptide against a pathogenic organism (*e.g.*, a virus) or a cancer, it may be preferable to use sequence information from a plurality of different polypeptides expressed by the organism or the cancer. Accordingly, in a preferred embodiment, segments from a plurality of different polypeptides are linked together to form a synthetic polypeptide according to the invention. It is preferable in this respect to utilise as many parent polypeptides as possible from, or in relation to, a particular source in the construction of the synthetic polypeptide. The source of parent polypeptides includes, but is not limited to, a pathogenic organism and a cancer. Suitably, at least about 30%, preferably at least 40%, more preferably at least 50%, even more preferably at least 60%, even more preferably at least 70%, even more preferably at least 80% and still even more preferably at least 90% of the parent polypeptides expressed by the source is used in the construction of the synthetic polypeptide. Preferably, parent polypeptides from a virus include, but are not restricted to, latent polypeptides, regulatory polypeptides or polypeptides expressed early during their replication cycle. Suitably, parent polypeptides from a parasite or bacterium include, but are not restricted to, secretory polypeptides and polypeptides expressed on the surface of

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the parasite or bacteria. It is preferred that parent polypeptides from a cancer or tumour are cancer specific polypeptides.

Suitably, hypervariable sequences within the parent polypeptide are excluded from the construction of the synthetic polypeptide.

5 The synthetic polypeptides of the inventions may be prepared by any suitable procedure known to those of skill in the art. For example, the polypeptide may be synthesised using solution synthesis or solid phase synthesis as described, for example, in Chapter 9 of Atherton and Shephard (1989, *Solid Phase Peptide Synthesis: A Practical Approach*. IRL Press, Oxford) and in Roberge *et al* (1995, *Science* **269**: 202). Syntheses
10 may employ, for example, either *t*-butyloxycarbonyl (*t*-Boc) or 9-fluorenylmethyloxycarbonyl (Fmoc) chemistries (see Chapter 9.1, of Coligan *et al.*, *CURRENT PROTOCOLS IN PROTEIN SCIENCE*, John Wiley & Sons, Inc. 1995-1997; Stewart and Young, 1984, *Solid Phase Peptide Synthesis*, 2nd ed. Pierce Chemical Co., Rockford, Ill; and Atherton and Shephard, *supra*).

15 Alternatively, the polypeptides may be prepared by a procedure including the steps of:

(a) preparing a synthetic construct including a synthetic polynucleotide encoding a synthetic polypeptide wherein said synthetic polynucleotide is operably linked to a regulatory polynucleotide, wherein said synthetic polypeptide comprises a plurality of
20 different segments of a parent polypeptide, wherein said segments are linked together in a different relationship relative to their linkage in the parent polypeptide;

(b) introducing the synthetic construct into a suitable host cell;

(c) culturing the host cell to express the synthetic polypeptide from said synthetic construct; and

25 (d) isolating the synthetic polypeptide.

The synthetic construct is preferably in the form of an expression vector. For example, the expression vector can be a self-replicating extra-chromosomal vector such as a plasmid, or a vector that integrates into a host genome. Typically, the regulatory polynucleotide may include, but is not limited to, promoter sequences, leader or signal

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sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and termination sequences, and enhancer or activator sequences. Constitutive or inducible promoters as known in the art are contemplated by the invention. The promoters may be either naturally occurring promoters, or hybrid promoters that combine elements of more than one promoter. The regulatory polynucleotide will generally be appropriate for the host cell used for expression. Numerous types of appropriate expression vectors and suitable regulatory polynucleotides are known in the art for a variety of host cells.

In a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The expression vector may also include a fusion partner (typically provided by the expression vector) so that the synthetic polypeptide of the invention is expressed as a fusion polypeptide with said fusion partner. The main advantage of fusion partners is that they assist identification and/or purification of said fusion polypeptide. In order to express said fusion polypeptide, it is necessary to ligate a polynucleotide according to the invention into the expression vector so that the translational reading frames of the fusion partner and the polynucleotide coincide.

Well known examples of fusion partners include, but are not limited to, glutathione-S-transferase (GST), Fc portion of human IgG, maltose binding protein (MBP) and hexahistidine (HIS₆), which are particularly useful for isolation of the fusion polypeptide by affinity chromatography. For the purposes of fusion polypeptide purification by affinity chromatography, relevant matrices for affinity chromatography are glutathione-, amylose-, and nickel- or cobalt-conjugated resins respectively. Many such matrices are available in "kit" form, such as the QIAexpress™ system (Qiagen) useful with (HIS₆) fusion partners and the Pharmacia GST purification system. In a preferred embodiment, the recombinant polynucleotide is expressed in the commercial vector pFLAG™.

Another fusion partner well known in the art is green fluorescent protein (GFP). This fusion partner serves as a fluorescent "tag" which allows the fusion polypeptide of the invention to be identified by fluorescence microscopy or by flow cytometry. The GFP tag is useful when assessing subcellular localisation of a fusion polypeptide of the invention,

or for isolating cells which express a fusion polypeptide of the invention. Flow cytometric methods such as fluorescence activated cell sorting (FACS) are particularly useful in this latter application. Preferably, the fusion partners also have protease cleavage sites, such as for Factor X_a, Thrombin and inteins (protein introns), which allow the relevant protease to partially digest the fusion polypeptide of the invention and thereby liberate the recombinant polypeptide of the invention therefrom. The liberated polypeptide can then be isolated from the fusion partner by subsequent chromatographic separation. Fusion partners according to the invention also include within their scope "epitope tags", which are usually short peptide sequences for which a specific antibody is available. Well known examples of epitope tags for which specific monoclonal antibodies are readily available include c-Myc, influenza virus, haemagglutinin and FLAG tags. Alternatively, a fusion partner may be provided to promote other forms of immunity. For example, the fusion partner may be an antigen-binding molecule that is immuno-interactive with a conformational epitope on a target antigen or to a post-translational modification of a target antigen (*e.g.*, an antigen-binding molecule that is immuno-interactive with a glycosylated target antigen).

The step of introducing the synthetic construct into the host cell may be effected by any suitable method including transfection, and transformation, the choice of which will be dependent on the host cell employed. Such methods are well known to those of skill in the art.

Synthetic polypeptides of the invention may be produced by culturing a host cell transformed with the synthetic construct. The conditions appropriate for protein expression will vary with the choice of expression vector and the host cell. This is easily ascertained by one skilled in the art through routine experimentation.

Suitable host cells for expression may be prokaryotic or eukaryotic. One preferred host cell for expression of a polypeptide according to the invention is a bacterium. The bacterium used may be *Escherichia coli*. Alternatively, the host cell may be an insect cell such as, for example, *SF9* cells that may be utilised with a baculovirus expression system.

The synthetic polypeptide may be conveniently prepared by a person skilled in the art using standard protocols as for example described in Sambrook, *et al.*, MOLECULAR CLONING. A LABORATORY MANUAL (Cold Spring Harbor Press, 1989), in particular

Sections 16 and 17; Ausubel *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY (John Wiley & Sons, Inc. 1994-1998), in particular Chapters 10 and 16; and Coligan *et al.*, CURRENT PROTOCOLS IN PROTEIN SCIENCE (John Wiley & Sons, Inc. 1995-1997), in particular Chapters 1, 5 and 6.

- 5 The amino acids of the synthetic polypeptide can be any non-naturally occurring or any naturally occurring amino acid. Examples of unnatural amino acids and derivatives during peptide synthesis include but are not limited to, use of 4-amino butyric acid, 6-aminohexanoic acid, 4-amino-3-hydroxy-5-phenylpentanoic acid, 4-amino-3-hydroxy-6-methylheptanoic acid, t-butylglycine, norleucine, norvaline, phenylglycine, ornithine, 10 sarcosine, 2-thienyl alanine and/or D-isomers of amino acids. A list of unnatural amino acids contemplated by the present invention is shown in TABLE C.

TABLE C

<i>Non-conventional amino acid</i>	<i>Non-conventional amino acid</i>
α -aminobutyric acid	L-N-methylalanine
α -amino- α -methylbutyrate	L-N-methylarginine
aminocyclopropane-carboxylate	L-N-methylasparagine
aminoisobutyric acid	L-N-methylaspartic acid
aminonorbornyl-carboxylate	L-N-methylcysteine
cyclohexylalanine	L-N-methylglutamine
cyclopentylalanine	L-N-methylglutamic acid
L-N-methylisoleucine	L-N-methylhistidine
D-alanine	L-N-methylleucine
D-arginine	L-N-methyllysine
D-aspartic acid	L-N-methylmethionine
D-cysteine	L-N-methylnorleucine
D-glutamate	L-N-methylnorvaline
D-glutamic acid	L-N-methylornithine

<i>Non-conventional amino acid</i>	<i>Non-conventional amino acid</i>
D-histidine	L-N-methylphenylalanine
D-isoleucine	L-N-methylproline
D-leucine	L-N-methylserine
D-lysine	L-N-methylthreonine
D-methionine	L-N-methyltryptophan
D-ornithine	L-N-methyltyrosine
D-phenylalanine	L-N-methylvaline
D-proline	L-N-methylethylglycine
D-serine	L-N-methyl-t-butylglycine
D-threonine	L-norleucine
D-tryptophan	L-norvaline
D-tyrosine	α -methyl-aminoisobutyrate
D-valine	α -methyl- γ -aminobutyrate
D- α -methylalanine	α -methylcyclohexylalanine
D- α -methylarginine	α -methylcyclopentylalanine
D- α -methylassparagine	α -methyl- α -naphthylalanine
D- α -methylasspartate	α -methylpenicillamine
D- α -methylcysteine	N-(4-aminobutyl)glycine
D- α -methylglutamine	N-(2-aminoethyl)glycine
D- α -methylhistidine	N-(3-aminopropyl)glycine
D- α -methylisoleucine	N-amino- α -methylbutyrate
D- α -methylleucine	α -naphthylalanine
D- α -methyllysine	N-benzylglycine
D- α -methylmethionine	N-(2-carbamylethyl)glycine
D- α -methylornithine	N-(carbamylmethyl)glycine

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<i>Non-conventional amino acid</i>	<i>Non-conventional amino acid</i>
D- α -methylphenylalanine	N-(2-carboxyethyl)glycine
D- α -methylproline	N-(carboxymethyl)glycine
D- α -methylserine	N-cyclobutylglycine
D- α -methylthreonine	N-cycloheptylglycine
D- α -methyltryptophan	N-cyclohexylglycine
D- α -methyltyrosine	N-cyclodecylglycine
L- α -methylleucine	L- α -methyllysine
L- α -methylmethionine	L- α -methylnorleucine
L- α -methylnorvaline	L- α -methylornithine
L- α -methylphenylalanine	L- α -methylproline
L- α -methylserine	L- α -methylthreonine
L- α -methyltryptophan	L- α -methyltyrosine
L- α -methylvaline	L-N-methylhomophenylalanine
N-(N-(2,2-diphenylethyl carbamylmethyl)glycine	N-(N-(3,3-diphenylpropyl carbamylmethyl)glycine
1-carboxy-1-(2,2-diphenyl-ethyl amino)cyclopropane	

The invention also contemplates modifying the synthetic polypeptides of the invention using ordinary molecular biological techniques so as to alter their resistance to proteolytic degradation or to optimise solubility properties or to render them more suitable as an immunogenic agent.

3. Preparation of synthetic polynucleotides of the invention

The invention contemplates synthetic polynucleotides encoding the synthetic polypeptides as for example described in Section 2 *supra*. Polynucleotides encoding segments of a parent polypeptide can be produced by any suitable technique. For example, such polynucleotides can be synthesised *de novo* using readily available machinery.

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Sequential synthesis of DNA is described, for example, in U.S. Patent No 4,293,652. Instead of *de novo* synthesis, recombinant techniques may be employed including use of restriction endonucleases to cleave a polynucleotide encoding at least a segment of the parent polypeptide and use of ligases to ligate together in frame a plurality of cleaved
5 polynucleotides encoding different segments of the parent polypeptide. Suitable recombinant techniques are described for example in the relevant sections of Ausubel, *et al. (supra)* and of Sambrook, *et al., (supra)* which are incorporated herein by reference. Preferably, the synthetic polynucleotide is constructed using splicing by overlapping extension (SOEing) as for example described by Horton *et al.* (1990, *Biotechniques* 8(5):
10 528-535; 1995, *Mol Biotechnol.* 3(2): 93-99; and 1997, *Methods Mol Biol.* 67: 141-149). However, it should be noted that the present invention is not dependent on, and not directed to, any one particular technique for constructing the synthetic construct.

Various modifications to the synthetic polynucleotides may be introduced as a means of increasing intracellular stability and half-life. Possible modifications include but
15 are not limited to the addition of flanking sequences of ribo- or deoxy- nucleotides to the 5' and/or 3' ends of the molecule or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the oligodeoxyribonucleotide backbone.

The invention therefore contemplates a method of producing a synthetic polynucleotide as broadly described above, comprising linking together in the same
20 reading frame at least two nucleic acid sequences encoding different segments of a parent polypeptide to form a synthetic polynucleotide, which encodes a synthetic polypeptide according to the invention. Suitably, nucleic acid sequences encoding at least 10 segments, preferably at least 20 segments, more preferably at least 40 segments and more preferably at least 100 segments of a parent polypeptide are employed to produce the synthetic
25 polynucleotide.

Preferably, the method further comprises selecting segments of the parent polypeptide, reverse translating the selected segments and preparing nucleic acid sequences encoding the selected segments. It is preferred that the method further comprises randomly linking the nucleic acid sequences together to form the synthetic polynucleotide.
30 The nucleic acid sequences may be oligonucleotides or polynucleotides.

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Suitably, segments are selected on the basis of size. Additionally, or in the alternative, segments are selected such that they have partial sequence identity or homology (*i.e.*, sequence overlap) with one or more other segments. A number of factors can influence segment size and sequence overlap as mentioned above. In the case of
5 sequence overlap, large amounts of duplicated nucleic acid sequences can sometimes result in sections of nucleic acid being lost during nucleic acid amplification (*e.g.*, polymerase chain reaction, PCR) of such sequences, recombinant plasmid propagation in a bacterial host or during amplification of recombinant viruses containing such sequences. Accordingly, in a preferred embodiment, nucleic acid sequences encoding segments having
10 sequence identity or homology with one or more other encoded segments are not linked together in an arrangement in which the identical or homologous sequences are contiguous. Also, it is preferable that different codons are used to encode a specific amino acid in a duplicated region. In this context, an amino acid of a parent polypeptide sequence is preferably reverse translated to provide a codon which, in the context of adjacent or local
15 sequence elements, has a lower propensity of forming an undesirable sequence (*e.g.*, a duplicated sequence or a palindromic sequence) that is refractory to the execution of a task (*e.g.*, cloning or sequencing). Alternatively, segments may be selected such that they contain a carboxyl terminal leucine residue or such that reverse translated sequences encoding the segments contain restriction enzyme sites for convenient splicing of the
20 reverse translated sequences.

The method optionally further comprises linking a spacer oligonucleotide encoding at least one spacer residue between segment-encoding nucleic acids. Such spacer residue(s) may be advantageous in ensuring that epitopes within the segments are processed and presented efficiently. Preferably, the spacer oligonucleotide encodes 2 to 3
25 spacer residues. The spacer residue is suitably a neutral amino acid, which is preferably alanine.

Optionally, the method further comprises linking in the same reading frame as other segment-containing nucleic acid sequences at least one variant nucleic acid sequence which encodes a variant segment having a homologous but not identical amino acid
30 sequence relative to other encoded segments. Suitably, the variant segment comprises conserved and/or non-conserved amino acid differences relative to one or more other encoded segments. Such differences may correspond to polymorphisms as discussed

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above. In a preferred embodiment, degenerate bases are designed or built in to the at least one variant nucleic acid sequence to give rise to all desired homologous sequences.

When a large number of polymorphisms is intended to be covered, it is preferred that multiple synthetic polynucleotides are constructed rather than a single synthetic polynucleotide, which encodes all variant segments. For example, if there is less than 85% homology between polymorphic polypeptides, then it is preferred that more than one synthetic polynucleotide is constructed.

Preferably, the method further comprises optimising the codon composition of the synthetic polynucleotide such that it is translated efficiently by a host cell. In this regard, it is well known that the translational efficiency of different codons varies between organisms and that such differences in codon usage can be utilised to enhance the level of protein expression in a particular organism. In this regard, reference may be made to Seed *et al.* (International Application Publication No WO 96/09378) who disclose the replacement of existing codons in a parent polynucleotide with synonymous codons to enhance expression of viral polypeptides in mammalian host cells. Preferably, the first or second most frequently used codons are employed for codon optimisation.

Preferably, gene splicing by overlap extension or "gene SOEing" (*supra*) is employed for the construction of the synthetic polynucleotide which is a PCR-based method of recombining DNA sequences without reliance on restriction sites and of directly generating mutated DNA fragments *in vitro*. By modifying the sequences incorporated into the 5'-ends of the primers, any pair of PCR products can be made to share a common sequence at one end. Under PCR conditions, the common sequence allows strands from two different fragments to hybridise to one another, forming an overlap. Extension of this overlap by DNA polymerase yields a recombinant molecule. However, a problem with long synthetic constructs is that mutations generally incorporate into amplified products during synthesis. In this instance, it is preferred that resolvase treatment is employed at various steps of the synthesis. Resolvases are bacteriophage-encoded endonucleases which recognise disruptions or mispairing of double stranded DNA and are primarily used by bacteriophages to resolve Holliday junctions (Mizuuchi, 1982; Youil *et al.*, 1995). For example, T7 endonuclease I can be employed in synthetic DNA constructions to recognise mutations and cleave corrupted dsDNA. The mutated DNA strands are then hybridised to

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non-mutant or correct DNA sequences, which results in a mispairing of DNA bases. The mispaired bases are recognised by the resolvase, which then cleaves the DNA nearby leaving only correctly hybridised sequences intact. Preferably a thermostable resolvase enzyme is employed during splicing or amplification so that errors are not incorporated in downstream synthesis products.

Synthetic polynucleotides according to the invention can be operably linked to a regulatory polynucleotide in the form a synthetic construct as for example described in Section 2 *supra*. Synthetic constructs of the invention have utility *inter alia* as nucleic acid vaccines. The choice of regulatory polynucleotide and synthetic construct will depend on the intended host.

Exemplary expression vectors for expression of a synthetic polypeptide according to the invention include, but are not restricted to, modified Ankara Vaccinia virus as for example described by Allen *et al.* (2000, *J. Immunol.* **164**(9): 4968-4978), fowlpox virus as for example described by Boyle and Coupar (1988, *Virus Res.* **10**: 343-356) and the herpes simplex amplicons described for example by Fong *et al.* in U.S. Patent No. 6,051,428. Alternatively, Adenovirus and Epstein-Barr virus vectors, which are preferably capable of accepting large amounts of DNA or RNA sequence information, can be used.

Preferred promoter sequences that can be utilised for expression of synthetic polypeptides include the P7.5 or PE/L promoters as for example disclosed by Kumar and Boyle. (1990, *Virology* **179**: 151-158), CMV and RSV promoters.

The synthetic construct optionally further includes a nucleic acid sequence encoding an immunostimulatory molecule. The immunostimulatory molecule may be fusion partner of the synthetic polypeptide. Alternatively, the immunostimulatory molecule may be translated separately from the synthetic polypeptide. Preferably, the immunostimulatory molecule comprises a general immunostimulatory peptide sequence. For example, the immunostimulatory peptide sequence may comprise a domain of an invasin protein (Inv) from the bacteria *Yersinia* spp as for example disclosed by Brett *et al.* (1993, *Eur. J. Immunol.* **23**: 1608-1614). This immune stimulatory property results from the capability of this invasin domain to interact with the $\beta 1$ integrin molecules present on T cells, particularly activated immune or memory T cells. A preferred embodiment of the invasin domain (Inv) for linkage to a synthetic polypeptide has been previously described

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in U.S. Pat. No. 5,759,551. The said Inv domain has the sequence: Thr-Ala-Lys-Ser-Lys-Lys-Phe-Pro-Ser-Tyr-Thr-Ala-Thr-Tyr-Gln-Phe [SEQ ID NO; 1467] or is an immune stimulatory homologue thereof from the corresponding region in another *Yersinia* species invasin protein. Such homologues thus may contain substitutions, deletions or insertions of amino acid residues to accommodate strain to strain variation, provided that the homologues retain immune stimulatory properties. The general immunostimulatory sequence may optionally be linked to the synthetic polypeptide by a spacer sequence.

In an alternate embodiment, the immunostimulatory molecule may comprise an immunostimulatory membrane or soluble molecule, which is suitably a T cell co-stimulatory molecule. Preferably, the T cell co-stimulatory molecule is a B7 molecule or a biologically active fragment thereof, or a variant or derivative of these. The B7 molecule includes, but is not restricted to, B7-1 and B7-2. Preferably, the B7 molecule is B7-1. Alternatively, the T cell co-stimulatory molecule may be an ICAM molecule such as ICAM-1 and ICAM-2.

In another embodiment, the immunostimulatory molecule can be a cytokine, which includes, but is not restricted to, an interleukin, a lymphokine, tumour necrosis factor and an interferon. Alternatively, the immunostimulatory molecule may comprise an immunomodulatory oligonucleotide as for example disclosed by Krieg in U.S. Patent No. 6,008,200.

Suitably, the size of the synthetic polynucleotide does not exceed the ability of host cells to transcribe, translate or proteolytically process and present epitopes to the immune system. Practitioners in the art will also recognise that the size of the synthetic polynucleotide can impact on the capacity of an expression vector to express the synthetic polynucleotide in a host cell. In this connection, it is known that the efficacy of DNA vaccination reduces with expression vectors greater than 20-kb. In such situations it is preferred that a larger number of smaller synthetic constructs is utilised rather than a single large synthetic construct.

4. Immunopotentiating compositions

The invention also contemplates a composition, comprising an immunopotentiating agent selected from the group consisting of a synthetic polypeptide as

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described in Section 2, and a synthetic polynucleotide or a synthetic construct as described in Section 3, together with a pharmaceutically acceptable carrier. One or more immunopotentiating agents can be used as actives in the preparation of immunopotentiating compositions. Such preparation uses routine methods known to persons skilled in the art. Typically, such compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid prior to injection may also be prepared. The preparation may also be emulsified. The active immunogenic ingredients are often mixed with excipients that are pharmaceutically acceptable and compatible with the active ingredient. Suitable excipients are, for example, water, saline, dextrose, glycerol, ethanol, or the like and combinations thereof. In addition, if desired, the vaccine may contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents, and/or adjuvants that enhance the effectiveness of the vaccine. Examples of adjuvants which may be effective include but are not limited to: aluminium hydroxide, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thur-MDP), N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine (CGP 11637, referred to as nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (CGP 1983A, referred to as MTP-PE), and RIBI, which contains three components extracted from bacteria, monophosphoryl lipid A, trehalose dimycolate and cell wall skeleton (MPL+TDM+CWS) in a 2% squalene/Tween 80 emulsion. For example, the effectiveness of an adjuvant may be determined by measuring the amount of antibodies resulting from the administration of the composition, wherein those antibodies are directed against one or more antigens presented by the treated cells of the composition.

The immunopotentiating agents may be formulated into a composition as neutral or salt forms. Pharmaceutically acceptable salts include the acid addition salts (formed with free amino groups of the peptide) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids such as acetic, oxalic, tartaric, maleic, and the like. Salts formed with the free carboxyl groups may also be derived from inorganic basis such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic basis as isopropylamine, trimethylamine, 2-ethylamino ethanol, histidine, procaine, and the like.

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If desired, devices or compositions containing the immunopotentiating agents suitable for sustained or intermittent release could be, in effect, implanted in the body or topically applied thereto for the relatively slow release of such materials into the body.

The compositions are conventionally administered parenterally, by injection, for example, either subcutaneously or intramuscularly. Additional formulations which are suitable for other modes of administration include suppositories and, in some cases, oral formulations. For suppositories, traditional binders and carriers may include, for example, polyalkylene glycols or triglycerides; such suppositories may be formed from mixtures containing the active ingredient in the range of 0.5% to 10%, preferably 1%-2%. Oral formulations include such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium carbonate, and the like. These compositions take the form of solutions, suspensions, tablets, pills, capsules, sustained release formulations or powders and contain 10%-95% of active ingredient, preferably 25%-70%.

Administration of the gene therapy construct to said mammal, preferably a human, may include delivery via direct oral intake, systemic injection, or delivery to selected tissue(s) or cells, or indirectly via delivery to cells isolated from the mammal or a compatible donor. An example of the latter approach would be stem cell therapy, wherein isolated stem cells having potential for growth and differentiation are transfected with the vector comprising the *Sox18* nucleic acid. The stem cells are cultured for a period and then transferred to the mammal being treated.

With regard to nucleic acid based compositions, all modes of delivery of such compositions are contemplated by the present invention. Delivery of these compositions to cells or tissues of an animal may be facilitated by microprojectile bombardment, liposome mediated transfection (e.g., lipofectin or lipofectamine), electroporation, calcium phosphate or DEAE-dextran-mediated transfection, for example. In an alternate embodiment, a synthetic construct may be used as a therapeutic or prophylactic composition in the form of a "naked DNA" composition as is known in the art. A discussion of suitable delivery methods may be found in Chapter 9 of CURRENT PROTOCOLS IN MOLECULAR BIOLOGY (Eds. Ausubel *et al.*; John Wiley & Sons Inc., 1997 Edition) or on the Internet site DNA vaccine.com. The compositions may be administered by intradermal (e.g., using panjet™ delivery) or intramuscular routes.

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The step of introducing the synthetic polynucleotide into a target cell will differ depending on the intended use and species, and can involve one or more of non-viral and viral vectors, cationic liposomes, retroviruses, and adenoviruses such as, for example, described in Mulligan, R.C., (1993 *Science* **260** 926-932) which is hereby incorporated by
5 reference. Such methods can include, for example:

- A. Local application of the synthetic polynucleotide by injection (Wolff *et al.*, 1990, *Science* **247** 1465-1468, which is hereby incorporated by reference), surgical implantation, instillation or any other means. This method can also be used in combination with local application by injection, surgical implantation, instillation or
10 any other means, of cells responsive to the protein encoded by the synthetic polynucleotide so as to increase the effectiveness of that treatment. This method can also be used in combination with local application by injection, surgical implantation, instillation or any other means, of another factor or factors required for the activity of said protein.
- 15 B. General systemic delivery by injection of DNA, (Calabretta *et al.*, 1993, *Cancer Treat. Rev.* **19** 169-179, which is incorporated herein by reference), or RNA, alone or in combination with liposomes (Zhu *et al.*, 1993, *Science* **261** 209-212, which is incorporated herein by reference), viral capsids or nanoparticles (Bertling *et al.*, 1991, *Biotech. Appl. Biochem.* **13** 390-405, which is incorporated herein by reference) or any
20 other mediator of delivery. Improved targeting might be achieved by linking the synthetic polynucleotide to a targeting molecule (the so-called "magic bullet" approach employing, for example, an antibody), or by local application by injection, surgical implantation or any other means, of another factor or factors required for the activity of the protein encoding said synthetic polynucleotide , or of cells responsive to said
25 protein.
- C. Injection or implantation or delivery by any means, of cells that have been modified *ex vivo* by transfection (for example, in the presence of calcium phosphate: Chen *et al.*, 1987, *Mole. Cell Biochem.* **7** 2745-2752, or of cationic lipids and polyamines: Rose *et al.*, 1991, *BioTech.* **10** 520-525, which articles are incorporated herein by reference),
30 infection, injection, electroporation (Shigekawa *et al.*, 1988, *BioTech.* **6** 742-751, which is incorporated herein by reference) or any other way so as to increase the

expression of said synthetic polynucleotide in those cells. The modification can be mediated by plasmid, bacteriophage, cosmid, viral (such as adenoviral or retroviral; Mulligan, 1993, *Science* **260** 926-932; Miller, 1992, *Nature* **357** 455-460; Salmons *et al.*, 1993, *Hum. Gen. Ther.* **4** 129-141, which articles are incorporated herein by reference) or other vectors, or other agents of modification such as liposomes (Zhu *et al.*, 1993, *Science* **261** 209-212, which is incorporated herein by reference), viral capsids or nanoparticles (Bertling *et al.*, 1991, *Biotech. Appl. Biochem.* **13** 390-405, which is incorporated herein by reference), or any other mediator of modification. The use of cells as a delivery vehicle for genes or gene products has been described by Barr *et al.*, 1991, *Science* **254** 1507-1512 and by Dhawan *et al.*, 1991, *Science* **254** 1509-1512, which articles are incorporated herein by reference. Treated cells can be delivered in combination with any nutrient, growth factor, matrix or other agent that will promote their survival in the treated subject.

Also encapsulated by the present invention is a method for treatment and/or prophylaxis of a disease or condition, comprising administering to a patient in need of such treatment a therapeutically effective amount of a composition as broadly described above. The disease or condition may be caused by a pathogenic organism or a cancer as for example described above.

In a preferred embodiment, the immunopotentiating composition of the invention is suitable for treatment of, or prophylaxis against, a cancer. Cancers which could be suitably treated in accordance with the practices of this invention include cancers of the lung, breast, ovary, cervix, colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone liver, oesophagus, brain, testicle, uterus, melanoma and the various leukemias and lymphomas.

In an alternate embodiment, the immunopotentiating composition is suitable for treatment of, or prophylaxis against, a viral, bacterial or parasitic infection. Viral infections contemplated by the present invention include, but are not restricted to, infections caused by HIV, Hepatitis, Influenza, Japanese encephalitis virus, Epstein-Barr virus and respiratory syncytial virus. Bacterial infections include, but are not restricted to, those caused by *Neisseria* species, *Meningococcal* species, *Haemophilus* species *Salmonella* species, *Streptococcal* species, *Legionella* species and *Mycobacterium* species. Parasitic

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infections encompassed by the invention include, but are not restricted to, those caused by *Plasmodium* species, *Schistosoma* species, *Leishmania* species, *Trypanosoma* species, *Toxoplasma* species and *Giardia* species.

The above compositions or vaccines may be administered in a manner compatible
5 with the dosage formulation, and in such amount as is therapeutically effective to alleviate patients from the disease or condition or as is prophylactically effective to prevent incidence of the disease or condition in the patient. The dose administered to a patient, in the context of the present invention, should be sufficient to effect a beneficial response in a patient over time such as a reduction or cessation of blood loss. The quantity of the
10 composition or vaccine to be administered may depend on the subject to be treated inclusive of the age, sex, weight and general health condition thereof. In this regard, precise amounts of the composition or vaccine for administration will depend on the judgement of the practitioner. In determining the effective amount of the composition or vaccine to be administered in the treatment of a disease or condition, the physician may
15 evaluate the progression of the disease or condition over time. In any event, those of skill in the art may readily determine suitable dosages of the composition or vaccine of the invention.

In a preferred embodiment, DNA-based immunopotentiating agent (*e.g.*, 100 μ g) is delivered intradermally into a patient at day 1 and at week 8 to prime the patient. A
20 recombinant poxvirus (*e.g.*, at 10^7 pfu/mL) from which substantially the same immunopotentiating agent can be expressed is then delivered intradermally as a booster at weeks 16 and 24, respectively.

The effectiveness of the immunisation may be assessed using any suitable technique. For example, CTL lysis assays may be employed using stimulated splenocytes
25 or peripheral blood mononuclear cells (PBMC) on peptide coated or recombinant virus infected cells using ^{51}Cr labelled target cells. Such assays can be performed using for example primate, mouse or human cells (Allen *et al.*, 2000, *J. Immunol.* 164(9): 4968-4978 also Woodberry *et al.*, *infra*). Alternatively, the efficacy of the immunisation may be monitored using one or more techniques including, but not limited to, HLA class I
30 Tetramer staining - of both fresh and stimulated PBMCs (see for example Allen *et al.*, *supra*), proliferation assays (Allen *et al.*, *supra*), Elispot™ Assays and intracellular INF-

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gamma staining (Allen *et al.*, *supra*), ELISA Assays - for linear B cell responses; and Western blots of cell sample expressing the synthetic polynucleotides.

5. *Computer related embodiments*

The design or construction of a synthetic polypeptide sequence or a synthetic polynucleotide sequence according to the invention is suitably facilitated with the assistance of a computer programmed with software, which *inter alia* fragments a parent sequence into fragments, and which links those fragments together in a different relationship relative to their linkage in the parent sequence. The ready use of a parent sequence for the construction of a desired synthetic molecule according to the invention requires that it be stored in a computer-readable format. Thus, in accordance with the present invention, sequence data relating to a parent molecule (*e.g.*, a parent polypeptide) is stored in a machine-readable storage medium, which is capable of processing the data to fragment the sequence of the parent molecule into fragments and to link together the fragments in a different relationship relative to their linkage in the parent molecule.

Therefore, another embodiment of the present invention provides a machine-readable data storage medium, comprising a data storage material encoded with machine readable data which, when used by a machine programmed with instructions for using said data, fragments a parent sequence into fragments, and links those fragments together in a different relationship relative to their linkage in the parent sequence. In a preferred embodiment of this type, a machine-readable data storage medium is provided that is capable of reverse translating the sequence of a respective fragment to provide a nucleic acid sequence encoding the fragment and to link together in the same reading frame each of the nucleic acid sequences to provide a polynucleotide sequence that codes for a polypeptide sequence in which said fragments are linked together in a different relationship relative to their linkage in a parent polypeptide sequence.

In another embodiment, the invention encompasses a computer for designing the sequence of a synthetic polypeptide and/or a synthetic polynucleotide of the invention, wherein the computer comprises wherein said computer comprises: (a) a machine readable data storage medium comprising a data storage material encoded with machine readable data, wherein said machine readable data comprises the sequence of a parent polypeptide; (b) a working memory for storing instructions for processing said machine-readable data;

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(c) a central-processing unit coupled to said working memory and to said machine-readable data storage medium, for processing said machine-readable data into said synthetic polypeptide sequence and/or said synthetic polynucleotide; and (d) an output hardware coupled to said central processing unit, for receiving said synthetic polypeptide sequence
5 and/or said synthetic polynucleotide.

In yet another embodiment, the invention contemplates a computer program product for designing the sequence of a synthetic polynucleotide of the invention, comprising code that receives as input the sequence of a parent polypeptide, code that fragments the sequence of the parent polypeptide into fragments, code that reverse
10 translates the sequence of a respective fragment to provide a nucleic acid sequence encoding the fragment, code that links together in the same reading frame each said nucleic acid sequence to provide a polynucleotide sequence that codes for a polypeptide sequence in which said fragments are linked together in a different relationship relative to their linkage in the parent polypeptide sequence, and a computer readable medium that stores
15 the codes.

A version of these embodiments is presented in Figure 23, which shows a system
10 including a computer 11 comprising a central processing unit ("CPU") 20, a working memory 22 which may be, *e.g.*, RAM (random-access memory) or "core" memory, mass storage memory 24 (such as one or more disk drives or CD-ROM drives), one or more
20 cathode-ray tube ("CRT") display terminals 26, one or more keyboards 28, one or more input lines 30, and one or more output lines 40, all of which are interconnected by a conventional bidirectional system bus 50.

Input hardware 36, coupled to computer 11 by input lines 30, may be implemented in a variety of ways. For example, machine-readable data of this invention
25 may be inputted via the use of a modem or modems 32 connected by a telephone line or dedicated data line 34. Alternatively or additionally, the input hardware 36 may comprise CD. Alternatively, ROM drives or disk drives 24 in conjunction with display terminal 26, keyboard 28 may also be used as an input device.

Output hardware 46, coupled to computer 11 by output lines 40, may similarly be
30 implemented by conventional devices. By way of example, output hardware 46 may include CRT display terminal 26 for displaying a synthetic polynucleotide sequence or a synthetic polypeptide sequence as described herein. Output hardware might also include a

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printer 42, so that hard copy output may be produced, or a disk drive 24, to store system output for later use.

In operation, CPU 20 coordinates the use of the various input and output devices 36,46 coordinates data accesses from mass storage 24 and accesses to and from working
5 memory 22, and determines the sequence of data processing steps. A number of programs may be used to process the machine readable data of this invention. Exemplary programs may use for example the steps outlined in the flow diagram illustrated in Figure 24. Broadly, these steps include (1) inputting at least one parent polypeptide sequence; (2) optionally adding to alanine spacers at the ends of each polypeptide sequence; (3)
10 fragmenting the polypeptide sequences into fragments (*e.g.*, 30 amino acids long), which are preferably overlapping (*e.g.*, by 15 amino acids); (4) reverse translating the fragment to provide a nucleic acid sequence for each fragment and preferably using for the reverse translation first and second most translationally efficient codons for a cell type, wherein the codons are preferably alternated out of frame with each other in the overlaps of
15 consecutive fragments; (5) randomly rearranging the fragments; (6) checking whether rearranged fragments recreate at least a portion of a parent polypeptide sequence; (7) repeating randomly rearranging the fragments when rearranged fragments recreate said at least a portion; or otherwise (8) linking the rearranged fragments together to produce a synthetic polypeptide sequence and/or a synthetic polynucleotide sequence; and (9)
20 outputting said synthetic polypeptide sequence and/or a synthetic polynucleotide sequence. An example of an algorithm which uses *inter alia* the aforementioned steps is shown in Figure 25. By way of example, this algorithm has been used for the design of synthetic polynucleotides and synthetic polypeptides according to the present invention for Hepatitis C 1a and for melanoma, as illustrated in Figures 26 and 27.

25 Figure 28 shows a cross section of a magnetic data storage medium 100 which can be encoded with machine readable data, or set of instructions, for designing a synthetic molecule of the invention, which can be carried out by a system such as system 10 of Figure 23. Medium 100 can be a conventional floppy diskette or hard disk, having a suitable substrate 101, which may be conventional, and a suitable coating 102, which may
30 be conventional, on one or both sides, containing magnetic domains (not visible) whose polarity or orientation can be altered magnetically. Medium 100 may also have an opening (not shown) for receiving the spindle of a disk drive or other data storage device 24. The

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magnetic domains of coating 102 of medium 100 are polarised or oriented so as to encode in manner which may be conventional, machine readable data such as that described herein, for execution by a system such as system 10 of Figure 23.

Figure 29 shows a cross section of an optically readable data storage medium 110 which also can be encoded with such a machine-readable data, or set of instructions, for designing a synthetic molecule of the invention, which can be carried out by a system such as system 10 of Figure 23. Medium 110 can be a conventional compact disk read only memory (CD-ROM) or a rewritable medium such as a magneto-optical disk, which is optically readable and magneto-optically writable. Medium 100 preferably has a suitable substrate 111, which may be conventional, and a suitable coating 112, which may be conventional, usually of one side of substrate 111.

In the case of CD-ROM, as is well known, coating 112 is reflective and is impressed with a plurality of pits 113 to encode the machine-readable data. The arrangement of pits is read by reflecting laser light off the surface of coating 112. A protective coating 114, which preferably is substantially transparent, is provided on top of coating 112.

In the case of a magneto-optical disk, as is well known, coating 112 has no pits 113, but has a plurality of magnetic domains whose polarity or orientation can be changed magnetically when heated above a certain temperature, as by a laser (not shown). The orientation of the domains can be read by measuring the polarisation of laser light reflected from coating 112. The arrangement of the domains encodes the data as described above.

In order that the invention may be readily understood and put into practical effect, particular preferred non-limiting embodiments will now be described as follows.

EXAMPLES

EXAMPLE 1

Preparation of an HIV Savine

Experimental Protocol

5 *Plasmids*

The plasmid pDNAVacc is ampicillin resistant and contains an expression cassette comprising a CMV promoter and enhancer, a synthetic intron, a multiple cloning site (MCS) and a SV40poly A signal sequence (Thomson *et al.*, 1998). The plasmid pTK7.5 and contains a selection cassette, a pox virus 7.5 early/late promoter and a MCS
10 flanked on either side by Vaccinia virus TK gene sequences.

Recombinant Vaccinia Viruses

Recombinant Vaccinia viruses expressing the *gag*, *env* (IIB) and *pol* (LAI) genes of HIV-1 were used as previously described and denoted VV-GAG, VV-POL, VV-ENV (Woodberry *et al.*, 1999; Kent *et al.*, 1998).

15 *Marker Rescue Recombination*

Recombinant Vaccinia viruses containing Savine constructs were generated by marker rescue recombination, using protocols described previously (Boyle *et al.*, 1985). Plaque purified viruses were tested for the TK phenotype and for the appropriate genome arrangement by Southern blot and PCR.

20 *Oligonucleotides*

Oligonucleotides 50 nmol scale and desalted were purchased from Life Technologies. Short oligonucleotides were resuspended in 100 µL of water, their concentration determined, then diluted to 20 µM for use in PCR or sequencing reactions. Long oligonucleotides for splicing reactions were denatured for 5 minutes at 94°C in
25 20 µL of formamide loading buffer then 0.5 µL gel purified on a 6% polyacrylamide gel.

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Gel slices containing full-length oligonucleotides were visualised with ethidium bromide, excised, placed in Eppendorf™ tubes, combined with 200 µL of water before being crushed using the plunger of a 1 mL syringe. Before being used in splicing reactions the crushed gel was resuspended in an appropriate volume of buffer and 1-2 µL of the
5 resuspendate used directly in the splicing reactions.

Sequencing

Sequencing was performed using Dye terminator sequencing reactions and analyzed by the Biomedical Resource Facility at the John Curtin School of Medical Research using an ABI automated sequencer.

10 *Restimulation of Lymphocytes from HIV Infected Patients*

Two pools of recombinant Vaccinia viruses containing VV-AC1 + VV-BC1 (Pool 1) or VV-AC2 + VV-BC2 + VV-CC2 (Pool 2) were used to restimulate lymphocytes from the blood samples of HIV-infected patients. Briefly CTL lines were generated from HIV-infected donor PBMC. A fifth of the total PBMC were infected with either Pool 1 or Pool 2
15 Vaccinia viruses then added back to the original cell suspension. The infected cell suspension was then cultured with IL-7 for 1 week.

CTL Assays

Restimulated PBMCs were used as effectors in a standard ⁵¹Cr-release CTL assay. Targets were autologous EBV-transformed lymphoblastoid cell lines (LCLs) infected with
20 the following viruses : Pool 1, Pool 2, VV-GAG, VV-POL or VV-ENV. Assay controls included uninfected targets, targets infected with VV-lacZ (virus control) and K562 cells.

Results

HIV Savine Design

A main goal of the Savine strategy is to include as much protein sequence
25 information from a pathogen or cancer as possible in such a way that potential T cell epitopes remain intact and so that the vaccine or therapy is extremely safe. An HIV Savine is described herein not only to compare this strategy to other strategies but also, to produce

an HIV vaccine that would provide the maximum possible population coverage as well as catering for the major HIV clades.

A number of design criteria was first determined to exploit the many advantages of using a synthetic approach. One advantage is that it is possible to use consensus protein sequences to design these vaccines. Using consensus sequences for a highly variable virus like HIV should provide better vaccine coverage because individual viral isolate sequences may have lost epitopes which induce CTL against the majority of other viral isolates. Thus, using the consensus sequences of each HIV clade rather than individual isolate sequences should provide better vaccine coverage. Taking this one step further, a consensus sequence that covers all HIV clades should theoretically provide better coverage than using just the consensus sequences for individual clades. Before designing such a sequence however, it was decided that a more appropriate and focussed HIV vaccine might be constructed if the various clades were first ranked according to their relative importance. To establish such a ranking the following issues were considered, current prevalence of each clade, the rate at which each clade is increasing and the capacity of various regions of the world to cope with the HIV pandemic (Figures 1 and 2). These criteria produced the following ranking, Clade E \geq clade A > clade C > clade B > clade D > other clades. Clades E and A were considered to almost equal since they are very similar except in their envelope protein sequences, which differ considerably.

Another advantage of synthesising a designed sequence is that it is possible to incorporate degenerate sequences into their design. In the case of HIV, this means that more than one amino acid can be included at various positions to improve the ability of the vaccine to cater for the various HIV clades and isolates. Coverage is improved because mutations in different HIV clades and also in individual isolate sequences, while mostly destroying specific T cell epitopes, can result in the formation of new potentially useful epitopes nearby (Goulder *et al.*, 1997). Incorporating degenerate amino acid sequences, however, also means that more than one construct must be made and mixed together. The number of constructs required depends on the frequency with which mutations are incorporated into the design. While this approach requires the construction of additional constructs, these constructs can be prepared from the same set of degenerate long oligonucleotides, significantly reducing the cost of providing such considerable interclade coverage.

A set of degeneracy rules was developed for the incorporation of amino acid mutations into the design which meant that a maximum of eight constructs would be required so that theoretically all combinations were present, as follows: 1) Two amino acids at three positions (or less) within any group of nine amino acids (*i.e.*, present in a CTL epitope); 2) Three amino acids at one position and two at another (or not) within any group of nine amino acids; 3) Four amino acids at one position and two at another (or not) within any group of nine amino acids. The reason why these rules were applied to nine amino acids (the average CTL epitope size) and not to larger stretches of amino acid sequence to cater for class II restricted epitopes, is because class II-restricted epitopes generally have a core sequence of nine amino acids in the middle which bind specifically to class II MHC molecules with the extra flanking sequences stabilising binding, by associating with either side of class II MHC antigens in a largely sequence independent manner (Brown *et al.*, 1993).

Using the HIV clade ranking described above, the amino acid degeneracy rules and in some situations the similarity between amino acids, a degenerate consensus protein sequence was designed for each HIV protein using the consensus protein sequences for each HIV clade compiled by the Los Alamos HIV sequence database (Figures 3-11) (HIV Molecular Immunology Database, 1997). It is important to note that in some situations the order with which each of the above design criteria was applied was altered. Each time this was done the primary goal however was to increase the ability of the vaccine to cater for interclade differences. Two isolate sequences, GenBank accession U51189 and U46016, for clade E and clade C, respectively, were used when a consensus sequence for some HIV proteins from these two clades was unavailable (Gao *et al.*, 1996; Salminen *et al.*, 1996). The design of a consensus sequence for the hypervariable regions of the HIV envelope protein and in some cases between these regions (hypervariable regions 1-2 and 3-5) was difficult and so these regions were excluded from the vaccine design.

Once a degenerate consensus sequence was designed for each HIV protein, an approach was then determined for incorporating all the protein sequences safely into the vaccine. One convenient approach to ensure that a vaccine will be safe is to systematically fragment and randomly rearrange the protein sequences together thus abrogating or otherwise altering their structure and function. The protein sequences still have to be immunologically functional however, meaning that the process used to fragment the

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sequences should not destroy potential epitopes. To decide on the best approach for systematically fragmenting protein sequences, the main criteria used was the size of T epitopes and their processing requirements. Class I-restricted T cell epitopes are 8-10 amino acids long and generally require 2-3 natural flanking amino acids to ensure their efficient processing and presentation if placed next to unnatural flanking residues (Del Val *et al.*, 1991; Thomson *et al.*, 1995). Class II-restricted T cell epitopes range between 12-25 amino acids long and do appear to require natural flanking residues for processing however, it is difficult to rule out a role for natural flanking residues in all cases due to the complexity of their processing pathways (Thomson *et al.*, 1998). Also class II-restricted epitopes despite being larger than CTL epitopes generally have a core sequence of 9-10 amino acids, which binds to MHC molecules in a sequence specific fashion. Thus, based on current knowledge, it was decided that an advantageous approach was to overlap the fragments by at least 15 amino acids to ensure that potential epitopes which might lie across fragment boundaries are not lost and to ensure that CTL epitopes near fragment boundaries, that are placed beside or near inhibitory amino acids in adjacent fragments, are processed efficiently. In deciding the optimal fragment size, the main criteria used were that size had to be small enough to cause the maximum disruption to the structure and function of proteins but large enough to cover the sequence information as efficiently as possible without any further unnecessary duplication. Based on these criteria the fragments would be twice the overlap size, in this case 30 amino acids long.

The designed degenerate protein sequences were then separated into fragments 30 amino acid long and overlapping by fifteen amino acids. Two alanine amino acids were also added to the start and end of the first and last fragment for each protein or envelop protein segment to ensure these fragments were not placed directly adjacent to amino acids capable of blocking epitope processing (Del Val *et al.*, 1991). The next step was to reverse translate each protein sequence back into DNA. Duplicating DNA sequences was avoided when constructing DNA sequences encoding a tandem repeat of identical or homologous amino acid sequences to maximise expression of the Savine. In this regard, the first and second most commonly used mammalian codons (shown in Figure 12) were assigned to amino acids in these repeat regions, wherein a first codon was used to encode an amino acid in one of the repeated sequences and wherein a second but synonymous codon was used for the other repeated sequence (*e.g.*, see the gag HIV protein in Figure 13). To cater

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for the designed amino acid mutations more than one base was assigned to some positions using the IUPAC DNA codes without exceeding more than three base variations (eight possible combinations) in any group of 27 bases (Figure 12). Where a particular combination of amino acids could not be incorporated, because too many degenerate bases would be required, some or all of the amino acid degeneracy was removed according to the protein consensus design rules outlined above. Also the degenerate codons were checked to determine if they could encode a stop codon, if stop codons could not be avoided then the amino acid degeneracy was also simplified again according to the protein consensus design rules outlined above.

10 The designed DNA segments were then scrambled randomly and joined to create twenty-two subcassettes approximately 840 bp in size. Extra DNA sequences incorporating sites for one of the cohesive restriction enzymes *XbaI*, *SpeI*, *AvrII* or *NheI* and 3 additional base pairs (to cater for premature Taq polymerase termination) were then added to each end of each subcassette (Figure 14). Some of these extra DNA sequences also contained, 15 the cohesive restriction sites for *SaII* or *XhoI*, Kozak signal sequences and start or stop codons to enable the subcassettes to be joined and expressed either as three large cassettes or one full length protein (Figures 14 and 15).

In designing the HIV Savine one issue that required investigation was whether such a large DNA molecule would be fully expressed and whether epitopes encoded near 20 the end of the molecule would be efficiently presented to the immune system. The inventors also wished to show that mixing two or more degenerate Savine constructs together could induce T cell responses that recognise mutated sequences. To examine both issues DNA coding for a degenerate murine influenza nucleoprotein CTL epitope, NP365-373, which differs by two amino acids at positions 71 and 72 in influenza strain A/PR/8/34 25 compared to the A/NT/60/68 strain and restricted by H2-Db, was inserted before the last stop codon at the end of the HIV Savine design (Figure 15). An important and unusual characteristic of both of these naturally occurring NP365-373 sequences, which enabled the present inventors to examine the effectiveness of incorporating mutated sequences, is that they generate CTL responses which do not cross react with the alternate sequence 30 (Townsend *et al.*, 1986). This is an unusual characteristic because epitopes not destroyed by mutation usually induce CTL responses that cross-react.

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Up to ten long oligonucleotides up to 100 bases long and two short amplification oligonucleotides were synthesised to enable construction of each subcassette (Life Technologies). In designing each oligonucleotide the 3' end and in most cases also the 5' end had to be either a 'c' or a 'g' to ensure efficient extension during PCR splicing. The overlap region for each long oligonucleotide was designed to be at least 16 bp with approximately 50% G/C content. Also oligonucleotide overlaps were not placed where degenerate DNA bases coded for degenerate amino acids to avoid splicing difficulties later. Where this was too difficult some degenerate bases were removed according to the protein consensus design rules outlined above and indicated in Figure 12. Figure 16 shows an example of the oligonucleotides design for each subcassette.

Construction of the HIV Savine

Five of each group of ten designed oligonucleotides were spliced together using stepwise asymmetric PCR (Sandhu *et al.*, 1992) and Splicing by Overlap Extension (SOEing) (Figure 17a). Each subcassette was then PCR amplified, cloned into pBluescriptTM II KS⁻ using *Bam*HI/*Eco*RI and 16 individual clones sequenced. Mutations, deletions and insertions were present in the large majority of the clones for each subcassette, despite acrylamide gel purification of the long oligonucleotides. In order to construct a functional Savine with minimal mutations, two clones for each subcassette with no insertions or deletions and hence a complete open reading frame and with minimal numbers of non-designed mutations, were selected from the sixteen available. The subcassettes were then excised from their plasmids and joined by stepwise PCR-amplified ligation using the polymerase blend ElongaseTM (Life Technology), T4 DNA ligase and the cohesive restriction enzymes *Xba*I/*Spe*I/*Avr*II/*Nhe*I, to generate two copies of cassettes A, B and C as outlined in Figure 14 and shown in Figure 17b. Predicted sequences for these cassettes are shown in Figure 30. Each cassette was then reamplified by PCR with ElongaseTM, cloned into pBluescriptTM II KS⁻ and 3 of the resulting plasmid clones sequenced using 12 of the 36 sequencing primers designed to cover the full length construct. Clones with minimal or no further mutations were selected for transfer into plasmids for DNA vaccination or used to make recombinant poxviruses. A summary of the number of designed and non-designed mutations in each Savine construct is presented in Table 1.

TABLE 1Summary of mutations

Construct	No. aas	Number of mutations			
		Designed	Expected in 2 clones	Actual in 2 clones	Non-designed
Cassette A	1896	249	124	107	5 (AC1), 8 (AC2)
Cassette B	1184	260	130	124	11 (BC1), 4 (BC2)
Cassette C	1969	276	138	121	10 (CC1), 14 (CC2)
Full length	5742	785	392	352	26 (FL1), 26 (FL2)

Summary of the mutations present in the two full-length clones constructed as determined by sequencing. Includes the number of mutations designed, expected and actually present in the 2 clones and the number of non-designed mutations in each cassette and full-length clone.

HIV Savine DNA vaccines and Recombinant Vaccinia viruses

To test the immunological effectiveness of the HIV Savine constructs the cassette sequences were transferred into DNA vaccine and poxvirus vectors. These vectors when used either separately in immunological assays described below or together in a 'prime-boost' protocol which has been shown previously to generate strong T cell responses *in vivo* (Kent *et al.*, 1997).

DNA Vaccination plasmids were constructed by excising the cassettes from the selected plasmid clones with *XbaI/XhoI* (cassette A) or *XbaI/SaII* (cassettes B and C) and ligating them into pDNAVacc cut with *XbaI/XhoI* to create pDVAC1, pDVAC2, pDVBC1, pDVBC2, pDVCC1, pDVCC2, respectively (Figure 18a). These plasmids were then further modified by cloning into their *XbaI* site a DNA fragment excised using *XbaI/AvrII* from pTUMERA2 and encoding a synthetic endoplasmic reticulum (ER) signal sequence from the Adenovirus E1A protein (Persson *et al.*, 1980) (Figure 18a). ER signal sequences have been shown previously to enhance the presentation of both CTL and T helper epitopes *in vivo* (Ishioka, G.Y., 1999; Thomson *et al.*, 1998). The plasmids pDVERAC1, pDVERBC1, pDVERCC1 and pDVERAC2, pDVERBC2, pDVERCC2 were then mixed

together to create, plasmid pool 1 and pool 2 respectively. Each plasmid pool collectively encodes one copy of the designed full-length HIV Savine.

Plasmids to generate recombinant Vaccinia viruses which express HIV Savine sequences were constructed by excising the various HIV Savine cassettes from the selected plasmid clones using *Bam*HI/*Xho*I (cassette A) or *Bam*HI/*Sal*I (cassettes B and C) and cloned into the marker rescue plasmid, pTK7.5, cleaved with *Bam*HI/*Sal*I. These pTK7.5-derived plasmids were then used to generate recombinant Vaccinia viruses by marker rescue recombination using established protocols (Boyle *et al.*, 1985) to generate VV-AC1, VV-AC2, VV-BC1, VV-BC2, VV-CC1 and VV-CC2 (Figure 18b).

Two further DNA vaccine plasmids were constructed each encoding a version of the full length HIV Savine (Figure 18c). Briefly, the two versions of cassette B were excised with *Xho*I and cloned into the corresponding selected plasmid clones containing cassette A sequences that were cut with *Xho*I/*Sal*I to generate pBSAB1 and pBSAB2 respectively. The joined A/B cassettes in pBSAB1 and pBSAB2 were excised with *Xba*I/*Xho*I and cloned into pDVCC1 and pDVCC2, respectively, and cleaved with *Xba*I/*Xho*I to generate pDVFL1 and pDVFL2. These were then further modified to contain an ER signal sequence using the same cloning strategy as outlined in figure 18a.

Restimulation of HIV specific lymphocytes from HIV infected patients

The present inventors examined the capacity of the HIV Savine to restimulate HIV-specific polyclonal CTL responses from HIV-infected patients. PBMCs from three different patients were restimulated *in vitro* with two HIV Savine Vaccinia virus pools (Pool 1 included VV-AC1 and VV-BC1; Pool 2 included VV-AC2, VV-BC2 and VV-CC2) then used in CTL lysis assays against LCLs infected either with one of the Savine Vaccinia virus pools or Vaccinia viruses which express gag, env or pol. Figure 19 clearly shows, that in all three assays, both HIV Savine viral pools restimulated HIV-specific CTL responses which could recognise targets expressing whole natural HIV antigens and not targets which were uninfected or infected with the control Vaccinia virus. Furthermore, in all three cases, both pools restimulated responses that recognised all three natural HIV antigens. This result suggests that the combined Savine constructs will provide broader immunological coverage than single antigen based vaccine approaches. The level of lysis in each case of targets infected with Savine viral pools was significantly higher than the

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lysis recorded for any other infected target. This probably reflects the combined CTL responses to gag, pol, and env plus other HIV antigens not analysed here but whose sequences are also incorporated into the Savine constructs.

CTL recognition of each HIV antigen is largely controlled by each patient's HLA background hence the pattern of CTL lysis for whole HIV antigens is different in each patient. Interestingly, this CTL lysis pattern did not change when the second Savine Vaccinia virus pool was used for CTL restimulation. In these assays, therefore, the inventors were unable to demonstrate clear differences between pools 1 and 2, despite pool 1 lacking a Vaccinia virus expressing cassette CC1 and despite the many amino acid differences between the A and B cassettes in each pool (see table 1).

From the foregoing, the present inventors have developed a novel vaccine/therapeutic strategy. In one embodiment, pathogen or cancer protein sequences are systemically fragmented, reverse translated back into DNA, rearranged randomly then joined back together. The designed synthetic DNA sequence is then constructed using long oligonucleotides and can be transferred into a range of delivery vectors. The vaccine vectors used here were DNA vaccine plasmids and recombinant poxvirus vectors which have been previously shown to elicit strong T cell responses when used together in a 'prime-boost' protocol (Kent *et al.*, 1997). An important advantage of scrambled antigen vaccines or 'Savines' is that the amount of starting sequence information for the design can be easily expanded to include the majority of the protein sequences from a pathogen or for cancer, thereby providing the maximum possible vaccine or therapy coverage for a given population.

An embodiment of the systematic fragmentation approach described herein was based on the size and processing requirements for T cell epitopes and was designed to cause maximal disruption to the structure and function of protein sequences. This fragmentation approach ensures that the maximum possible range of T cell epitopes will be present from any incorporated protein sequence without the protein being functional and able to compromise vaccine safety

Another important advantage of Savines is that consensus protein sequences can be used for their design. This feature is only applicable when the design needs to cater for pathogen or cancer antigens whose sequence varies considerably. HIV is a highly

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mutagenic virus, hence this feature was utilised extensively to design a vaccine which has the potential to cover not only field isolates of HIV but also the major HIV clades involved in the current HIV pandemic. To construct the HIV Savine, one set of long oligonucleotides was synthesised, which included degenerate bases in such a way that 8
5 constructs are theoretically required for the vaccine to contain all combinations in any stretch of 9 amino acids. The inventors believe that this approach can be improved for the following reasons: 1) While degenerate bases should be theoretically equally represented, in practice some degenerate bases were biased towards one base or the other, leading to a lower than expected frequency of the designed mutations in the two full length HIV
10 Savines which were constructed (see Table 1). 2) Only sequence combinations actually present in the HIV clade consensus sequences are required to get full clade coverage, hence the number of full length constructs needed could be reduced. To reduce the number of constructs however, separate sets of long oligonucleotides would have to be synthesised, significantly increasing the cost, time and effort required to generate a vaccine capable of
15 such considerable vaccine coverage.

A significant problem during the construction of the HIV Savine synthetic DNA sequence was the incorporation of non-designed mutations. The most serious types of mutations were insertions, deletions or those giving rise to stop codons, all of which change the frame of the synthesised sequences and/or caused premature truncation of the
20 Savine proteins. These types of mutation were removed during construction of the HIV Savines by sequencing multiple clones after subcassette and cassette construction and selecting functional clones. The major source of these non-designed mutations was in the long oligonucleotides used for Savine synthesis, despite their gel purification. This problem could be reduced by making the initial subcassettes smaller thereby reducing the
25 possibility of corrupted oligonucleotides being incorporated into each subcassette clone. The second major cause of non-designed mutations was the large number of PCR cycles required for the PCR and ligation-mediated joining of the subcassettes. Including extra sequencing and clone selection steps during the subcassette joining process should help to reduce the frequency of non-designed mutations in future constructs. Finally, another
30 method that could help reduce the frequency of such mutations at all stages is to use resolvase treatment. Resolvases are bacteriophage-encoded endonucleases which recognise disruptions to double stranded DNA and are primarily used by bacteriophages to resolve

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Holliday junctions (Mizuuchi, 1982; Youil *et al.*, 1995). T7 endonuclease I has already been used by the present inventors in synthetic DNA constructions to recognise mutations and cleave corrupted dsDNA to allow gel purification of correct sequences. Cleavage of corrupted sequences occurs because after a simple denaturing and hybridisation step mutated DNA hybridises to correct DNA sequences and results in a mispairing of DNA bases which is able to be recognised by the resolvase. This method resulted in a 50% reduction in the frequency of errors. Further optimisation of this method and the use of a thermostable version of this type of enzyme could further reduce the frequency of errors during long Savine construction.

Two pools of Vaccinia viruses expressing Savine cassettes were both shown to restimulate HIV-specific responses from three different patients infected with B clade HIV viruses. These results provide a clear indication that the HIV Savine should provide broad coverage of the population because each patient had a different HLA pattern yet both pools were able to restimulate HIV-specific CTL responses in all three patients against all three natural HIV proteins tested. Also, both pools were shown to restimulate virtually identical CTL patterns in all three patients. This result was unexpected because some responses should have been lost or gained due to the amino acid differences between the two pools and because Pool 1 is only capable of expressing 2/3 of the full length HIV Savine. There are two suggested reasons why the pattern of CTL lysis was not altered between the two viral pools. Firstly, the sequences in the Savine constructs are nearly all duplicated because the fragment sequences overlap. Hence the loss of a third of the Savine may not have excluded sufficient T cell epitopes for differences to be detected in only three patient samples against only three HIV proteins. Secondly, while mutations often destroy T cell epitopes, if they remain functional, then the CTL they generate frequently can recognise alternate epitope sequences. Taken together this finding indirectly suggests that combining only two Savine constructs may provide robust multiclade coverage. Further experiments are being carried out to directly examine the capacity of the HIV Savine to stimulate CTL generated by different strains of HIV virus. The capacity of the two HIV-1 Savine Vaccinia vector pools to stimulate CD4+ T cell HIV-1 specific responses from infected patients was also tested (Figure 20). Both patients showed significant proliferation of CD4+ T cells although both pools did not show consistent patterns suggesting that the two pools may provide wider vaccine coverage than using either pool independently.

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The present inventors have generated a novel vaccine strategy, which has been used to generate what the inventors believe to be the most effective HIV candidate vaccine to date. The inventors have used this vaccine to immunise naïve mice. Figure 21 shows conclusively that the HIV-1 Savine described above can generate a Gag and Nef CTL response in naïve mice. It should be noted, however, that the Nef CTL epitope appeared to exist only in Pool 1 since it was not restimulated by Pool 2. This is further proof of the utility of combining HIV-1 Savine Pool 1 and Pool 2 components together to provide broader vaccine coverage.

The HIV-1 Savine Vaccinia vectors have also been used to restimulate *in vivo* HIV-1 responses in pre-immune *M. nemestrina* monkeys. These experiments (Figure 22) showed, by INF- γ ELISPOT and CD69 expression on both CD4 and CD8 T cells, that the ability of the HIV-1 SAVINE to restimulate HIV-1 specific responses in vivo is equivalent or perhaps better than another HIV-1 candidate vaccine.

This is a generic strategy able to be applied to many other human infections or cancers where T-cell responses are considered to be important for protection or recovery. With this in mind the inventors have begun constructing Savines for melanoma, cervical cancer and Hepatitis C. In the case of melanoma, the majority of the currently identified melanoma antigens have been divided into two groups, one containing antigens associated with melanoma and one containing differentiation antigens from melanocytes, which are often upregulated in melanomas. Two Savine constructs are presently being constructed to cater for these two groups. The reason for making the distinction is that treatment of melanoma might first proceed using the Savine that incorporates fragments of melanoma specific antigens only. If this Savine fails to control some metastases then the less specific Savine containing the melanocyte-specific antigens can then be used. It is important to point out that other cancers also express many of the antigens specific to melanomas *e.g.*, testicular and breast cancers. Hence the melanoma specific Savine may have therapeutic benefits for other cancers.

A small Savine is also being constructed for cervical cancer. This Savine will contain two antigens, E6 and E7, from two strains of human papilloma virus (HPV), HPV-16 and HPV-18, directly linked with causing the majority of cervical cancers worldwide. There is a large number of sequence differences in these two antigens between the two

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strains which would normally require two Savines to be constructed. However since this Savine is small, the antigen fragments from both strains are being scrambled together. While it is normally better for the Savine approach to include all or a majority of the antigens from a virus, in this case only E6 and E7 are expressed during viral latency or in cervical carcinomas. Hence in the interests of simplicity, the rest of the HPV genome will not be included although all HPV antigens would be desirable in a Savine against genital warts.

Two Savines have also been constructed for two strains of hepatitis C, a major cause of liver disease in the world. Hepatitis C is similar to HIV in the requirements for a vaccine or therapeutic. However, the major hepatitis C strains share significantly lower homology, 69-79%, with one another than do the various HIV clades. To cater for this the inventors have decided to construct two separate constructs to cater for the two major strains present in Australia, types 1a and 3a, which together cause approximately 80-95% of hepatitis C infections in this country. Both constructs will be approximately the same size as the HIV Savine but will be blended together into a single vaccine or therapy.

Overall it is believed that the Savine vaccine strategy is a generic technology likely to be applied to a wide range of human diseases. It is also believed that because it is not necessary to characterise each antigen, this technology will be actively applied to animal vaccines as well where research into vaccines or therapies is often inhibited by the lack of specific reagents, modest research budgets and poor returns on animal vaccines.

EXAMPLE 2

Hepatitis C Savine

Synthetic immunomodulatory molecules have also been designed for treating Hepatitis C. In one example, the algorithm of Figure 25 was applied to a consensus polyprotein sequence of Hepatitis C 1a to facilitate its segmentation into overlapping segments (30 aa segments overlapping by 15 aa), the rearrangement of these segments into a scrambled order and the output of Savine nucleic acid and amino acid sequences, as shown in Figure 26. Exemplary DNA cassettes (A, B and C) are also shown in Figure 26, which contain suitable restriction enzyme sites at their ends to facilitate their joining into a single expressible open reading frame.

EXAMPLE 3

Melanoma Savine

The algorithm of Figure 25 was also applied to melanocyte differentiation antigens (gp100, MART, TRP-1, Tyros, Trp-2, MC1R, MUC1F and MUC1R) and to
5 melanoma specific antigens (BAGE, GAGE-1, gp100In4, MAGE-1, MAGE-3, PRAME, TRP2IN2, NYNSO1a, NYNSO1b and LAGE1), as shown in Figure 27, to provide separate Savine nucleic acid and amino acid sequences for treating or preventing melanoma.

EXAMPLE 4

Resolvase Repair Experiment

10 A resolvase can be used advantageously to repair errors in polynucleotides. The following procedure outlines resolvase repair of a synthetic 340 bp fragment in which DNA errors were common.

Method

The 340 bp fragment was PCR amplified and gel purified on a 4% agarose gel.
15 After spin purifying, 10ul of the eluate corresponding to approximately 100 ng was subjected to the resolvase repair treatment. The rest of the DNA sample was stored for later cloning as the untreated control.

2 μ L of 10xPCR buffer, 2 μ L of 20 mM $MgCl_2$ and 6 μ L of MilliQ™ water (MQW) and Taq DNA polymerase were added to the 10 μ L DNA sample. The mixture
20 was subjected to the following thermal profile; 95°C for 5min, 65°C for 30min, cooled and held at 37°C. Five μ L of 10xT7 endonuclease I buffer, 8 μ L of 1/50 μ L of T7endoI enzyme stock and 17 μ L of MQW were added, mixed and incubated for 30 min. Loading buffer was added to the sample and the sample was electrophoresed on a 4% agarose gel. A faint band corresponding to the full length fragment was excised and subjected to 15 further
25 cycles of PCR. The amplified fragment was agarose gel purified and, along with the untreated DNA sample, cloned into pBluescript. Eleven plasmid clones for each DNA sample were sequenced and the number and type of errors compared (see table)

Buffers were as follows:

10x T7 endonuclease buffer

2.5ml 1M TRIS pH7.8, 0.5ml 1M MgCl₂, 25 µL 1 M DTT, 50 µL 10mg/mL BSA, 2 mL MQW made up to a total of 5 mL.

5 T7 endonuclease I stock

Concentrated sample of enzyme prepared by, and obtained from, Jeff Babon (St Vincent's Hospital) was diluted 1/50 using the following dilution buffer: 50 µL 1 M TRIS pH7.8, 0.1µL 1M EDTA pH8, 5 µL 100 mM glutathione, 50 µL 10mg/mL BSA, 2.3 mL MQW, 2.5 mL glycerol made up to a total of 5 mL.

10 Results

The results are summarised in Tables 2 and 3.

TABLE 2

Total Errors	
Untreated	Resolvase treated
A/T to G/C = 6	A/T to G/C = 1
G/C to A/T = 12	G/C to A/T = 7
A/T to deletion = 1	A/T to deletion = 1
G/C to deletion = 6	G/C to deletion = 3

TABLE 3

Clone summary	
Untreated	Resolvase treated
6/11 contained deletions	3/11 contained deletions
9/11 contained mutations	7/11 contained mutations

Clone summary	
Untreated	Resolvase treated
2/11 correct	3/11 correct

Discussion/Conclusion

While overall the number of correct clones obtained was not significantly different, there was a significant difference in the level of errors. This reduction in errors becomes more significant as greater numbers of long oligonucleotides are joined into the one construct *i.e.*, increasing the difference between untreated *versus* treated samples in the chance of obtaining a correct clone. It is believed that combining another resolvase such as T4 endonuclease VII may further enhance repair or increase the bias against errors.

Importantly, this experiment was not optimised *e.g.*, by using proofreading PCR enzymes or optimised conditions. Finally if the repair reaction is carried out during normal PCR, for example, by including a thermostable resolvase, it is believed that amplification of already damaged long oligonucleotides, and the normal accumulation of PCR induced errors, even using error reading polymerases during PCR, could be reduced significantly. The repair of damaged long oligonucleotides is particularly important for synthesis of long DNA fragment such as in Savines because, while the rate of long oligonucleotide damage is typically <5%, after joining 10 oligonucleotides, the error rate approaches 50%. This is true even using the best proofreading PCR enzymes because these enzymes do not verify the sequence integrity using correct oligonucleotide templates that exist as a significant majority (95%) in a joining reaction.

The disclosure of every patent, patent application, and publication cited herein is incorporated herein by reference in its entirety.

The citation of any reference herein should not be construed as an admission that such reference is available as "Prior Art" to the instant application

Throughout the specification the aim has been to describe the preferred embodiments of the invention without limiting the invention to any one embodiment or specific collection of features. Those of skill in the art will therefore appreciate that, in

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light of the instant disclosure, various modifications and changes can be made in the particular embodiments exemplified without departing from the scope of the present invention. All such modifications and changes are intended to be included within the scope of the appended claims.

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WHAT IS CLAIMED IS:

1. A synthetic polypeptide comprising a plurality of different segments of at least one parent polypeptide, wherein the segments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide.
2. The synthetic polypeptide of claim 1, consisting essentially of different segments of a single parent polypeptide.
3. The synthetic polypeptide of claim 1, consisting essentially of different segments of a plurality of different parent polypeptides.
4. The synthetic polypeptide of claim 1, wherein the segments in said synthetic polypeptide are linked sequentially in a different order or arrangement relative to their linkage in said at least one parent polypeptide.
5. The synthetic polypeptide of claim 4, wherein the segments in said synthetic polypeptide are randomly rearranged relative to their order or arrangement in said at least one parent polypeptide.
6. The synthetic polypeptide of claim 1, wherein the size of an individual segment is at least 4 amino acids.
7. The synthetic polypeptide of claim 6, wherein the size of an individual segment is from about 20 to about 60 amino acids.
8. The synthetic polypeptide of claim 7, wherein the size of an individual segment is about 30 amino acids.
9. The synthetic polypeptide of claim 7, comprising at least 30% of the parent polypeptide sequence.
10. The synthetic polypeptide of claim 1, wherein at least one of said segments comprises partial sequence identity or homology to one or more other said segments.
11. The synthetic polypeptide of claim 10, wherein the sequence identity or homology is contained at one or both ends of an individual segment.

12. The synthetic polypeptide of claim 11, wherein one or both ends of said segment comprises at least 4 contiguous amino acids that are identical to, or homologous with, an amino acid sequence contained within one or more other of said segments.
13. The synthetic polypeptide of claim 10, wherein the size of an individual segment is about twice the size of the sequence that is identical or homologous to the or each other said segment.
14. The synthetic polypeptide of claim 13, wherein the size of an individual segment is about 30 amino acids and the size of the sequence that is identical or homologous to the or each other said segment is about 15 amino acids.
15. The synthetic polypeptide of claim 1, wherein an optional spacer is interposed between some or all of the segments.
16. The synthetic polypeptide of claim 15, wherein the spacer alters proteolytic processing and/or presentation of adjacent segment(s).
17. The synthetic polypeptide of claim 16, wherein the spacer comprises at least one neutral amino acid.
18. The synthetic polypeptide of claim 16, wherein the spacer comprises at least one alanine residue.
19. The synthetic polypeptide of claim 1, wherein the at least one parent polypeptide is associated with a disease or condition.
20. The synthetic polypeptide of claim 1, wherein the at least one parent polypeptide is selected from a polypeptide of a pathogenic organism, a cancer-associated polypeptide, an autoimmune disease-associated polypeptide, an allergy-associated polypeptide or a variant or derivative of these.
21. The synthetic polypeptide of claim 1, wherein the at least one parent polypeptide is a polypeptide of a virus.
22. The synthetic polypeptide of claim 21, wherein the virus is selected from a Human Immunodeficiency Virus (HIV) or a Hepatitis virus.
23. The synthetic polypeptide of claim 22, wherein the virus is a Human Immunodeficiency Virus (HIV) and the at least one parent polypeptide is selected from env, gag, pol, vif, vpr, tat, rev, vpu and nef, or a combination thereof.

24. The synthetic polypeptide of claim 1, wherein the at least one parent polypeptide is a cancer-associated polypeptide.
25. The synthetic polypeptide of claim 24, wherein the cancer is melanoma.
26. The synthetic polypeptide of claim 25, wherein the at least one parent polypeptide is a melanocyte differentiation antigen.
27. The synthetic polypeptide of claim 25, wherein the at least one parent polypeptide is a melanocyte differentiation antigen selected from gp100, MART, TRP-1, Tyros, TRP2, MC1R, MUC1F, MUC1R or a combination thereof.
28. The synthetic polypeptide of claim 25, wherein the at least one parent polypeptide is a melanoma-specific antigen.
29. The synthetic polypeptide of claim 25, wherein the at least one parent polypeptide is a melanoma-specific antigen selected from BAGE, GAGE-1, gp100In4, MAGE-1, MAGE-3, PRAME, TRP2IN2, NYNSO1a, NYNSO1b, LAGE1 or a combination thereof.
30. A synthetic polynucleotide encoding a synthetic polypeptide comprising a plurality of different segments of at least one parent polypeptide, wherein the segments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide.
31. A method for producing the synthetic polynucleotide encoding a synthetic polypeptide comprising a plurality of different segments of at least one parent polypeptide, wherein the segments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide, said method comprising:
- linking together in the same reading frame a plurality of nucleic acid sequences encoding different segments of the at least one parent polypeptide to form a synthetic polynucleotide whose sequence encodes said segments linked together in a different relationship relative to their linkage in the at least one parent polypeptide.
32. The method of claim 31, further comprising fragmenting the sequence of a respective parent polypeptide into fragments and linking said fragments together in a different relationship relative to their linkage in a respective parent polypeptide sequence.

33. The method of claim 32, wherein the fragments are randomly linked together.
34. The method of claim 31, further comprising reverse translating the sequence of a respective parent polypeptide or a segment thereof to provide a nucleic acid sequence encoding said parent polypeptide or said segment.
35. The method of claim 34, wherein an amino acid of a respective parent polypeptide sequence is reverse translated to provide a codon, which has higher translational efficiency than other synonymous codons in a cell of interest.
36. The method of claim 35, wherein an amino acid of said parent polypeptide sequence is reverse translated to provide a codon which, in the context of adjacent or local sequence elements, has a lower propensity of forming an undesirable sequence that is refractory to the execution of a task.
37. The method of claim 35, wherein an amino acid of said parent polypeptide sequence is reverse translated to provide a codon which, in the context of adjacent or local sequence elements, has a lower propensity of forming an undesirable sequence selected from a palindromic sequence or a duplicated sequence, which is refractory to the execution of a task selected from cloning or sequencing.
38. The method of claim 31, further comprising linking a spacer oligonucleotide encoding at least one spacer residue between segment-encoding nucleic acids.
39. The method of claim 38, wherein spacer oligonucleotide encodes 2 to 3 spacer residues.
40. The method of claim 38 or claim 39, wherein the spacer residue is a neutral amino acid.
41. The method of claim 38 or claim 39, wherein the spacer residue is alanine.
42. The method of claim 31, further comprising linking in the same reading frame as other segment-containing nucleic acid sequences at least one variant nucleic acid sequence which encodes a variant segment having a homologous but not identical amino acid sequence relative to other encoded segments.

43. The method of claim 42, wherein the variant segment comprises conserved and/or non-conserved amino acid differences relative to one or more other encoded segments.
44. The method of claim 43, wherein the differences correspond to sequence polymorphisms.
45. The method of claim 44, wherein degenerate bases are designed or built in to the at least one variant nucleic acid sequence to give rise to all desired homologous sequences.
46. The method of claim 31, further comprising optimising the codon composition of the synthetic polynucleotide such that it is translated efficiently by a host cell.
47. A synthetic construct comprising a synthetic polynucleotide encoding a synthetic polypeptide comprising a plurality of different segments of at least one parent polypeptide, wherein the segments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide, wherein said synthetic polynucleotide is operably linked to a regulatory polynucleotide.
48. The synthetic construct of claim 47, further including a nucleic acid sequence encoding an immunostimulatory molecule.
49. The synthetic construct of claim 48, wherein the immunostimulatory molecule comprises a domain of an invasin protein (Inv).
50. The synthetic construct of claim 48, wherein the immunostimulatory molecule comprises the sequence set forth in SEQ ID NO: 1467 or an immune stimulatory homologue thereof.
51. The synthetic construct of claim 48, wherein the immunostimulatory molecule is a T cell co-stimulatory molecule.
52. The synthetic construct of claim 48, wherein the immunostimulatory molecule is a T cell co-stimulatory molecule selected from a B7 molecule or an ICAM molecule.
53. The synthetic construct of claim 48, wherein the immunostimulatory molecule is a B7 molecule or a biologically active fragment thereof, or a variant or derivative of these.

54. The synthetic construct of claim 48, wherein the immunostimulatory molecule is a cytokine selected from an interleukin, a lymphokine, tumour necrosis factor or an interferon.

55. The synthetic construct of claim 48, wherein the immunostimulatory molecule is an immunomodulatory oligonucleotide.

56. An immunopotentiating composition, comprising an immunopotentiating agent selected from the synthetic polypeptide of claim 1, the synthetic polynucleotide of claim 30 or the synthetic construct of claim 47, together with a pharmaceutically acceptable carrier.

57. The composition of claim 56, further comprising an adjuvant.

58. A method for modulating an immune response, which response is preferably directed against a pathogen or a cancer, comprising administering to a patient in need of such treatment an effective amount of an immunopotentiating agent selected from the synthetic polypeptide of claim 1, the synthetic polynucleotide of claim 30, the synthetic construct of claim 47, or the composition of claim 56.

59. A method for treatment and/or prophylaxis of a disease or condition, comprising administering to a patient in need of such treatment an effective amount of an immunopotentiating agent selected from selected from the synthetic polypeptide of claim 1, the synthetic polynucleotide of claim 30, the synthetic construct of claim 47, or the composition of claim 56.

60. A computer program product for designing the sequence of a synthetic polypeptide comprising a plurality of different segments of at least one parent polypeptide, wherein the segments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide, said program product comprising:

- code that receives as input the sequence of said at least one parent polypeptide;
- code that fragments the sequence of a respective parent polypeptide into fragments;
- code that links together said fragments in a different relationship relative to their linkage in said parent polypeptide sequence; and

- a computer readable medium that stores the codes.

61. The computer program product of claim 60, further comprising code that randomly rearranges said fragments.

62. The computer program product of claim 60, further comprising code that links the sequence of a spacer residue to the sequence of said at least one parent polypeptide or to said fragments.

63. A computer program product for designing the sequence of a synthetic polynucleotide encoding a synthetic polypeptide comprising a plurality of different segments of at least one parent polypeptide, wherein the segments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide, comprising:

- code that receives as input the sequence of at least one parent polypeptide;
- code that fragments the sequence of a respective parent polypeptide into fragments;
- code that reverse translates the sequence of a respective fragment to provide a nucleic acid sequence encoding said fragment;
- code that links together in the same reading frame each said nucleic acid sequence to provide a polynucleotide sequence that codes for a polypeptide sequence in which said fragments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide sequence; and
- a computer readable medium that stores the codes.

64. The computer program product of claim 63, further comprising code that randomly rearranges said nucleic acid sequences.

65. The computer program product of claim 64, further comprising code that reverse translates an amino acid of a respective parent polypeptide sequence to provide a codon, which has higher translational efficiency than other synonymous codons in a cell of interest.

66. The computer program product of claim 63, further comprising code that reverse translates an amino acid of a respective parent polypeptide sequence to provide a codon

which, in the context of adjacent or local sequence elements, has a lower propensity of forming an undesirable sequence that is refractory to the execution of a task.

67. The computer program product of claim 63, further comprising code that links a spacer oligonucleotide to one or more of said nucleic acid sequences.

68. A computer for designing the sequence of a synthetic polypeptide comprising a plurality of different segments of at least one parent polypeptide, wherein the segments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide, wherein said computer comprises:

- (a) a machine-readable data storage medium comprising a data storage material encoded with machine-readable data, wherein said machine-readable data comprise the sequence of at least one parent polypeptide;

- (b) a working memory for storing instructions for processing said machine-readable data;

- (c) a central-processing unit coupled to said working memory and to said machine-readable data storage medium, for processing said machine readable data to provide said synthetic polypeptide sequence; and

- (d) an output hardware coupled to said central processing unit, for receiving said synthetic polypeptide sequence.

69. The computer of claim 68, wherein the processing of said machine readable data comprises fragmenting the sequence of a respective parent polypeptide into fragments and linking together said fragments in a different relationship relative to their linkage in the sequence of said parent polypeptide.

70. The computer of claim 68, wherein the processing of said machine readable data comprises randomly rearranging said fragments.

71. The computer of claim 68, wherein the processing of said machine readable data comprises linking the sequence of a spacer residue to the sequence of said at least one parent polypeptide or to said fragments.

72. A computer for designing the sequence of a synthetic polynucleotide encoding a synthetic polypeptide comprising a plurality of different segments of at least one parent polypeptide, wherein the segments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide, wherein said computer comprises:

(a) a machine-readable data storage medium comprising a data storage material encoded with machine-readable data, wherein said machine-readable data comprise the sequence of at least one parent polypeptide;

(b) a working memory for storing instructions for processing said machine-readable data;

(c) a central-processing unit coupled to said working memory and to said machine-readable data storage medium, for processing said machine readable data to provide said synthetic polynucleotide sequence; and

(d) an output hardware coupled to said central processing unit, for receiving said synthetic polynucleotide sequence.

73. The computer of claim 72, wherein the processing of said machine readable data comprises fragmenting the sequence of a respective parent polypeptide into fragments, reverse translating the sequence of a respective fragment to provide a nucleic acid sequence encoding said fragment and linking together in the same reading frame each said nucleic acid sequence to provide a polynucleotide sequence that codes for a polypeptide sequence in which said fragments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide sequence.

74. The computer of claim 72, wherein the processing of said machine readable data comprises randomly rearranging said nucleic acid sequences.

75. The computer of claim 72, wherein the processing of said machine readable data comprises reverse translating an amino acid of a respective parent polypeptide sequence to provide a codon, which has higher translational efficiency than other synonymous codons in a cell of interest.

76. The computer of claim 72, wherein the processing of said machine readable data comprises reverse translating an amino acid of a respective parent polypeptide sequence to provide a codon which, in the context of adjacent or local sequence elements, has a lower propensity of forming an undesirable sequence that is refractory to the execution of a task.

77. The computer of claim 72, wherein the processing of said machine readable data comprises linking a spacer oligonucleotide to one or more of said nucleic acid sequences.

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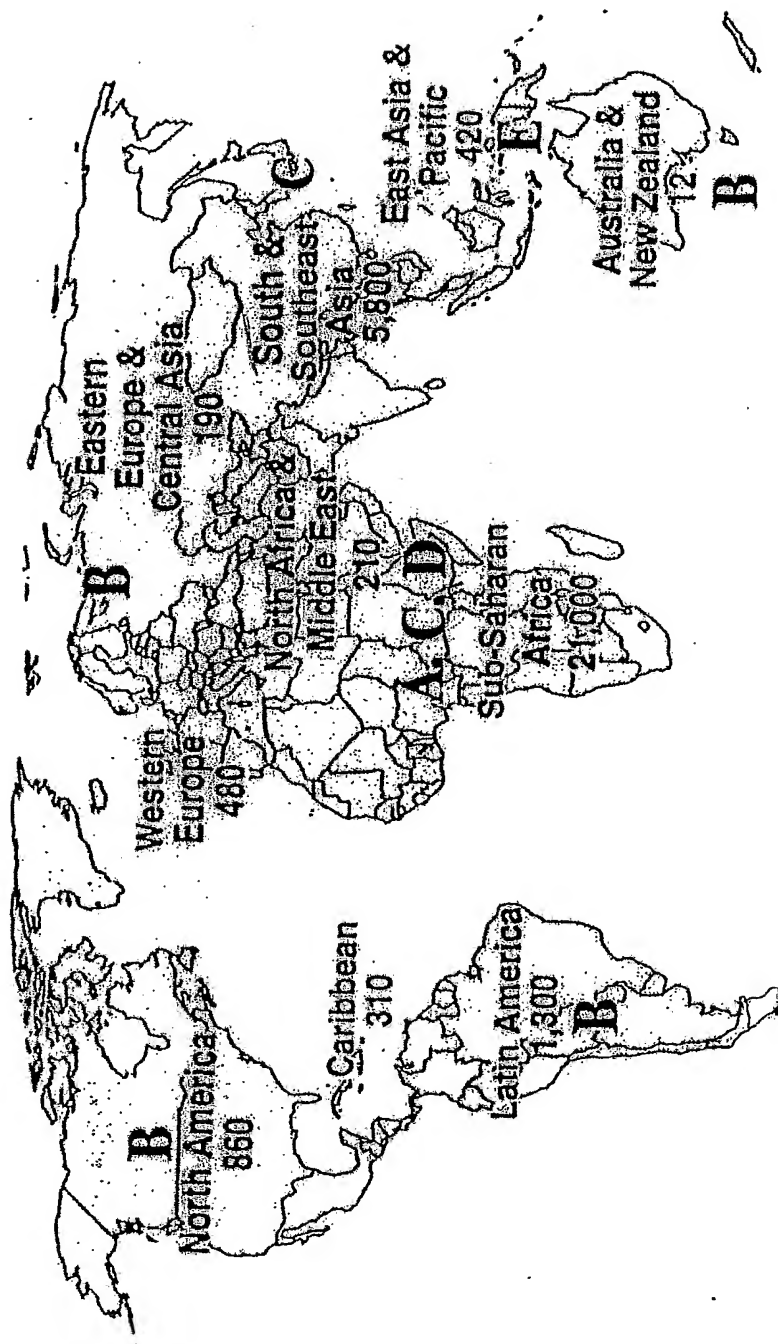


FIGURE 1

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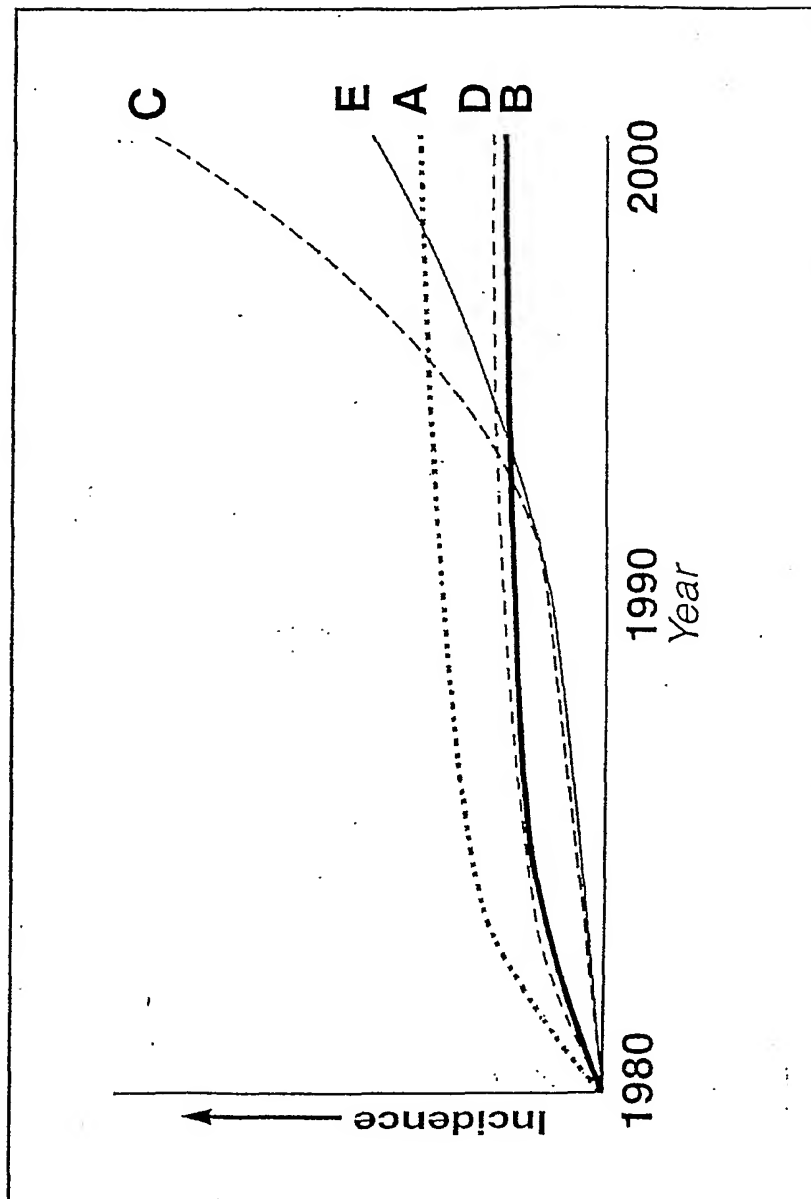


FIGURE 2

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	p17 ->	/<-	nls	->/		
	/<-	membrane binding	->/			
DESIGNED SEQ	MGARASVLGGKLD	AW EKIRLR	PGGKKKKYKMKHLV	WASRELERFALNPGLLE	TAEGCQQILEQLQS	ALKT
MUTATED AAs		R E	RL I	S S K G P Q		
E-ISOLATE	MGARASVLGGKLD	AW EKIRLR	PGGKKKKYKMKHLV	WASRELERFALNPGLLE	TAEGCQQILIEQLQ	STLKT
CONSENSUS-A	mGARASvLsggkL	DawekIrLRPgGkKkYrL	KHlvwAsreLerFaLnPslLe	TaegcqqimeQlqs	alkT	
CONSENSUS-B	-----e-r-----	k---i-----v-g---s---	R--lg---ps-q-			
CONSENSUS-C	-----i-r-----	?-----h-Mi-----	g---s---k--ik--P--Q-			
CONSENSUS-D	-----?-----	?-----i-----	G---s---k--ig--P--iq-			
CONSENSUS-F	-----	-----i-g---s---	rk-Ig---ps-Q-			
CONSENSUS-G	-----?-----	?-----?-----	?-----G---T-----	P?-Q-		
CONSENSUS-H	-----?-----	?-----?-----	?-----?-----	L-?I---P---		
CONSENSUS-O	---?---T-S---	---?---S-?---	---?---C-?---	---?E?LLQ--EP---		
CONSENSUS-CPZ	---?---?---?---	---?---?---M?---	---?---?---?---	---?K?---?P?---		
			/<- nls ->/			
DESIGNED SEQ	GSEELKSLYNTIATL	WC VHQR	IEVKDTKEALDK	IEEEQKKSQQK.....	TQQAAA..DT.GS...	SSKV
MUTATED AAs	T R F V		D R	V N K	N Q	
E-ISOLATE	GSEELKSLYNTIATL	WC VHQR	IEVKDTKEALDK	IEEVQKKSQQK.....	QQAAA..DT.GS...	SSKV
CONSENSUS-A	g?eElkSLfNtvat	LycvHqrIdvkDtKeAldkiEeignKskqk	?????tqqaaA..?T.gs?	..sskv		126
CONSENSUS-B	-s---r--y-----	e-----E---k-----	a-----??d---n??-q-			128
CONSENSUS-C	-T---r--?-----	??-e-r-----E---?Q-----	k.ad?-k-----			120
CONSENSUS-D	-s-----?-----	e-e-----e-m-E---k-----	a---t..D..rn...-Q-			125
CONSENSUS-F	-S---r--y---v--f---vE-----	L-E---q-----?---dk.....				123
CONSENSUS-G	-T---?---?---?---?---e-----	eEV-Ka-kn-Q-----?---?---e?..n...-q-				110
CONSENSUS-H	-T---Q---LL-?-----	?-----?---?---?---Q??-----	T?..DK.??...??-?			106
CONSENSUS-O	-S??-?---W-AI?V-W---	N-??I?---QQ-IQ-LK-V.M?-RKS...A-AAKE.....	...?RQ?			106
CONSENSUS-CPZ	?S????-??V-W-?-----	??-?---?---?---K?????Q??T-S---	???G????-????-???????			61
	p17 \/ p24					
DESIGNED SEQSQNYPIVQNAQGQM	VHQPLSPRTLNAWVKV	IEEKGFNPEVIMFSALE	SEGATPQDLNMLNIV	GGH	
MUTATED AAs		L AI	V A S	T T	T T	
E-ISOLATESQNYPIVQNAQGQM	VHQPLSPRTLNAWVKV	IEEKGFNPEVIMFSALE	SEGATPQDLNMLNIV	GGH	
CONSENSUS-A	????SqNYPIVQNaqGQm	?hQ?lSPrTLNawVKviEekaFspEVIPmFsaLSEGATpQdLNmMLNiVgGH				190
CONSENSUS-Bl---V--ai-----	v-----T---T---				194
CONSENSUS-CL---v--ai-----	?---T-----T---T---				185
CONSENSUS-DL---V--ai-----	t---T---				191
CONSENSUS-Fl---V--i-----	T---T---				188
CONSENSUS-Gi-----v-----	t---T---				174
CONSENSUS-H?V--AI-----	V-----A---?				170
CONSENSUS-O	...?-----?-----V--AI-----	AV-----N--I---M-----??Y-I-T---AI---				168
CONSENSUS-CPZ	---?---?---?---?---?---?---V---?---?---?---?---?---T---A---?					107
DESIGNED SEQ	QAAMQMLKETINEEAAEW	DRVHPVHAGPIPPGQMREPRGSDIAGTTSTLQEIQIGWMTN...	NNPPIVGD			
MUTATED AAs		D I	VA I	A S V E		
E-ISOLATE	QAAMQMLKETINEEAAEW	DRVHPVHAGPIPPGQMREPRGSDIAGTTSTLQEIQIGWMTN...	NNPPIVGD			
CONSENSUS-A	QAAMQMLKdtInEAAewDr	?HPVhAgPippgQmREPrGSDIAGtTstlqEqigwmTs...	NNPiPVGD			256
CONSENSUS-B	-----e-----l-----	a-----n-----e-----				261
CONSENSUS-C	-----l-----vA-----	a---?-----				251
CONSENSUS-D	-----E-----l-----	A-----?-----e-----				257
CONSENSUS-F	-----L---q-----i-----	q-----v---e-----				255
CONSENSUS-G	-----I---?Q-----I---?	R-----e-----				239
CONSENSUS-H	-----?-----?-----	?-----A---?-----				233
CONSENSUS-O	-G-L-V--EV-----?---T--P???-L---I---T-----	Q---?---T-R.??-??-				229
CONSENSUS-CPZ	-G---V--EV-----L--T---???-L---?-----	---?---?---?---?---?---				160
		/<- MHR ->/				

FIGURE 3
SUBSTITUTE SHEET (RULE 26)

p24 \ / \ / 'p2' \ / p7

15-

ISOLATE-E SILKALGTGATLEEMMTACQGVGGPSHKARVLAEAMSA...QH.AN...IMMQRGNF.KGQTR.IKCFN

CONSENSUS-A	sILraLg?gAtLeEMMTacQgVggPgHKArvLAEAmSqv...q??n??iMmQrGnf.rgqkr?iKCFN	384
CONSENSUS-B	T--K--Pa-----tn-s.at?-----n-rKtv---	394
CONSENSUS-C	T-----P-s-----s-----a..nn-----s--K-p-iv----	382
CONSENSUS-D	t--K--P?-P-----s-----a..tn.s.ta-----K-prki----	390
CONSENSUS-F	T--K--P-----P-----a..TN.-?a-----ks--K-R-iv----	386
CONSENSUS-G	T--?-P-----P-----A..SG.-A.-A.-?-K??-.K-P??-?----	360
CONSENSUS-H	?-?-P-----SI-----P-----?..TN.-?A.-?-K--K-R-I?----	353
CONSENSUS-O	Q--K?--P?-----V-----T--??-----A?AQQDLKGGYTA.VF--QN.P?R-G----	358
CONSENSUS-CPZ	?--K-----?-----?-----?-----?Q.-?-?.VF?-?-?G?-?-?----	262

Zn-motif ->/ /<-Zn-motif ->/ pol cds -> p7. \/'p1' \/'p6

DESIGNED SEQ CGKEGHLARNCRAPRKKGCWKCGKEGHQMKDCT..E.RQANFLGKIWPSNKG.RPGNFPQSKP.....
MUTATED AAS I K R S H L R

ISOLATE-E CGKEGHLARNCRAPRKKGCWCKGKEGHQMKDCT..E.RQANFLGKIWPSNKG.RPGNFPSQSKP.....

CONSENSUS-A	CGkEGHlArNCrAPrKkGCwKCGkEGHQmKdCT.?e.rQANFlgkiwpSsKG.RPgNfPQsRp.....	443
CONSENSUS-B	-----i-k-----h-----l-----???????	453
CONSENSUS-C	-----i-k-----?-----?-----L-----???????	439
CONSENSUS-D	-----i-k-----h-----l-----	449
CONSENSUS-F	-----i-k-----r-----n-----L-----	445
CONSENSUS-G	-----?-----?-----?-----H-----L-?-?	414
CONSENSUS-H	-----?-----?-----?-----?-----L-----	406
CONSENSUS-I	-----?-----?-----?-----?-----Y-PGGT-----YV-???	411
CONSENSUS-CPZ	-----?-----K-----R-----R-Q-----?-----?-----V-----?-----?-----V-?????	306

vpr binding

vpr binding

b6

terminus

$\langle \dots \rangle$

✓ (minor)

(minor) V

$$/ \leftarrow \rightarrow /$$

/ (80%)

DESIGNED SEQEPTAPPAE.....NF.GFGEETT.PS....PKQE QKD....KEHYPPASL KSLFGNDPLSQ
MUTATED AAs S R Q P L̄ L S

ISOLATE-EEPTAPPAE.....NW.GMGEE.....QKD....KEHPPPSVSLKSLFGNDPLSQ

CONSENSUS-AEPTApPAE.....?f?gmgeeit.s?...pkgeqkd...??ke??ppl?slKSlFGNDplSQ	485
CONSENSUS-B	??..???-----e-.....s..rf---t-tps????q---pi-...---ly?--a--r-----s--\$	500
CONSENSUS-C	???????-----???????S..rF---t..pa.....p-??-?-?---t-----x	479
CONSENSUS-DS..-F-----Ps...q-----??-----ly-----a-----	495
CONSENSUS-FS..-F-----PS.....egly--a--	482
CONSENSUS-G-?------?-? ???--?-?S.....-P??.....-LY?-----	440
CONSENSUS-HS..-F-----M..P.....??-...?-?-?-----	436
CONSENSUS-O?-S---M-----?VK.?Q...EN-?-G...-?-LY.-FA-----T-Q\$	444
CONSENSUS-CPZI.....Y.??Q--?K.Q?.....?-----?L-?-?-----?--?--	333

CONSENSUS A-CPZ FROM LOS ALAMOS HIV SEQUENCE DATABASE
ISOLATE-E SEQ FROM ISOLATE 93TH253 THAILAND

Underlined AA are not present in all overlapping segments

FIGURE 3 (Cont)

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DESIGNED SEQ FFRE.NLAFQQGKAREF.....SSE..QTGANSSASRKLGDDGG.....AER..Q
 MUTATED AAS P E P R PT D

ISOLATE-E FFRE.NLAFQQGKAREF.....SSE..QTGANSSASRKLGDDGG.....AER..Q

CONSENSUS-A FFRE.NLAFQQGEAR?F.....SSE..QT??NS?TSR?LWDGG?D??L?....???G?E?..Q 35
 CONSENSUS-B ----.d---p--k--e-????????????----Ra--p-r-E-qVw-r-nnS-S???-EA-adr... 49
 ISOLATE-C ----.T-----K--E-----P-----RA--P-T---QV.RGSN....T.FSEAGAER..Q
 CONSENSUS-D ----.d---p--K-GEL.....RA--P---E-RVW-r-NP-S....eT-A-R... 48
 CONSENSUS-O ---?.?-?SGGH---QL.....CA..TS-PI-P-?.....GSE.....GT-ES?---G?? 35
 CONSENSUS-U ----.P--K--E-----P-----RA--P---E-RVW-G-K.T-S....ET-A-R... 48
 CONSENSUS-CPZ ----.?????????--L.....CA-????--?--?--?--?--?--?--?--?--?--?--? 13

protease
 \/
 <- gag cds end

DESIGNED SEQ GT..SSSFSPQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEDINLPGKWPKMIGGIGGFIKVRQYD
 MUTATED AAS LN V I EM R

ISOLATE-E GT..SSSFSPQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEDINLPGKWPKMIGGIGGFIKVRQYD

CONSENSUS-A G?..??SF?FPQITLWQRPLVTI?I?GQLIEALLDTGADDTVLEDINLPGKWPK?IGGIGGFIKVRQYD 96
 CONSENSUS-B ----.tv--s-----ik-g--K-----eM---r---M----- 116
 ISOLATE-C ----.LN-----IK-G--K-----E-----M-----
 CONSENSUS-D ----.TV--n-----IK-G--K-----Em-----M----- 115
 CONSENSUS-O R...A-??CL--P--D--I--A-VG-H-C-?-----NN-Q-E-?-?-M-----KE-? 94
 CONSENSUS-U ----.IV--S-----V--RVG--K-----E-----M----- 115
 CONSENSUS-CPZ ?-??-? 55

protease \ / p66, p51

DESIGNED SEQ QILIEICGKKAIGTVLVGPTPVNIIGRNMLTQIGCTLNFPISPIDTVPVKLKPGMDGPKVKQWPLTEEKI
 MUTATED AAS I H L L R E

ISOLATE-E QILIEICGKKAIGTVLVGPTPVNIIGRNMLTQIGCTLNFPISPIDTVPVKLKPGMDGPKVKQWPLTEEKI

CONSENSUS-A QILIEICGKK?IGTVLVGPTPVNIIGRNMLTQIGCTLNFPISPIETVPVKLK?MDGPKVKQWPLTEEKI 164
 CONSENSUS-B ----.H-A-----L-----G----- 186
 ISOLATE-C ----.I-----A-----M--L-R-----G-----
 CONSENSUS-D ----.?-A-----L-----G----- 184
 CONSENSUS-O NVTV-??-?EVQ-----?--I--GL-----AP-----G-----S?--- 159
 CONSENSUS-U ----.IV--S-----V--RVG--K-----E-----M----- 185
 CONSENSUS-CPZ ?V?-?-??R?V?--? 106

| M41L D67N | K70R

DESIGNED SEQ KALTEICKEMEEEGKISKIGPENPYNTPVFAIKKKDSTKWRKLVDFRELNKRTQDFWEVQLGIPHPAGLK
 MUTATED AAS A T K R I

ISOLATE-E KALTEICKEMEEEGKISKIGPENPYNTPVFAIKKKDSTKWRKLVDFRELNKRTQDFWEVQLGIPHPAGLK

CONSENSUS-A KALT?IC?EMEKEGKISKIGPENPYNTPVFAIKKKDSTKWRKLVDFRELNKRTQDFWEVQLGIPH?AGLK 231
 CONSENSUS-B ----.vE--T-----P----- 256
 ISOLATE-C ----.A--E--Q-----R-----P-----
 CONSENSUS-D ----.E--T-----R-----I-----P----- 254
 CONSENSUS-O E--A--O--O-----R-----I-----?-----?-----PG--- 227

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DESIGNED SEQ	QPIELPEKDSWTVNDIQKLVGKLNWASQIYAGIKVKQLCKLLRGTKALTDIVPLTEEAEELEENREI..	
MUTATED AAS	V E P R A E T A	
ISOLATE-E	QPIELPEKDSWTVNDIQKLVGKLNWASQIYAGIKVKQLCKLLRGTKALTDIVPLTEEAEELEENREI..	
CONSENSUS-A	QP??LPEKDSWTVNDIQKLVGKLNWASQIYAGIK?KQLC?LLRGAKALTDIV?LTEEAEELEENREI..	421
CONSENSUS-B	--Iv-----V---k---t---EviP-----	464
ISOLATE-C	--IQ-----P---VR---K-----T-----	
CONSENSUS-D	--sIk---E-----p---VR---K---T---EViP-----	462
CONSENSUS-O	--?IQ--?-?V-----?-Q--RV?E--K-I--T-S--EV-P-S?--E---?..	419
CONSENSUS-U	--IQ--D-E-----P---V---K-----P-A-----	463
CONSENSUS-CPZ	--?I---???-----?-P-----I--?-?-?-?-?-?-?-?-?-?-?	329
DESIGNED SEQ	.LREPVGHVYDPSKDLVAEVQKQGQDQWTYQIYQEPFKNLKTGKYSRKRSASHTNDVRQLTEVVQKIATE	
MUTATED AAS	K I I G F F(error) A M G K AA V	
ISOLATE-E	.LRIPVGHVYDPSKDLVAEVQKQGQDQWTYQIYQEPFKNLKTGKYSRKRSASHTNDVRQLTEVVQKIATE	
CONSENSUS-A	.LK?PVHGVYDPSKDLVAEVQKQGQDQWTYQIYQEPFKNLKTGKYA?KRSASHTNDVKQLTEVVQKV??E	484
CONSENSUS-B	..-e-----s---i---i---g-----rm-G-----A---iat-	533
ISOLATE-C	..-E---F---S---I---I---N---F-F-----F---T-----A---IAL-	
CONSENSUS-D	..-E---S---I---i---hG-----Rm-G-----a-a---IsT-	531
CONSENSUS-O	..-E---Q-D---WV?I---?---?---?EH-----?RQKAS---IR--A---?---SQ-	479
CONSENSUS-U	..-E---S---I---I---G---QY-----RIK-----A---IAQ-	532
CONSENSUS-CPZ	??-??-?-?-?-?-?-?-?-?-I---?---?---?---?---?---R??-?-?-?-?-I---	367
DESIGNED SEQ	SIVIWGKTPKFRLP IQRETWETWWMEYWQATWIPEWEFVNTPLVLKWLWYQLEKDPVGAETFFYVDGAASR	
MUTATED AAS	K K A TD E A V N	
ISOLATE-E	SIVIWGKTPKFRLP IQRETWETWWMEYWQATWIPEWEFVNTPLVLKWLWYQLEKDPVGAETFFYVDGAASR	
CONSENSUS-A	SIVIWGK?PKFRLP IQ?ETWE?WWMEYWQATWIPEWEFVNTPLVLKWLWYQLEKDP?GAETFFYVDGAANR	550
CONSENSUS-B	-----t---k---K---t-----e-v-----	602
ISOLATE-C	-----T---K---A---TD-----E---A-V-----	
CONSENSUS-D	-----T---K---T---?-----E---I-----	600
CONSENSUS-O	?-?-L---?-VTR---T---A?-----S---I---?---?E-----?	541
CONSENSUS-U	-----T---K---A---T-----TE---V-----	602
CONSENSUS-CPZ	-----?---?---?---?A---?---?---?---?---?---P??-?-?-?-?-L-	416
DESIGNED SEQ	ETKLGKAGYVTDGRGRQKVISLTETTNQKTELHAIHLALQDSGSEVNIVTDSQYALGIIQAQPDRESEEVV	
MUTATED AAS	IV D Q Q L L K L	
ISOLATE-E	ETKLGKAGYVTDGRGRQKVISLTETTNQKTELHAIHLALQDSGSEVNIVTDSQYALGIIQAQPDRESEEVV	
CONSENSUS-A	ETK?GKAGYVTDGRGRQKVSLTETTNQKTELHAIHLALQDSGSEVNIVTDSQYALGIIQAQPDRESE?V	618
CONSENSUS-B	---l-----d-----q-----l-----k---l---	672
ISOLATE-C	---I-----I-----Q---Q-----L---K---I---	
CONSENSUS-D	---L-----Pf-D-----Q---N-----L-----K---L---	670
CONSENSUS-O	?-L-----EQ-K-?IIK-?-A-M-?L?-KE?-?-?-SS-TQ-?-PI-	602
CONSENSUS-U	---K-----Q-----K-----I---	672
CONSENSUS-CPZ	??-?-?-?-?-?-?-?-QA--?-?L?-?-?-?-?-?-?-?-?-?-L-	459
DESIGNED SEQ	SQIIEELIKKEKVYLSWVPAHKGIGGNEQVDKLVISGIRKVLFLDGINKAQEEHRYHSNWRTMASDFNL	
MUTATED AAS	N K R A SA D K NE	
ISOLATE-E	SQIIEELIKKEKVYLSWVPAHKGIGGNEQVDKLVISGIRKVLFLDGINKAQEEHRYHSNWRTMASDFNL	
CONSENSUS-A	NQIIEKLI?K?KVYLSWVPAHKGIGGNEQVDKLV?GIRKVLFLDGIDKAQE?HE?YH?NW?AMASDFNL	681
CONSENSUS-B	s---q---K-E---a-----a-----e-K-s-r-----	742
ISOLATE-C	---Q---S-ER-----S-----E-K-S-R-NE-I	
CONSENSUS-D	s---Q---K-E---A-----Q-----E-K-N-R-----	740
CONSENSUS-O	Q---E-TK-E?---T-----KI---KD-R---E---Q---D-K-S---L-?-G-	669
CONSENSUS-U	---Q---Q-D-----S-----E-K-S-R-----	742
CONSENSUS-CPZ	??-?-?-K?E?I-----?---?---?---?---S---?---?---?	510
DESIGNED SEQ	PPIVAKEIVANCDCQLKGEAMHGQVDCSPGIWQLDCTHLEGKVILVAVHVASGYIEAEVIPAETGQETA	
MUTATED AAS	P S I N I	

FIGURE 4 (Cont)

SUBSTITUTE SHEET (RULE 26)

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ISOLATE-C	--L-----R-----N---A---GIQ-----E-	
CONSENSUS-D	--l-----V-----A---GIK-----D-	880
CONSENSUS-O	--L---A-----P---??M-A---??IQH-----A---S-Q---D-	798
CONSENSUS-U	-----V-----A---IK-----E-	882
CONSENSUS-CPZ	--L---?---T---?---A---?I-----?---?---?---D-	631
DESIGNED SEQ	AEHLKTAVQMAVFIHNFKRKGGIGGYSAGERIIDIIATDIQTKELQKQITKIQNFRVYYRDSRDPWKG	
MUTATED AAS	R V S N L L	
ISOLATE-E	AEHLKTAVQMAVFIHNFKRKGGIGGYSAGERIIDIIATDIQTKELQKQITKIQNFRVYYRDSRDPWKG	
CONSENSUS-A	AEHLKTAVQMAVFIHNFKRKGGIGGYSAGERIIDIIA?DIQTKELQKQI?KIQNFRVYYRDSRDPWKG	880
CONSENSUS-B	-----v-----t-----T-----l-----	952
ISOLATE-C	-----R-----S-----N-L-----	
CONSENSUS-D	-----i-----	950
CONSENSUS-O	---?---V---T---?---L-SQ---T---L-?N-----	865
CONSENSUS-U	-----M-T-----T-----N-----	952
CONSENSUS-CPZ	--?---?---?---T?---?---?---T---??---?---L-?---?---?---	687
vif cds ->		
DESIGNED SEQ	AKLLWKGEAVVIQDNSDIKVVPRRKAKIIRDYGKQMGDDCVAGRQDED	
MUTATED AAS	A S	
ISOLATE-E	AKLLWKGEAVVIQDNSDIKVVPRRKAKIIRDYGKQMGDDCVAGRQDED	
CONSENSUS-A	AKLLWKGEAVVIQDNSDIKVVPRRKAKIIRDYGKQMGDDC?AGRQDED	929
CONSENSUS-B	-----V-s-----	1002
ISOLATE-C	-----A-V-----	
CONSENSUS-D	-----V-----V-S-----	1000
CONSENSUS-O	-Q-----KG-----T-SM-N--T-SSESMEQPGEIP	925
CONSENSUS-U	-----V-G---KHGTAW	1008
CONSENSUS-CPZ	-?-----QGEL-----V-S--N--KHGTAW	742

CONSENSUS A-CPZ FROM LOS ALAMOS HIV SEQUENCE DATABASE
 ISOLATE-C FROM GENBANK U46016 HIV-1 SUBTYPE C (ETHIOPIA)
 ISOLATE-E FROM GENBANK U51189 HIV-1 SUBTYPE E ISOLATE 93TH253 (THAILAND)

FIGURE 4 (Cont)

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```
<- pol cds
```

DESIGNED SEQ	MENRW.Q.VMIVWQVDRMRIRTWNSLVKHHMYISKKAKQWGFYRHHYESQHHPKVSSEVHIPLGE..ARLVI	
MUTATED AAS	L K K H N FD R D I	
ISOLATE-E	MENRW.Q.VMIVWQVDRMRIRTWNSLVKHHMYISKKAKQWGFYRHHYESQHHPKVSSEVHIPLGE..ARLVI	
CONSENSUS-A	MENRW.Q.VMIVWQVDRMrIRTWNSLVKHHMYVSKKAKGWGFYRHHfEsRhpkvsSEVHIPLGd..ARLvv	66
CONSENSUS-B	-----?-.-----k-----i-g-----y-t-xi-----i	66
ISOLATE-C	MENRW Q VLIWQVDRMKIRTWNSLVKHHMHISRRANGWVYRHHYDSRHHPKVSSEVHIPLGE ARLII	
CONSENSUS-D	-----K-----?R-----Yd-p-----I-----E-----	65
CONSENSUS-O	-----L-----?--QKVKA-----Y-K-?-?-??N-?-?-Y--N-?-?-Y--V??--??--	54
CONSENSUS-CPZ	?????.?-??-----??-?-?-?-I???-????-?-?-Y????-???-?-?-?????K-?-	34
DESIGNED SEQ	RTYWGLQTGEKQWQLGHGVSIEWRQKRYSTQVDPDLADQLIHLYQFDCFSdstIRRAILGQIVRRRCEYP	
MUTATED AAS	K H R H Q L S G <u>H</u> <u>H</u> A A HR S Q	
	K Y	
ISOLATE-E	RTYWGLQTGEKQWQLGHGVSIEWRQKRYSTQIDPDLADQLIHLYQFDCFSdstIRRAILGQVRRRCEYP	
CONSENSUS-A	RTYWGLHTGErDWHLGHGVSIEWrQKRYSTQvDPDLADqLIHLhYfdCFsdsAIRkAILGeivRPRCEYQ	136
CONSENSUS-B	t-----q-----k-----y-----e-----n-----h-----s-----	136
ISOLATE-C	KTYWGLQTGERDWHLGHGVSIEWRLRSYNTQVDPGLADHLIHMHYFDCFAESAIRKAILGQVRSRCDYQ	
CONSENSUS-D	k-----?-----Q-----KR-----G-----MY-----E-----h-----S-----	132
CONSENSUS-O	T-----MP-----?E-----?Y?-K--I--ET--RM-----T--T?--?-----QR-LTK--?	118
CONSENSUS-CPZ	T??-?-??-?-?-?-?-?-?G?-?-?-?-T--??-??-?-?-?-??-?-?-?-?????-?-K	76

```
vpr cds ->
```

DESIGNED SEQ	SGHNKVGSLQYLAL.KAL...ITPKKIRPPLPSVKKLTEDRWNKPKIKGHRENHTMNGH
MUTATED AAs	A T K K E T R G
ISOLATE-E	SGHNKVGSLQYLAL.KAL...TTPKKIRPPLPSVKKL TEDRWNKPKIKGHRENPTMNGH\$
CONSENSUS-A	AGHNKVGS LQYLAL .KAL...VaPtkaKPPLPSvkKLtEDRWnePQKTRGRHRGsR?mNgH\$
CONSENSUS-B	-----a---..it-k-i-----?-?-K----K-----ht-----
ISOLATE-C	AGHNKVGS LQYLAL TAL IKPKAKPPLPSVSKLVEDKW NKPKQKTRGRRGNHTMNGH
CONSENSUS-D	-----?-?-t---..i--k-I-----K-----R-----?-?-HT---
CONSENSUS-O	?-SQ-T-?-?-?-?-V....k????-Q?-----K???I-DQL?-?-S----
CONSENSUS-CPZ	?-?Q-?-?-?-?-?-?-r????-??-K??R???-?EN?TR---

FIGURE 5

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[illegible]

FIGURE 7

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		high-affinity binding site nls			
\ / 3' sj		exon \ / exon		/ <- -> /	
DESIGNED SEQ	MAGRSGSTDE ELL RAVRIINILYQSNPYPSSEG	TRQTRKNRRRRWRARQ	QIRAI	SERILSTCLGRS	
MUTATED AAs	D K I K	S A R	E	.HS W NF P	
ISOLATE-E	MAGRSGSTDE ELL RAVRIINILYQSNPYPSSEG	TRQTRKNRRRRWRARQ	QIRAI	SERILSTCLGRS	
CONSENSUS-A	MAgRSG?sDE.eLL.KaIRIKiLYQSNPyPkPkG.SRQARKNRRRRWRARQ	QIDSLSeRILStCLGRP			66
CONSENSUS-B	-----d-----tV-l--f-----p-s-e-.T---R-----e-----r-i--w----y---s				67
ISOLATE-C	MAGRSGDSDE ELL KAVRIIKILYQSNPYPTPEG	TRQARRNRRRRWRARQ	QIH	TLSE	RILSNFLGRP
CONSENSUS-F	-----N-?T-----R-?-Y-----E-.T---R-----?-R??-?-S-----				61
CONSENSUS-O	-----E-...Q?-?Q--Q-----?-?-?-N-----R--A-V-?-A?-?-A-VVHG?				56
CONSENSUS-U	-----DA--...RVV-----P-E-.T--T-----RAI--F-----S				67
CONSENSUS-CPZ	----?E-?????-??-VK-----?-?-?-R-?-?-?-?-?-?-V-?-?-?-				41
Leu-rich effector domain / <- -> /					
DESIGNED SEQ	AEPVPLQLPPLERLHLDCSEDCGTSQTQSQGTETGVGRPQISGESSVILGPGTKN				
MUTATED AAs	N SD	N L AV S			
ISOLATE-E	TEPVPLQLPPLERLHLDCSEDCGTSQTQSQGTETGVGRPQISGESSVILGPGTKN				
CONSENSUS-A	AEPVPLQLPPLERLhLDCsEdcgTSgTQq?qq?etGVGrpQvsVEssavLGSgTKn				120
CONSENSUS-B	-----t-----?-----?-----s--il---p---e---E\$				115
ISOLATE-C	AEPVPLQLPPLERLNLDCSESDTSQTQSQGTETGVGNP	PREMATURE TRUNCATED			
CONSENSUS-F	E-----?---?IN?--?E.Q-A?E.....S--T-G--H-----E\$				105
CONSENSUS-O	Q?NN?VD-----Q-?IRDp-?D?L????TVDPRAEDN\$CL-NLCS	CNT??????N\$			95
CONSENSUS-U	-----I---C-----G-----P--T-----S-PI-G---TI-----E\$				123
CONSENSUS-CPZ	PK-GD-E--E-DK-S-Q-V-TTQDV--SNTSQPQ-AT-ETVPAGGNYSI--K-A--				97

FIGURE 8

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DESIGNED SEQ		MTPL	EIIAIVAFIVALIIAIVVWTIAYI	EYRKLRLQR	RIDRL	IKTRERA	EDSGNES	
MUTATED AAs			L	L	VF	K	K	
CONSENSUS-A	mtPL???	eIcAivGLiVALILAIvVWTivGI.eyKklkqr.....	Kidrl?ikRirERA.EDSGNES	57				
CONSENSUS-B	-qs-	q-?--a-v--a-i-----f-?-r-i-R-----?	-----d-----	56				
ISOLATE-C	MVDLLAKVDYRIVIVAFIVALIIAIVVWTIAYI	EYRKLRLQR	RIDRL IKTRERA	EDSGNES				
CONSENSUS-D	-Q--	v-l--A-v---i-----f--crr-kr-----	-----w--d-----?	57				
CONSENSUS-F	-S??	LAIS?TA-----I-----?Y--R--R-----	N--YE?--?-----	51				
CONSENSUS-O	-H??	?LL-?I??SAL??INV??-?.F?..LR?Y-??QDR?E?E-LER.LR--?IR.D-DY--		42				
CONSENSUS-U	-Q--	T-T-----V-F-A-----S-Y--R-IR-K.....	LD-----	57				
CONSENSUS-CPZ	--??	????L??????W?-CI???I????-??YK???.....	??????-?.??I?????.?????-	14				
DESIGNED SEQ		EGDTEE	LSTM	VDM	GNYDLGVDNNL			
MUTATED AAs		R	AL					
CONSENSUS-A	?GDT?E.L?kL...VEM.GnydlgvdnNL\$							78
CONSENSUS-B	e--qe--sa-????-H?apwdvdD--							79
ISOLATE-C	DGDTEE	LSTM	VDM	GNLRLLDVNDL				
CONSENSUS-D	E--rE--sa-----HhAPwd?Ddm-							80
CONSENSUS-F	E--AE--A?-----G--PFIP-DI---							73
CONSENSUS-O	N?EE-QEVM?-...??SH-F?NPM.FE??							59
CONSENSUS-U	D---E--ST....M--YEYILDND---							81
CONSENSUS-CPZ	-?EE--??-?????????FANP?.???DE							23

FIGURE 9

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      <- vpU cds
signal peptide / gp120

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DESIGNED SEQ	MRVKETQMNWPNL WK	W GTLILGLVIIC SA SD NLWVTVYVGVPVWRDADTTLFCAS	
MUTATED AAs	R	M M M E E T	
CONSENSUS-A	Mrvmgig?nyq?l.wr??...	??W.gtmilg??iic.na??e.?lWVtVyYGVpVWkdaeTTLfcAS	49
CONSENSUS-B	??-k-rk-h-?-----	??-l-mIm--s-----e-t-----	53
CONSENSUS-C	--r--?r-w-qw-.i.....	--ILGFwmlm--.v-g.n-----e-k-----	53
CONSENSUS-D	--r?-er--h-?-----	--L--mLM--.sv.a??-----E-t-----	52
CONSENSUS-E	--Ket-m-wpn-.k-.....	--l-lv--?s-.Sd.N-----r-d-----	55
CONSENSUS-F	-?-R-M-R-W-H-.GK.....	--LLF--iL-----n-----e-T-----	53
CONSENSUS-G	-?-k--r-W-H-.k.....	--L--LV--.s.sn.n-----E--D-----	54
CONSENSUS-O	-t-tMKaM?KrNr.Kl.....	-?lylamALi-P-.LS--??Q-YA--s----E--?Pv----	51
CONSENSUS-U	-??-E?-R-??-?.....	-??-?-----?-----?-----	36
CONSENSUS-CPZ	-?????-??-?.....	-?????-?-???.T.--.??-?-----?P?-----?	19

DESIGNED SEQ	DAKAHETFEVHNVW	ATHACVPTDPNPQEIHLE	NVTENFNMWKNNNMVEQM	QEDVISLWD	QSLKPCVKLT	
MUTATED AAs	YD	VV	D	D	H	I
CONSENSUS-A	dAkAydtE?HNvWv?ATHaCVPTDPnPgEi?le.NVTE?FnmwkNnMVeQmheDiISLWD.qSLkPCvKt					113
CONSENSUS-B	-----v-----	-----vv-?-?	n-----			119
CONSENSUS-C	-----e?-v-----	-----mv-----	n-----	d--d-----		119
CONSENSUS-D	-----s-k?-a-i-----		N-----			117
CONSENSUS-E	-----He-v-----		n-----	q--v-----?		121
CONSENSUS-F	-----S-Ek-v-----		n-d-----	T-----		120
CONSENSUS-G	-----s-s-----		n-----		E-----	120
CONSENSUS-O	-----NLTS-q-I-.sQ-----	-----?-?-yp-?-	d--I--Y--d-----		qm-----	114
CONSENSUS-U	-----?-?-?-?-?-?-?-?-?-?	-----?-?-?-?-?-?				91
CONSENSUS-CPZ	?-???S-----?					56

DESIGNED SEQ	PLCVTLNCTNANLINVN	HYPERVARIABLE REGIONS 1/2	
MUTATED AAs			
CONSENSUS-A	PLCVTL?C.?????????n?t?????????n?t?????n?????..?????????.....m		126
CONSENSUS-B	-----n-.td-----?-?-----??-----??..????-		133
CONSENSUS-C	-----n-.-----?-----t-?-?-----.....??		132
CONSENSUS-D	-----n-.t-----?-?-----t-?-?-----?????????		131
CONSENSUS-E	-----n-.tna-----.-l-----nv-i-nvsnii-g-it.....?????		150
CONSENSUS-F	-----n-?t-a-----.-a-----t-?-?-q-----..?tlkE		139
CONSENSUS-G	-----n-.t-----.-V-t-----?-?-?.....NcT-?en-nNstv-----???		143
CONSENSUS-O	F---Qm-.td-----.-l-----.....		129
CONSENSUS-U	-----n-.t-----.-e-----P????..???		105
CONSENSUS-CPZ	-?-????-.....?-?-?-----P????..???		60

DESIGNED SEQ	HYPERVARIABLE REGIONS 1/2	
MUTATED AAs		
CONSENSUS-A	?..?e....ikNCsfNmTtelrdkkqkvysLfYrldvVqi???????n?????.....n?????????	160
CONSENSUS-B	e??g-?????-i-si-v-e-a--k--p-d-----?-----????-----	169
CONSENSUS-C	-?-.....-a--?-A-----i-pl-----s-----	166
CONSENSUS-D	-?-g....m-----i-?v---kq-ha-k-----t-----	165
CONSENSUS-E	..d....Vr-----hA--k-i-----s---?..?-----	185
CONSENSUS-F	eP.ga....Q-----v---Q?-Ha-----I-p-s-----ns-----??-----	177
CONSENSUS-G	..e....m-----i--i---ktE-A--k-----p-n-----?ss-----sd	182
CONSENSUS-O	..n-??..m-?-?-V-V-k---E-KQA--Vs-L?k?N-ts---T-----m	164
CONSENSUS-U	??-?-.....i-----kt?-a--k-----P-n-----n-----?-----	137
CONSENSUS-CPZ	??-?-.....???-?-??-???-??????-??-????-T-----	73

DESIGNED SEQ YRLINCNTSVIKQACPKVSFDPIPIHYCAPAGYAILKCNCKNFNGTGPCKNVSSVQCTHG IKPVVSTQL
MUTATED AAs S A T I T E F N K T T R

FIGURE 10
SUBSTITUTE SHEET (RULE 26)

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CONSENSUS-D -----t-----n-k-----r----- 234
CONSENSUS-E -----V-K-----i-D-----t-y-----N-n-----S----- 254
CONSENSUS-F -----?-----T-----Wd-----Y-----N-k----- 245
CONSENSUS-G -----v-T-K-----n-d-----r-n----- 251
CONSENSUS-O -?-t--STt-?------y--F--N?T-----l-?-itV-T-----T----- 228
CONSENSUS-U -----?-k-----n-K----- 205
CONSENSUS-CPZ -????--T?--?-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?-H-----?-?-?-?-?- 120

```

<- V3 neutralization loop

DESIGNED SEQ LLNGSLAEE EIIIRSENLTNNAKTIIVHLNESVEINCTRP NNNTR K HYPERVARIABLE REGION 3/4/5
 MUTATED AAs VV F D V Q K V S T

```

CONSENSUS-A LLnGSLAe???v?irSenitnNaktiiVql??pV?InCtRP.nnntr.ks???vri???gpGq??afiya. 279
CONSENSUS-B -----e.e-v-----f-d-----nes-e-----?-----ih-----r-----t. 296
CONSENSUS-C -----e.i-----l-----v-----h-n-s-e-v-----i-----t----- 291
CONSENSUS-D -----E.EiI-----l-----?-----nes-----?y?---qr---tp---?---l-t? 288
CONSENSUS-E -----e.eIi-----L-----h-NKS-e-----s-----t-----it-----v--r. 312
CONSENSUS-F -----e.dii---q---sd-----h-Nes-q-----I?-----r----- 302
CONSENSUS-G -----e.eI-----?---d---v-----nksie-----I?-----f----- 305
CONSENSUS-H -----?-----D-T-N-----K-----?-----I?-----?-----?----- 39
CONSENSUS-O I---T-Skg.kIr-Mgk--?dsg-N---T-N--?i-mt-e---g-?-v.Qe---i?-----m--W-S. 279
CONSENSUS-U -----E.E-i-----?---d-----net-k-----?-----?-----v----- 261
CONSENSUS-CPZ -?-????--?-?????K?????V?????-E??-??-?-?.G-?-?.??...?Q-----M..T--N. 142

```

V3 neutralization loop -> * *** ^ ^ ^ CD4

DESIGNED SEQ HYPERVARIABLE REGION 3/4/5
 MUTATED AAs

```

CONSENSUS-A tgdi.....iG.dirqAhCnvsr?eWn?tlq?V....a?QLr?..f???nkt....??iIF?n.ssGGD 320
CONSENSUS-B --?-???-----i--ak--n--kqi....v-k--e??q-----v-nq?----- 342
CONSENSUS-C -----I?-k-e-----?kK-ae..h-p-----k-?----- 334
CONSENSUS-D -?r?????..?-?-----i-?a?-k--q-----k-gd?.ll-----t--kp----- 331
CONSENSUS-E -----k-y-EINGTk--e?-kq....tek-ke..H--n-----qP?p----- 360
CONSENSUS-F --?-?-----k-----gtq-----e-----?a?-ks..h--?-----k-ns----- 344
CONSENSUS-G -----?-----em--n-----?-----i-----?-----t-ns--a----- 344
CONSENSUS-H ?-?-?-----?-----I??-?-?-?-?-?-?-?-?-?..H?-----P----- 65
CONSENSUS-O M-.l???n?k???s-?-Y-?YnaTd-?ka-kqt....eRYLe..Lv...-?-----vtm?-n?s-?- 321
CONSENSUS-U -----i--t?--n--q-----k..y--n--?-----ns?----- 306
CONSENSUS-CPZ ?E??.....?-T-?-?-?N?T?-?-????-????-?-?-?-?-?-?A-???-?..???-- 157

```

| CD4 * * *** ^ ^ ^ ^ ^ ^ ^

DESIGNED SEQ HYPERVARIABLE REGION 3/4/5
 MUTATED AAs

```

CONSENSUS-A lEitthsFnCggef?FYCnts?lF.nstW????????...n?t.?????..?n?t????..???sndtI 355
CONSENSUS-B p--vm-----tg-----?-----?-----?-----?-----?----- 374
CONSENSUS-C -----r-----y-----p...?g-?-----?-----?-----?----- 366
CONSENSUS-D p-----?-----?-----?-----?-----?-----?-----?----- 361
CONSENSUS-E --m-h--r-----t-----n-cig-----e-m....gc--g-----?----- 398
CONSENSUS-F -----m--r-----?-----?-----?-----?-----?-----?----- 372
CONSENSUS-G -----r-----g--?s?-----n??-----?-----?-----?----- 373
CONSENSUS-H ?-??-?-?-?-?-?-?K-----?-----?-----N--?-G-----?----- 92
CONSENSUS-O ?-v-hlh--H-----m--y-Fsc-----?-----?-----?-----n-----?g-? 356
CONSENSUS-U -----t-----?-----?-----?-----d---?-----?-----?----- 336
CONSENSUS-CPZ P-V??-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?-I-----G?? 175

```

* CD4 | * ^ ^ ^ | CD4 ^ ^ ^

DESIGNED SEQ HYPERVARIABLE REGION 3/4/5
 MUTATED AAs

```

CONSENSUS-A t..lq.CrI.kqIvnm.wQrvqg.AmYapPIq.g?irb?sNITGllLTRDGg??...nns??...???? 401
CONSENSUS-B -??-p-----i-----e-k-----?---q--s-----?-----?-----?----- 419
CONSENSUS-C --p-----i-----e-r-----?---n-t-k-----?-----?-----?----- 411
CONSENSUS-D --p-----i-----?---k-----e-----?---s-----?-----?-----?----- 405

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FIGURE 10 (Cont)

SUBSTITUTE SHEET (RULE 26)

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		gp120 / gp41										
DESIGNED SEQ	TFRPGGGDIKDNWRSELYKYKVVKIEPLGVAPTR AKRRVV	EREKRA	VG	IGAMIFGFLGA								
MUTATED AAs	I NMR E K I K Q L FL											
CONSENSUS-A	?netFrPgGgdmdrDNWrsELYkYKvVkiePlGvaPtr.akrRVV...	eREKRA??vg.lGavflgflGa	462									
CONSENSUS-B	-t-i-----k-----q-----?i-m-----		480									
CONSENSUS-C	-?-----e-k-----?-----?i-----		470									
CONSENSUS-D	-----r-----?-----I-----m-----		465									
CONSENSUS-E	-----NiK-----Q-----i-----I-----Mif-----		508									
CONSENSUS-F	-?-----n-k-----e-----q-----k-----?--l-----		478									
CONSENSUS-G	-----k-----R-----G-----?-----		481									
CONSENSUS-H	-?V-----?--?--?--?--?--?--?--?--?--?--?--?		187									
CONSENSUS-O	--?--l--?--k--I--T--f--rvK--FS--ki--RP?Igt?t?H-----ML--v--S--		462									
CONSENSUS-U	-?-----?-----?-----M-----?-----		435									
CONSENSUS-CPZ	?????-?????-?--?--?--?--?--?--S-----??R?????--?--Q--?--?--?--?--?--?		227									
DESIGNED SEQ	AGSTMGAASITLTVQARQLLSGIVQQQSNLLRAIEAQOHLQLTVWGIKQLQARVLAVERYLKD QKFLG											
MUTATED AAs	M L N M I QL											
CONSENSUS-A	AGSTmGAAsITLTVqArqLlSGIVqqQsNllrAIEaQqhlLkLTvWGIKQLQARvLAvErYlRd.QQLLG	531										
CONSENSUS-B	-----?-----n-----q-----k-----?	548										
CONSENSUS-C	-----?-----m-Q-----t-----i-----k-----	539										
CONSENSUS-D	-----?-----N-----Q-----k-----	533										
CONSENSUS-E	-----Q-----K-----Kf-----	577										
CONSENSUS-F	-----n-----Q-----?	546										
CONSENSUS-G	-----V-----Q-----?	549										
CONSENSUS-H	-----?-----?-----?	227										
CONSENSUS-O	-----ATa-----tHt--?K-----D-----Q-----R--S-----R--R--L--L--TliQN-----n	529										
CONSENSUS-U	-----??-??-?-----?--?--N-----Q-----ES-----	496										
CONSENSUS-CPZ	-----??-??-?-----?--?--?-----Q--S--V-----?-----?-----?-----?	279										
* * ^^^ ^^^ ^^^												
DESIGNED SEQ	LWGCsGKIICtTAVPWNSSW	S NKSLEEIWNMTWMWEWEREISNYTNQIYE ILTESQNQQ										
MUTATED AAs	I L N T F D IQ SL K											
CONSENSUS-A	IWGCsGKIICtTnVPWNsSW.....S.Nks??dIWdnMTWlqWdKEIsnYT?iIY?.LiEesqnqQ	586										
CONSENSUS-B	-----a-----a-----?--l--?--?--me-er--d--l--t-----	603										
CONSENSUS-C	-----a-----q-----m--r-----dt--r--L--d-----	597										
CONSENSUS-D	-----h-----r--L--e--?--mE--ER--d--Gl--s-----?	589										
CONSENSUS-E	L-----I-----A-----t-----r--fEE--n-----iE--eR-----Nq--e--ILT-----	636										
CONSENSUS-F	L-----qEe--?--ME--e-----SnE--R-----?	603										
CONSENSUS-G	-----t-----fnE-----Ie--eR--N--q--n--l-----?	606										
CONSENSUS-O	L--K-----Y--S--K--?t--?G.....??neS--?L--Q--qq--n--vSS?--e--e--Q?A--?	580										
CONSENSUS-U	L-----T-----LVTL--L--ME--R-----QV--G--L--D--K--	555										
CONSENSUS-CPZ	L--??-??-?--T--N--?????????..??-?--?--?--Q--?LV?--?G?--?..?L?A?--?	312										
\ / 3'sj												
DESIGNED SEQ	DRNEQELLELDKWASLWNWFDITNWLWYIKIFIMIVGGLIGLRIVFAVLsIVNRVRQGYSPLSFQTLTPA											
MUTATED AAs	KD A N SK V I I T											
CONSENSUS-A	EkNEqdlLaLDkwanLwnWfdIsnWLWYIriFimIVGGLIGLRivfaVlsIInRVRqGYSP1sFQtltP?	655										
CONSENSUS-B	-----e--e-----?--t-----k-----v-----v-----?l-a	671										
CONSENSUS-C	-----k-----s--?-----?--t-----k-----i-----V-----n	664										
CONSENSUS-D	-----e--?-----S-----s--T-----k-----lv-----l-a	657										
CONSENSUS-E	DR--K--e-----S-----T-----K-----i-----V-----p?Hh	705										
CONSENSUS-F	-----e-----S-----K-----K-----v-----K-----?--hi-S	672										
CONSENSUS-G	-----?S--s--s-----k-----v-----?HH	674										
CONSENSUS-O	-----K?--E--E--Si--l--TK-----K--A--I--A--v--ViMI--NlVKNI-----Q--L--IP??h	647										
CONSENSUS-U	--S--K--E-----S-----G--T-----K-----T--F-----L--T	625										
CONSENSUS-CPZ	-?-????-?E--?--?S-----T?-----K--?--?--?I?-----?????-??R?-----?--?--?--?	355										

V/ 3'sj

DESIGNED SEQ	DRNEQELLELDKWasLWNWFDITNWLWYIKIFIMIVGGLIGLRIVFAVLSIVNRVRQGYSPLSFQTLIPA										
MUTATED AAs	KD A N SK V I I T										
CONSENSUS-A	EkNEqdLLaLDkWanLwnWFDIsnWLWYIriFimIVGGLIGLRIVfaVlsiInRVRqGYSPLSFQtltp?	655									
CONSENSUS-B	-----e--e-----s-----?--t-----k-----v-----v-----?l--a	671									
CONSENSUS-C	-----k-----s--?-----?--t--k-----i-----V-----n	664									
CONSENSUS-D	-----e--?-----S-----s--T--k-----lv-----l--a	657									
CONSENSUS-E	DR--K--e-----S-----T--K-----i-----V-----p?Hh	705									
CONSENSUS-F	-----e-----S-----K-----V--K-----?--hi--S	672									
CONSENSUS-G	-----?S--s--s-----k-----V-----?HH	674									
CONSENSUS-O	-----K?--E--E--Si--l--TK-----K--A--I--A--v--ViMI--NlVKNI--Q--L--IP??h	647									
CONSENSUS-U	--S--K--E--S--G--T--K-----T--F-----L--T	625									
CONSENSUS-CPZ	-?-??-?E--?S-----T-----K--?--?--?I?-----????-??R?-----?--?--?--?	355									

<- tat cds

DESIGNED SEQ	PRG PDRPEGIEEEGG EQDRDRSVRLVSGFLALAWDDLRLSLCLFSYHRLRLDLILI A AR IVELLGHS										
MUTATED AAs	LGR RG G N S N F V T R										

FIGURE 10 (Cont)

SUBSTITUTE SHEET (RULE 26)

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CONSENSUS-O	q?E.agT-G-TG-g---e--p-Wtp-Pq---?-LYT---TII-Wt--L-SNLaSg.I.....qk	702
CONSENSUS-U	--G.----G-T-----E-NN--V--N-----E-----I-----L---V.....KG-R..	685
CONSENSUS-CPZ	Q?- .?????E-?-?-- .??--?-???-??-???-?-----N-GIW--QS-TSLACN.V.W-##LKT---L	398

<- rev cds

DESIGNED SEQ	SLRGLRRG	WEALKYL WNLQYWQELKISAVSLLNATAIAVAEGTDRVIEVAQRAGRAILHI	
MUTATED AAs	K Q	G W G L L N I GW I V W N	
CONSENSUS-A	slkgrlrlg.....weglkyL.wNLllyWgrELK?SainLldtiAiavAgwtDRvIEigOrigRAilnI		780
CONSENSUS-B	?.....??-.....-a--w.---q--sq---n--vs--nat-----Eg-----vv--a?---h-		789
CONSENSUS-C	--r--qr-----a-----Gs-vq--l--k--S-----EG--i--??-?-----?		787
CONSENSUS-DR-----a-----q--?q--n--S-----Eg---?--v--a?--v-h-		773
CONSENSUS-E	-----R-----G-----Q--I--S--naT-----VA-gaW---h-		832
CONSENSUS-F	.?R--R-----A--l-.G--t--Q--N--s--N-T--v--Eg---?--?AL--?-----		787
CONSENSUS-G	i-----q--N-----?-----N-----vv--aC-----		800
CONSENSUS-O	lI?y-g--LWILGQktIeaCR-c?Av?Q--LQ--qn--T-----?--V--N--gi-lGi---?G---		767
CONSENSUS-UR-----A--G--V--Q--N--S--NAT--V--EG--I--V--C-----		741
CONSENSUS-CPZ	I-HS---L.....R-R-CL-.GGIIQ--K--I--S--AT-----EG--I--AF-VTL-I-R--		460

DESIGNED SEQ	PRRIRQGLERALL
MUTATED AAs	T F

CONSENSUS-A	PrRIRQGLERaLl\$	793
CONSENSUS-B	-?-----	801
CONSENSUS-C	-----F-a--q-	800
CONSENSUS-D	-?-----	785
CONSENSUS-E	-----	845
CONSENSUS-F	-?-----?	798
CONSENSUS-G	-----	813
CONSENSUS-O	-----?--	779
CONSENSUS-U	-----F-----	754
CONSENSUS-CPZ	-----	473

FIGURE 10 (Cont)

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DESIGNED SEQ	MGGKWSKSSLVGWPEVRERIRQT	PPAAEGVGAVSQD	LDKHGAITSSNTPA	
MUTATED AAs	C P A RA	A A R	<u>Y</u> L A	
ISOLATE-E	MGGKWSKSSIVGWPQVRERIKQT	PPAAEGVGAVSQD	LDKHGAVTSSNM	
CONSENSUS-A	MGGKWSKsSiVgWPeVrkRmRqT.....?PtAAkGVGAvSQD.....LDkhGAiTSSnt??			48
CONSENSUS-B	-----?--?--?--e---ra?????????????--Ep--d-----r-----e-----aa			46
ISOLATE-C	MGGTMSKCSVPVGWPAIRERIRRA	APAAEGVGAASRD	LDKYGALTSSNTPA	
CONSENSUS-D	-----AI-E-I-r-?????.....dP--D-----R-----E-----as			50
CONSENSUS-O	--NA??-?KF?--??--?--R?.....??P?-?PC-P---??-RE.....-A?R-G-?-H-PQ			38
CONSENSUS-U	--?--?--?--?--E-I-?-???.-----P???.-----?--?--?--?--?--?--A-			31
\vskip6pt				
	* SH3-binding SH3-binding			
DESIGNED SEQ	NNADCWVLK AQE E EG VGFPVRPQVPLRPMTYKGAFDLSFFLKEKGGLEGLVYSKKRQEILDWLW			
MUTATED AAs	P A E E	A V L	D I Q D	
ISOLATE-E	NNADCWVLK AQE E EG VGFPVRPQVPLRPMTYKGAFDLSFFLKEKGGLEGLVYSKKRQEILDWLW			
CONSENSUS-A	tnpsCawLE?Aqe?.d..e?.VGFPVRPQVPLRPMTYKGAvDLShFLKEKGGLDGLIys?kRQEILDWLW			110
CONSENSUS-B	--ad-----e??-e?-----a-?-----e---?--q---d-----			108
ISOLATE-C	NNPDCAWLE AQEE E EE VGFPVRPQVPLRPMTYKGAFDLSFLKEKGGLEGLIYSKKRQEILDWLW			
CONSENSUS-D	--ad-----ES.-E-----e-----E--W-K-----			115
CONSENSUS-O	N-AAL-F-?.SH?..?..-?-----?--F--F-----?--H--A-----?			93
CONSENSUS-U	N-??-??-?.??-..E?-E-----?--F--?-----?--?-----			83
\vskip6pt				
	* SH3-binding			
DESIGNED SEQ	YHTQGFFPDWHNYTPGPGIRY PLTFGWCFKLVPVDPREVE EINKGENNCLLHPMSQHGMEDEREVL			
MUTATED AAs	N Y Q T	S A E	ICL D K	
ISOLATE-E	YHTQGFFPDWHNYTPGPGIRY PLCFGWCFKLVPVDPREVE EDNKGENNCLLHPMSQHGIEDEREVL			
CONSENSUS-A	YnTQGfFPDQWQNYTPGPGtRf.PLTFGWCFKLVPvDPaEVE.eat?GEnNSLLHPICQHGMdDe?revLm			176
CONSENSUS-B	-h---y-----?--y?-----e-ek-----ne-----msl-----pE-----?			174
ISOLATE-C	YNTQGFFPDWQNYTPGPGVRY PLTFGWCFKLVPVDPSEVE EINEGENNCLLHPASLHGMEDEDREVLK			
CONSENSUS-D	-----I-----I-Y-----e-----q-----E--t-c-----?-----E-pE-q--k			182
CONSENSUS-O	-?-----?-----?-----L-----S?E-A-RLGNT?-?A?-----A-?--?E-?H?-I-?			150
CONSENSUS-U	-H---?-----?-----?-----?-----?-----N-----C-----?S-----?E-----?			138
\vskip6pt				
	*			
DESIGNED SEQ	WKFDsRLARRHIARELRPEFY KDC			
MUTATED AAs	H L M H Y			
ISOLATE-E	WKFDsALARRHIARELRPEFY KDC			
CONSENSUS-A	WkFDsRlAlkhRa?ElhPefY.KDC\$			199
CONSENSUS-B	-r-----fh-m-r-----y-----?TSMCLQGTFRWGISREARLGGTGEWRALRCCT			230
ISOLATE-C	WKFDsHLARRHMARELHPEY KDC			
CONSENSUS-D	-R-N---fE-K-R-m-----			206
CONSENSUS-O	-?--RS-G?T-?--??--LF?--?			166
CONSENSUS-U	-----S-??-?-R-?--?--?--			157

FIGURE 11

GAG OVERLAPPING SEGMENTS

M G A R A S V L S G G K L D A W E K I R L R P G G K K Y K	Segment 1
atg ggc gcc agg gcc agc rtc ctc agm ggc rag ctg gac gcc tgg gaa aag att agg ctc agg cct ggc gga aag aaa aag tat arg	R
W E K I R L R P G G K K Y K M K H L V W A S R E L E R F A	Segment 2
tgg gag aaa atc aga ctg aga ccc gga ggc aaa aag aaa tac ara mtg aaa cac mtt gtg tgg gcc tcc agg gaa ctg gaa agg ttt gcc	
M K H L V W A S R E L E R F A L N P G L L E T A E G C Q Q I	Segment 3
L I	S K
mtg aag cat mtc gtc tgg gct agc aga gag ctc gag aga ttc gct ctg aat ccc rgc ctg ctc gag aca kcc gaa ggc tgt mag caa att	
L N P G L L E T A E G C Q Q I L E Q L Q S A L K T G S E E L	Segment 4
ctc aac cct rgc ctc ctg gaa acc kct gag gga tgt maa cag atc ctg gra cag ctc cag ycc gcc ctc mag aca ggc wcc gaa gag ctc	
L E Q L Q S A L K T G S E E L K S L Y N T I A T L W C V H Q	Segment 5
ctc grg caa ctg caa yct gct ctg maa acc gga wca gag gaa ctg arg tcc ctg twt aac aca rtc gct acc ctc tgg tgt gtg cat cag	
K S L Y N T I A T L W C V H Q R I E V K D T K E A L D K I E	Segment 6
ara agc ctc twc aat acc rtc gcc aca ctg tgg tgc gtc cac caa agg att gas gtc arg gac aca aag gaa gcc ctc gac aaa atc gaa	

FIGURE 12

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R I E V K D T K E A L D K I E E E Q K K S Q Q K T Q Q A A A
 Segment 7
 D R
 aga atc gaw gtg ara gat acc aaa gag gct ctg gat aag att gag gag gwg caa aas aaa agc mag caa aag aca caa cag gct gcc gct
 E E Q K K S Q Q K T Q Q A A D T G S S S K V S Q N Y P I V
 Segment 8
 V N K
 gaa gwa cag aaw aag tcc maa cag aaa acc cag caa gcc gcc gat aca ggc arc tcc agc mag gtc agc caa aac tat ccc att gtg
 D T G S S K V S Q N Y P I V Q N A Q G Q M V H Q P L S P R
 Segment 9
 N Q
 gac acc gga art agc tcc maa gtg tcc cag aat tac cct atc gtc cag aat syc caa ggc caa atg gtc cac caa scc mtc tcc ccc aga
 Q N A Q G Q M V H Q P L S P R T L N A W V K V I E E K G F N
 Segment 10
 L A I
 caa aac syc cag gga cag atg gtg cat cag sct.mtt agc cct agg acc ctc aac gct tgg gtc aag gtc rtc gaa gag aaa gsc ttt arc
 T L N A W V K V I E E K G F N P E V I P M F S A L S E G A T
 Segment 11
 V A S
 aca ctg aat gcc tgg gtg aaa gtg rtt gag gaa aag gsa ttc art ccc gaa gtg att ccc atg ttt wcc gct ctg tcc gag gga gcc aca

FIGURE 12 (Cont)

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P E V I P M F S A L S E G A T P Q D L N M M L N I V G G H Q
 Segment 12
 cct gag gtc atc cct atg ttc wca gcc ctc agc gaa ggc gct acc ccc caa gac ctg aat ayg atg ctc aac ayc gtc ggc gga cac caa
 T T

P Q D L N M M L N I V G G H Q A A M Q M L K E T I N E E A A
 Segment 13
 cct cag gat ctc aac ayg atg aat ayt gtg gga ggc cat cag gcc gct atg caa atg ctg aaa gas aca atc aat gag gaa gcc gct
 T D

A A M Q M L K E T I N E E A A E W D R V H P V H A G P I P P
 Segment 14
 gct gcc atg cag atg ctc aag gaw acc att aac gaa gag gct gcc gag tgg gac aga rtc cat ccc gtc cat gcc gga ccc rtt scc cct
 D I V A

E W D R V H P V H A G P I P P G Q M R E P R G S D I A G T T
 Segment 15
 gaa tgg gat agg rtt cac cct gtg cac got ggc cct rtc sct ccc ggc caa ats aga gag cct agg gga agc gat atc gct ggc aca acc
 I V A

G Q M R E P R G S D I A G T T S T L Q E Q I G W M T N N P P
 Segment 16
 gga cag atr agg gaa ccc aga ggc tcc gac att gcc gga acc aca agc aca ctg caa gag caa atc gsa tgg atg aca arc aat ccc cct
 I A S

S T L Q E Q I G W M T N N P P I P V G D I Y K R W I I L G L
 Segment 17
 tcc acc ctc cag gaa cag att gsc tgg atg aca art aac cct ccc rtc cct gtc gga gas att tac aaa agg tgg att atc ctc ggc ctg
 A S V E

FIGURE 12 (Cont)

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I P V G D I Y K R W I I L G L N K I V R M Y Q P V S I L D I Segment 18
 V E S
 rtt ccc gtg ggc gaw atc tat aag aga tgg atc att ctg gga ctc aac aaa atc gtg aga atg tat yma ccc gtc agc att ctg gat atc

 N K I V R M Y Q P V S I L D I R Q G P K E P F R D Y V D R F Segment 19
 S K
 aat aag att gtc agg atg tac yma cct ctc tcc atc ctc gac att arg caa ggc cct aag gaa ccc ttt agg gat tac gtc gac aga ttc

 R Q G P K E P F R D Y V D R F Y K T L R A E Q A T Q E V K N Segment 20
 K F S D
 ara cag gga ccc aaa gag cct ttc aga gac tat gtg gat agg ttt twc aaa acc ctc agg gct gag caa gcc wca cag gaw gtg aaa aac

 Y K T L R A E Q A T Q E V K N W M T E T L L V Q N A N P D C Segment 21
 F S D D
 twt aag aca ctg aga gcc gaa cag gct wcc caa gas gtc aag aat tgg atg acc gas aca ctg ctc gtg caa aac gct aac cct gac tgt

 W M T E T L L V Q N A N P D C K S I L K A L G T G A T L E E Segment 22
 D T R P S
 tgg atg aca gaw acc ctc ctg gtc cag aat gcc aat ccc gat tgc aag wcc atc ctc arg gct ctg gga mcc gga gcc wca ctg gaa gag

 K S I L K A L G T G A T L E E M M T A C Q G V G G P S H K A Segment 23
 T R P S G
 aaa wca att ctg ara gcc ctc ggc mca ggc gct wcc ctc gag gaa atg atg aca gcc tgt cag gga gtg gga ggc cct rgc cat aag gct

FIGURE 12 (Cont)

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M M T A C Q G V G G P S H K A R V L A E A M S Q A T H A N I
 atg atg acc gct tgc caa ggc gtc ggc gga ccc rgt cac aaa gcc agg gtc ctg gca gag gct atg tcc cag gyg amc mac gct aac att
 Segment 24
 V N N
 R V L A E A M S Q A T H A N I M M Q R G N F K G Q K R I I K
 Segment 25
 V
 P
 aga gtg ctg gcc gaa gcc atg agc caa gyc amc mat gcc aat atc atg atg cag aga ggc aat ttc ara ggc cma aag aga atc rtc aaa
 M M Q R G N F K G Q K R I I K C F N C G K E G H L A R N C R
 Segment 26
 R
 P
 atg atg caa agg gga aac ttt arg gga cmg aaa agg att rtc aag tgc ttt aac tgt gga aag gaa ggc cat mtc gct arg aat tgc aga
 C F N C G K E G H L A R N C R A P R K K G C W K C G K E G H
 Segment 27
 I
 K
 tgt ttc aat tgc ggc aaa gag gga cac mtt gcc ara aac tgt agg gcc cct aga aag aaa ggc tgt tgg aaa tgc gga arg gaa ggc cat
 R
 A P R K K G C W K C G K E G H Q M K D C T E R Q A N F L G K
 Segment 28
 R
 gct ccc agg aaa aag gga tgc tgg aag tgt ggc ara gag gga cac cag atg aag gat tgc aca gag aga cag gct aac ttt ctg gga aag
 Q M K D C T E R Q A N F L G K I W P S N K G R P G N F P Q S
 Segment 29
 H
 L
 S
 caa atg aaa gac tgt acc gaa agg caa gcc aat ttc ctg ggc aaa atc tgg ccc tcc mrc aaa ggc aga ccc gga aac ttt cgc caa agc

FIGURE 12 (Cont)

I W P S N K G R P G N F P Q S K P E P T A P P A E N F G F G
H L R S
Segment 30
att tgg cct agc mrc aag gga agg cct ggc aat ttc cyg cag tcc arg cct gag cct acc gct ccc cct ggc gaa arc ttt rga ttc ggc
S
K P E P T A P P A E N F G F G E E T T P S P K Q E Q K D K E
R S R Q P
Segment 31
ara ccc gaa ccc aca gcc cct ccc gct gag art ttc rgg ttc gga gag gaa acc aca ccc tcc cma aag caa gag cma aag gat aag gag
Q
E E T T P S P K Q E Q K D K E H Y P P S A S L K S L F G N D
Q P L L
Segment 32
gaa gag aca acc cct agc cmg aaa cag gaa cmg aaa gac aaa gaa cwc tac ccc cct tya gcc agc ctc aag tcc ctg ttt ggc aat gac
L
(H) Y P P S A S L K S L F G N D P L S Q
L S
Segment 33
cwc tat cct ccc tya gct tcc ctg aaa agc ctc ttc gga aac gat ccc tya tcc caa

FIGURE 12 (Cont)

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POL OVERLAPPING SEGMENTS

F F R E N L A F Q Q G K A R E F S S E Q T G A N S S A S R K	Segment 1
ttc ttt agg gaa amc ctg gct ttc cmg caa ggc raa gcc aga gag ttt ycc agc gaa cag aca rga gcc aat agc ycc rcc tcc agg aaa	
F S S E Q T G A N S S A S R K L G D G G A E R Q G T S S S	Segment 2
ttc yct tcc gag caa aca rgg gct aac tcc yct rca agc aga aag ctg gga gac gga ggc gga gcc gas aga cag gga aca agc tcc agc	
L G D G G A E R Q G T S S S F S F P Q I T L W Q R P L V T	Segment 3
ctc ggc gat ggc gga ggc gct gaw agg caa ggc acc tcc agc tcc ytc arc ttt ccc caa atc aca ctg tgg caa agg cct ctg gtc acc	
F S F P Q I T L W Q R P L V T I K I G G Q L K E A L L D T G	Segment 4
ytt art ttc cct cag att acc ctc tgg cag aga ccc ctc gtg aca rtc aaa atc ggc gga cag ctc awa gag gct ctg ctc gac aca ggc	
I K I G G Q L K E A L L D T G A D D T V L E D I N L P G K W	Segment 5
rtt aag att gga ggc caa ctg awa gaa gcc ctc ctg gat aca gga gcc gat gac acc gtc ctg gaa gaw ats aat ctg cct ggc arg tgg	
A D D T V L E D I N L P G K W K P K M I G G I G G F I K V R	Segment 6
gct gac gat aca gtg ctc gag gas ats aac ctc ccc gga ara tgg aag cct aag atg att ggc gga atc ggc gga ttc att aag gtg aga	

FIGURE 12 (Cont)

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K P K M I G G I G G F I K V R Q Y D Q I L I E I C G K K A I Segment 7
 aaa ccc aaa atg atc gga ggc att gga ggc ttt atc aaa gtc agg cag tat gac caa atc mtt atc gaa atc tgt gga mas aag gct atc
 Q Y D Q I L I E I C G K K A I G T V L V G P T P V N I I G R Segment 8
 caa tac gat cag att mtt att gag att tgc ggc mas aaa gcc att ggc aca gtg ctc gtg gga cct acc cct gtg aat atc att ggc aga
 G T V L V G P T P V N I I G R N M L T Q I G C T L N F P I S Segment 9
 gga acc gtc ctg gtc ggc ccc aca ccc gtc aac att atc gga agg aac mtg ctg aca cag mtt ggc ygc acc ctc aac ttt ccc att agc
 N M L T Q I G C T L N F P I S P I D T V P V K L K P G M D G Segment 10
 aat mtg ctc acc caa mtc gga ygc aca ctg aat ttc cct atc tcc ccc att gas aca gtg cct gtg aaa ctg aaa ccc gga atg gat ggc
 P I D T V P V K L K P G M D G P K V K Q W P L T E E K I K A Segment 11
 cct atc gaw acc gtc ccc aag ctc aag cct ggc atg gac gga ccc aaa gtg aaa cag tgg ccc ctc acc gaa gag aaa atc aaa gcc
 P K V K Q W P L T E E K I K A L T E I C K E M E E G K I S Segment 12
 cct aag gtc aag caa tgg cct ctg aca gag gaa aag att aag gct ctg aca gmg att tgc ama gag atg gag vaa gag gga aag att agc

FIGURE 12 (Cont)

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L T E I C K E M E E G K I S K I G P E N P Y N T P V F A I Segment 13
 A T K Q
 ctc acc gmg atc tgt ama gaa atg gaa vaa gaa ggc aaa atc tcc arg att ggc cct gag aat ccc tat aac aca ccc rtc ttt gcc att
 K I G P E N P Y N T P V F A I K K K D S T K W R K L V D F R Segment 14
 R I
 arg atc gga ccc gaa aac cct tac aat acc cct rtc ttc gct atc aag aaa aag gac tcc acc aaa tgg aga aag ctc gtg gat ttc aga
 K K K D S T K W R K L V D F R E L N K R T Q D F W E V Q L G Segment 15
 aaa aag aaa gat agc aca aag tgg agg aaa ctg gtc gac ttt agg gag ctc aac aaa agg aca cag gat ttc tgg gag gtc dag ctc ggc
 E L N K R T Q D F W E V Q L G I P H P A G L K K K S V T V Segment 16
 gaa ctg aat aag aga acc caa gac ttt tgg gaa gtg caa ctg gga atc cct cac cct gct gga ctg aaa aag tcc gtg aca gtg
 I P H P A G L K K K S V T V L D V G D A Y F S V P L D E S Segment 17
 K D
 G
 att ccc cat ccc gcc ggc ctc aag aaa aag gtc acc gtc ctg gat gtg gga gac gct tac ttt agc gtc ccc ctc gac raa rrc

FIGURE 12 (Cont)

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L D V G D A Y F S V P L D E S F R K Y T A F T I P S I N N E
 Segment 18
 K D T
 G
 ctc gac gtc ggc gat gcc tat ttc tcc gtg cct ctg gat raa rrc ttc aga aag tat acc gct ttc aca atc cct agc aya aac aat gag
 F R K Y T A F T I P S I N N E T P G I R Y Q Y N V L P Q G W
 Segment 19
 TTT
 ttt agg aaa tac aca gcc ttt acc att ccc tcc ayc aat aac gaa acc cct ggc att agg tat cag tat aac gtc ctg cct cag gga tgg
 T P G I R Y Q Y N V L P Q G W K G S P A I F Q S S M T K I L
 Segment 20
 P
 P Q
 aca ccc gga atc aga tac caa tac aat gtg ctc ccc caa ggc tgg aag gga tcc ccc scc att ttc caa agc tcc atg mcc maa atc ctc
 K G S P A I F Q S S M T K I L E P F R I K N P E M V I Y Q Y
 Segment 21
 P Q
 K Q D
 aaa ggc agc cct sct atc ttt cag tcc agc atg mca mag att ctg gag cct ttt agg awa maa aac cct gas atg gtc atc tat cag tat
 E P F R I K N P E M V I Y Q Y M D D L Y V G S D L E I G Q H
 Segment 22
 K Q D
 gaa ccc ttc aga awa mag aat ccc gaw atg gtg att tac caa tac atg gac gat ctg tat gtg gga agc gat ctg gaa atc gga cag cat

FIGURE 12 (Cont)

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M D D L Y V G S D L E I G Q H R T K I E E L R A H L L R W G
 Segment 23
 atg gat gac ctc tac gtc ggc tcc gac ctc gag att ggc caa cac agg rcc aaa atc gaa gag ctc agg sma cac ctc ctg ara tgg gga
 R T K I E E L R A H L L R W G F T T P D K K H Q K E P P F L
 Segment 24
 (A) E Q
 aga rca aag att gag gaa ctg aga smg cat ctg ctc ara tgg ggc ttc aca acc cct gac aaa aag cat cag aaa gag cct ccc ttt ctg
 F T T P D K K H Q K E P P F L W M G Y E L H P D R W T V Q P
 Segment 25
 ttt acc aca ccc gat aag aaa cac caa aag gaa ccc cct ttc ctc tgg atg gga tac gaa ctg cat ccc gat agg tgg acc gtc cag cct
 W M G Y E L H P D R W T V Q P I E L P E K D S W T V N D I Q
 Segment 26
 tgg atg ggc tat gag ctc cac cct gac aga tgg aca gtg caa ccc atc swg ctc ccc gaa aag gas tcc tgg aca gtg aat gac att cag
 I E L P E K D S W T V N D I Q K L V G K L N W A S Q I Y A G
 Segment 27
 V Q P
 att swg ctg cct gag aaa gaw agc tgg acc gtc aac gat atc caa aag ctc gtg gga aag ctc aac tgg gcc tcc cag att tac scc gga

FIGURE 12 (Cont)

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L K T G K Y S R K R S A H T N D V R Q L T E V V Q K I A T E Segment 34
 A M G K A A (V)
 ctc aag acc ggc aaa tac kct agg awg agg rgt gcc cat acc aat gac ctc arg caa ctg aca gmG gyt gtg caa aag rtt gcc aca gag

D V R Q L T E V V Q K I A T E S I V I W G K T P K F R L P I Segment 35
 K A A V K
 gat ctg ara cag ctc acc gma gyc gtc cag aaa rtc gct acc gaa agc att gtg att tgg gga aag aca ccc aaa ttc ara ctg cct atc

S I V I W G K T P K F R L P I Q R E T W E T W M E Y W Q A Segment 36
 K K A T D
 tcc atc gtc atc tgg ggc aaa acc cct aag ttt arg ctc ccc att cag ara gag aca tgg gaa rcc tgg tgg ayg gas tat tgg caa gcc

Q R E T W E T W M E Y W Q A T W I P E W E F V N T P P L V Segment 37
 K A T D
 caa arg gaa acc tgg gag rct tgg tgg ayg gam tac tgg cag gct acc tgg atc oct gag tgg gag ttt gtg aat acc oct ccc ctc gtg

T W I P E W E F V N T P P L V K L W Y Q L E K D P I V G A E Segment 38
 E A V
 aca tgg att ccc gaa tgg gaa ttc gtc aac aca ccc cct ctg gtc aag ctc tgg tat cag ctc gag aaa gas cct atc gyt ggc gyt gag

K L W Y Q L E K D P I V G A E T F Y V D G A A S R E T K L G Segment 39
 E A V N
 aaa ctg tgg tac caa ctg gaa aag gam ccc att gyc gga gyc gaa acc ttt tac gtc gac gga gcc gct arc aga gag aca aag ctc ggc

FIGURE 12 (Cont)

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T F Y V D G A A S R E T K L G K A G Y V T D R G R Q K V I S Segment 40
 aca ttc tat gtg gat ggc gct gcc art agg gaa acc aaa ctg gga aag gct ggc tat gtg aca gac aga ggc aga cag aaa rtc rtt agc
 I V
 K A G Y V T D R G R Q K V I S L T E T T N Q K T E L H A I H Segment 41
 I V D Q
 aaa gcc gga tac gtc acc gat agg gga agg caa aag rtt rtc tcc ctg aca gas aca acc aat cag aaa acc gaa ctg caw gcc att cam
 L T E T N Q K T E L H A I H L A L Q D S G S E V N I V T D Segment 42
 D Q Q L
 ctc acc gam acc aca aac caa aag aca gag ctc cam gct atc caw ctg gct ctg caa gac tcc ggc tyg gag gtc aac att gtg aca gac
 L A L Q D S G S E V N I V T D S Q Y A L G I I Q A Q P D R S Segment 43
 L K
 ctc gcc ctc cag gat agc gga tyg gaa gtg aat atc gtc acc gat agc caa tac gct ctg gga atc att cwg gct cag cct gac ara agc
 S Q Y A L G I I Q A Q P D R S E S E V V S Q I I E E L I K K Segment 44
 L K L N K Q
 tcc cag tat gcc ctc ggc att atc cwa gcc caa ccc gat arg tcc gag tcc gag stc gtg art cag att atc gaa vag ctc atc aaa aag
 E S E V V S Q I I E E L I K K E K V Y L S W V P A H K G I G Segment 45
 L N K S R A
 gag tcc gag stc gtg art cag att atc gaa vag ctc atc aaa aag gaa arg gtc tac ctc kcc tgg gtg cct gcc cac aag gga atc gga

FIGURE 12 (Cont)

E K V Y L S W V P A H K G I G G N E Q V D K L V I S G I R K Segment 46
R A S A
gag ara gtg tat ctg kct tgg gtc ccc gct cat aaa ggc att ggc gga aac gaa cag gtc gac aaa ctg gtc akc kct ggc att agg aaa

G N E Q V D K L V I S G I R K V L F L D G I N K A Q E E H E Segment 47
S A D
ggc aat gag caa gtg gat aag ctg gtg akt kcc gga atc aga aag gtg ctg ttc ctg gga atc rat aag gct cag gaa gag cac gaa

V L F L D G I N K A Q E E H E R Y H S N W R T M A S D F N L Segment 48
D K N E
gtc ctg ttt ctg gat ggc att rac aaa gcc caa gag gaa cat gag arg tat cac tcc aac tgg agg aca atg gct arc gam ttc aat ctg

(R) Y H S N W R T M A S D F N L P P I V A K E I V A N C D K C Segment 49
K N E P S C
ara tac cat agc aat tgg aga acc atg gcc art gas ttt aac ctg ccc cct atc gtc sct aag gaa atc gtc gcc wrt tgc gat aag tgt

P P I V A K E I V A N C D K C Q L K G E A M H G Q V D C S P Segment 50
P S I N C
cct ccc att gtg scc aaa gag att gtg gct wrt tgt gac aaa tgc cag ctg aag gga gag gct atk cac gga cag gtc rac tgt agc cct

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FIGURE 12 (Cont)

Q L K G E A M H G Q V D C S P G I W Q L D C T H L E G K V I Segment 51
I
caa ctg aaa ggc gaa gcc ats cat ggc caa gtg rat tgc tcc ccc ggc att tgg caa ctg gat tgc aca cac ctc gag gga aag rtt atc
N
G I W Q L D C T H L E G K V I L V A V H V A S G Y I E A E V Segment 52
I
gga atc tgg cag ctc gac tgt acc cat ctg gaa ggc aaa rtc att ctg gtc gcc gtc cac gtc tcc ggc tac att gag gct gag gtc
L V A V H V A S G Y I E A E V I P A E T G Q E T A Y F L L K Segment 53
I
ctc gtg gct gtg cat gtg agc gga tat atc gaa gcc gaa gtc gtc atc cct gcc gaa acc gga cag gaa acc gct tac ttt mtc ctc aag
I
I P A E T G Q E T A Y F L L K L A G R W P V K V I H T D N G Segment 54
I
att ccc gct gag aca ggc caa gag aca gcc tat ttc mtt ctg aaa ctg gct ggc aga tgg cct gtg ara ryc att cac aca gac aat ggc
R T
L A G R W P V K V I H T D N G S N F T S A A V K A A C W A Segment 55
R T
ctc gcc gga agg tgg ccc gtc arg rya atc cat acc gat aac gga agc aat ttc aca agc rct rcc gtc aag gct gcc tgc tgg tgg gct
T T
S N F T S A A V K A A C W A N I K Q E F G I P Y N P Q S Q Segment 56
T T
tcc aac ttt acc tcc rct rct gtg aaa gcc gct tgt tgg tgg gcc rrt atc maa cag gaa ttc gga atc cct tac aat ccc caa agc caa
G Q

FIGURE 12 (Cont)

N I K Q E F G I P Y N P Q S Q G V V E S M N K E L K K I I G Segment 57
G Q
rrc att mag caa gag ttt ggc att ccc tat aac cct cag toc cag ggc gtc gtc gaa agc atg aac aaa gag ctc aag aaa atc att ggc
G V V E S M N K E L K K I I G Q V R E Q A E H L K T A V Q M Segment 58
D
gga gtc gtc gag toc atg aat aag gaa ctg aaa aag att atc gga cag gtc agg gam cag gct gag cat ctg aaa acc gct gtc caa atg
Q V R E Q A E H L K T A V Q M A V F I H N F K R K G G I G G Segment 59
D R
caa gtc aga gas caa gcc gaa cac ctc aag aca gcc gtc cag atg gcc gtc ttc att cac aat ttc aaa agg ara ggc gga atc gga ggc
A V F I H N F K R K G G I G G Y S A G E R I I D I I A T D I Segment 60
R V S
gct gtc ttt atc cat aac ttt aag aga arg gga ggc att ggc gga tac tcc gcc gga gag aga atc rtt gac att atc gct asc gat atc
Y S A G E R I I D I I A T D I Q T K E L Q K Q I T K I Q N F Segment 61
V S N L
tat agc gct ggc gaa agg att rtc gat atc att gcc wcc gac att cag tat aag gaa ctg caa aas caa atc mya aag att cag aat ttc
Q T K E L Q K Q I T K I Q N F R V Y R D S R D P I W K G P Segment 62
N L L
caa tac aaa gag ctc cag aam cag att myc aaa atc caa aac ttt agg gtc tac tat agg gat agc aga gac cct mtc tgg aag gga ccc

FIGURE 12 (Cont)

R V Y Y R D S R D P I W K G P A K L L W K G E G A V V I Q D

Segment 63

aga gtg tat tac aga gac tcc agg gat ccc mtt tgg aaa ggc cct gcc aaa ctg ctg tgg aaa ggc gaa ggc gct gtc atc caa gac

L

A K L L W K G E G A V V I Q D N S D I K V V P R R K A K I I

Segment 64

gct aag ctg ctg tgg aag gga gag gga gcc gtc gtc att cag gat aac tcc gac att aag gtc gtc cct agg aga aag gct aag att atc

N S D I K V V P R R K A K I I R D Y G K Q M A G D D C V A G

Segment 65

aat agc gat atc aaa gtg gtc ccc aga agg aaa gcc aaa atc att agg gat tac gga aag caa atg gct ggc gmt gac tgt gtc gct rgc

A

S

R D Y G K Q M A G D D C V A G R Q D E D

Segment 66

agg gat tac gga aag caa atg gct ggc gmt gac tgt gtc gct rgc agg caa gac gaa gac

A

S

FIGURE 12 (Cont)

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VIF OVERLAPPING SEGMENTS

M E N R W Q V M I V W Q V D R M R I R T W N S L V K H H M Y	Segment 1
atg gaa aac aga tgg caa gtg atc gtc tgg caa gtg gat agg atg arg att agg aca tgg aaw agc ctc gtg aaa cac cat atg yat	
M R I R T W N S L V K H H M Y I S K K A K G W F Y R H H Y E	Segment 2
atg ara atc aga tac tgg aas acc ctg gtc aag cat cac atg yac atc tcc aag aaa gcc aaw ggc tgg ttc tat agg cat cac twt gas	
I S K K A K G W F Y R H H Y E S Q H P K V S S E V H I P L G	Segment 3
att agc aaa aag gct aas gga tgg ttt tac aga cac cat twc gaw agc cra cac cct aag gtc agc tcc gag gtc cac att ccc ctc ggc	
S Q H P K V S S E V H I P L G E A R L V I R T Y W G L Q T G	Segment 4
tcc crg cat ccc aaa gtg tcc agc gaa gtg cat atc cct ctg gga gas gct agg ctc rtc att arg aca tac tgg ggc ctc cas aca ggc	
E A R L V I R T Y W G L Q T G E K D W Q L G H G V S I E W R	Segment 5
gaw gcc aga ctg rtt atc ara acc tat tgg gga ctg caw acc gga gag ara gac tgg cas ctc ggc caw ggc gtc agc att gag tgg agg	

FIGURE 12 (Cont)

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E K D W Q L G H G V S I E W R Q K R Y S T Q V D P D L A D Q
 R H Q L S K
 Segment 6
 gaa arg gat tgg caw ctg gga cas gga gtg tcc atc gaa tgg aga mwg aaa ags tat agc aca cag gtc gac cct grc ctc gcc gat cas
 Q K R Y S T Q V D P D L A D Q L I H L Q Y F D C F S D S T I
 L S G H Y A
 Segment 7
 K
 mwg aag agm tac tcc acc caa gtg gat ccc grt ctg gct gac caw ctg att cac ctc yas tat ttc gat tgc ttt kcc gat agc rca atc
 L I H L Q Y F D C F S D S T I R R A I L G Q I V R R R C E Y
 H A H R S
 Segment 8
 Y
 ctc atc cat ctg yaw tac ttt gac tgt ttc kct gac tcc rcc att agg aga gcc att ctg gga cas aka gtg agm agg aga tgc gaa tac
 R R A I L G Q I V R R R C E Y P S G H N K V G S L Q Y L A L
 H R S Q A
 Segment 9
 aga agg gct atc ctc ggc caw aka gtc ags aga agg tgt gag tat cmg kcc gga cac aat aag gtc ggc tcc ctg caa tac ctc gcc ctc
 P S G H N K V G S L Q Y L A L K A L I T P K K I R P P L P S
 Q A T K
 Segment 10
 cma kct ggc cat aac aaa gtg gga agc ctc cag tat ctg gct ctg amg gct ctg att amg cct aag aaa atc ara ccc cct ctg cct agc

FIGURE 12 (Cont)

K
T

A
L

I
T

P
K

K
K

I
R

P
K

P
L

P
S

V
K

K
K

L
T

E
D

R
W

N
K

P
Q

K
I

T

ama gcc ctc atc ama ccc aaa aag att arg cct ccc ctc ccc tcc gtg aaa aag ctc acc gaa gac ara tgg aat rag cct caa aag aya

Segment 11

V
K

K
L

T
E

D
R

W
N

K
P

Q
K

I
K

G
H

R
E

N
H

T
M

N
G

H

gtc aag aaa ctg aca gag gat arg tgg aac raa ccc cag aaa ayc aag gga crc aga gra aat cac aca atg aat ggc cat

Segment 12

FIGURE 12 (Cont)

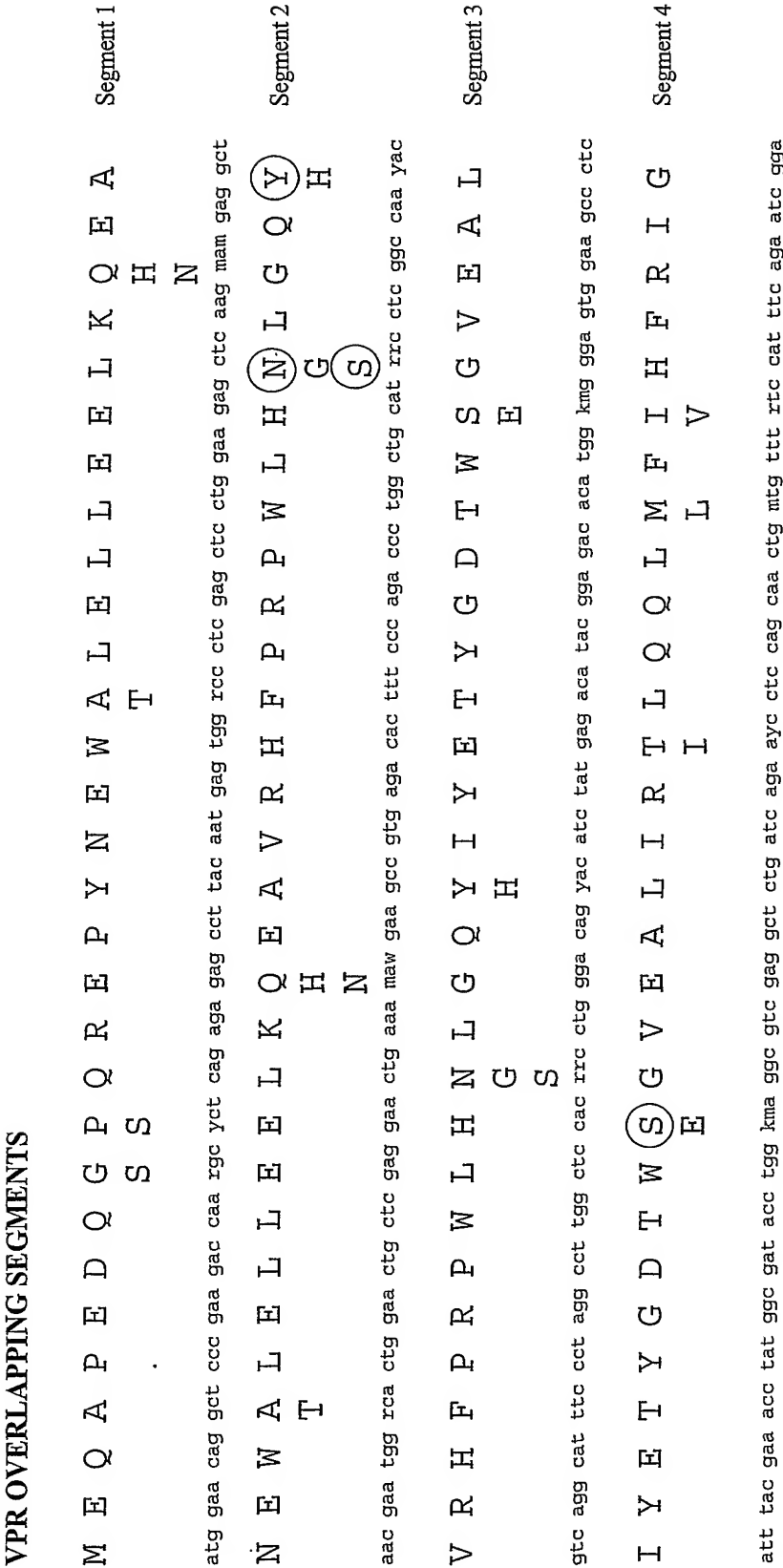


FIGURE 12 (Cont)

I
R
T
L
Q
Q
L
M
F
I
H
F
R
I
G
C
Q
H
S
R
I
G
I
L
R
Q
R
R
A
R

I
L
V

Segment 5

att agg ayc ctg caa cag ctc mtg ttc rtt cac ttt agg att ggc tgc crg cac toc agg att ggc att myc aga cag aga agg gsc aga

C
Q
H
S
R
I
G
I
L
R
Q
R
R
A
R
N
G
A
S
R
S

R
G
S

Segment 6

tgt cra cat agc aga atc gga atc myc agg caa agg aga gst agg aac gga kcc toc agg tcc

FIGURE 12 (Cont)

TAT OVERLAPPING SEGMENTS

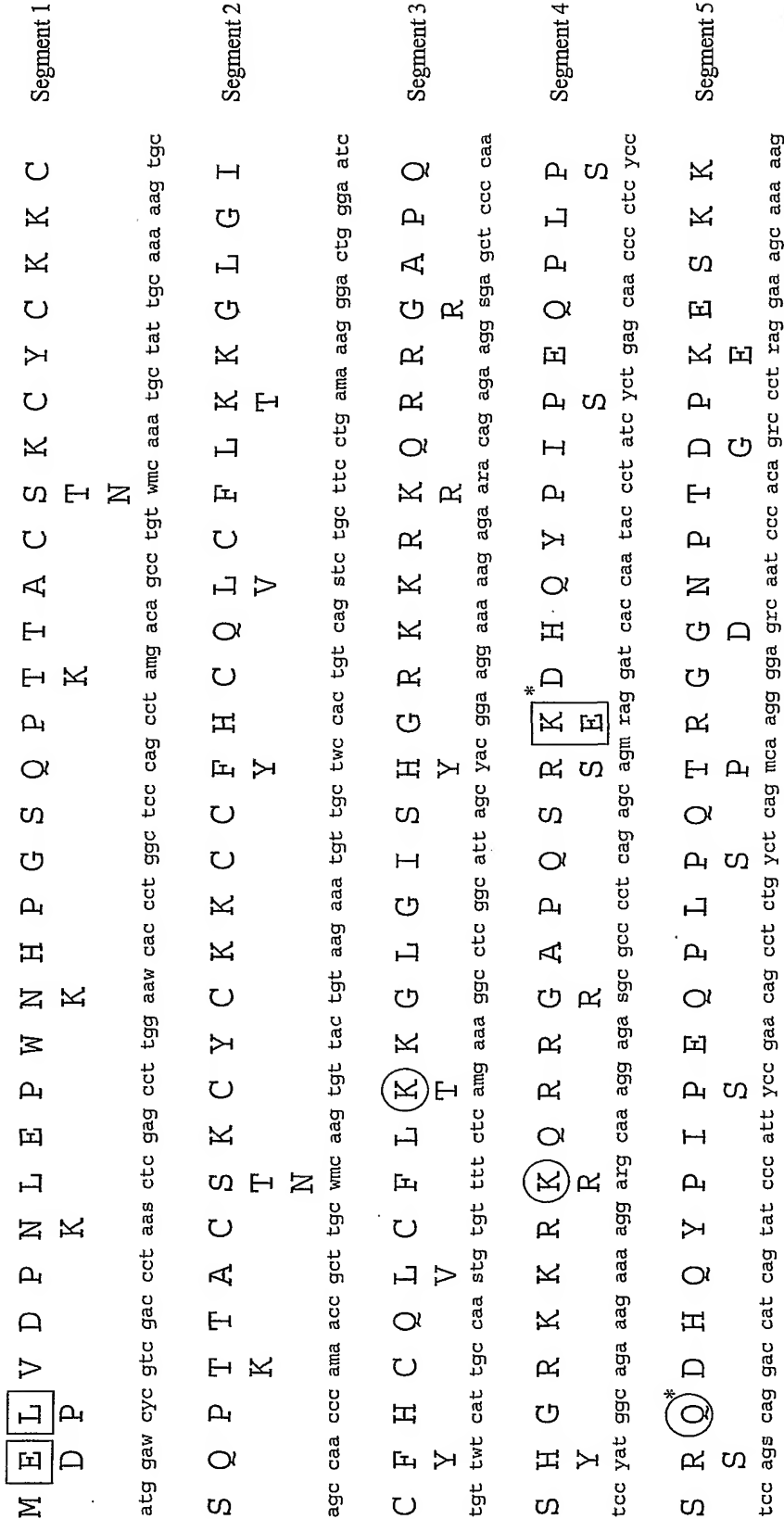


FIGURE 12 (Cont)

Segment 6

Q	T	R	G	Ⓜ	N	P	T	D	P	K	E	S	K	K	E	V	A	S	K	T	E	T	D	P	C	D	
P			D	G						F					K		E		A						F		
caa mcc aga ggc grt aac cct acc grt ccc raa gag tcc aag aaa rag gtc gmg tcc aag rca gag aca gac cct tkt gac																											

* different

FIGURE 12 (Cont)

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REV OVERLAPPING SEGMENTS

M A G R S G S T D E E L L R A V R I I N I L Y Q S N P Y P S	Segment 1
D K I	
N	
atg gct ggc aga agc gga rrc aca gac gaa gag ctc ctg arg gct rtc aga atc att aas att ctg tat cag tcc aac cct tac cct wcc	
V R I I N I L Y Q S N P Y P S S E G T R Q T R K N R R R W	Segment 2
I K	
rtt agg att atc aaw atc ctc tac caa agc aat ccc tat ccc wca agc gaa ggc wcc agg caa rcc aga arg aat agg aga tgg	
S E G T R Q T R K N R R R W R A R Q R Q I R A I S E R I L	Segment 3
S A R	
tcc gag gga wca aga cag rct agg ara aac aga agg aga tgg agg gmg agg caa agg caa atc circ kcc atc tcc gag wgg att ctg	
R A R Q R Q I R A I S E R I L S T C L G R S A E P V P L Q L	Segment 4
E H S W N F P	
aga gma aga cag aga cag att crt ket att agc gaa wgg atc ctc agc amc tlc ctc ggc aga ycc gct gag cct gtg cct cta caa ctg	
S T C L G R S A E P V P L Q L P P L E R L H L D C S E D C G	Segment 5
N F P	
tcc amc tkt ctg gga agg yct gcc gaa ccc gtc ccc cag ctc ccc ctg gaa agg ctc mac ctc gac tgt agc gaa gac wgt grc	

FIGURE 12 (Cont)

Segment 6

Segment 7

Segment 8

P P L E R L H L D C S E D C G T S G T Q Q S Q G T E T G V G
N S D
cct ccc ctc gag aga ctg mac ctg gat tgc tcc gag gat wgc grt acc tcc ggc aca cag caa agc caa ggc aca gag aca gga gtg gga

T S G T Q Q S Q G T E T G V G R P Q I S G E S S V I L G P G
N L A V S
aca agc gga acc caa cag tcc cag gga acc gaa acc ggc gtc ggc mrc cct cag att tyg gga gag tcc agc gyt rtc ctc ggc ycc gga

R P Q I S G E S S V I L G P G T K N
N L A V S
mrc ccc caa atc tya ggc gaa agc tcc ggc rtt ctg gga yct ggc acc aaa aac

FIGURE 12 (Cont)

VPU OVERLAPPING SEGMENTS

M T P L E I I A I V A F I V A L I I A I V V W T I A Y I E Y	Segment 1
<div>[S] [Q] [R] [L]</div> atg aca ycc ctc sag ara atc gct atc gtc gcc ytt atc gtc gcc ctc atc mta gcc att gtc gtc tgg aca atc gyc twc att gag tat	
L I I A I V V T I A Y I E Y R K L L R Q R R I D R L I K R	Segment 2
<div>[L] [V] [F] [K] [K] [E]</div> ctg att mtc gct atc gtc gtc tgg acc att gyg twt atc gaa tac arg aaa ctg ctc arg caa agg ara atc gat agg ctc atc raa agg	
R K L R Q R R I D R L I K R T R E R A E D S G N E S E G D	Segment 3
<div>[K] [K] [E] [I]</div> ara aag ctc ctg ara cag aga arg att gac aga ctg att rag aga ayc aga gag gcc gaa gac tcc ggc aat gag tcc gag gga gac	
T R E R A E D S G N E S E G D T E E L S T M V D M G N Y D L	Segment 4
<div>[I] [R] [A] [L]</div> aya agg gaa agg gct gag gat agc gga aac gaa agc gaa gcc gat asa gaa gag ctc agc rca wtg gtc gac atg ggc aat tac gat ctg	
T E E L S T M V D M G N Y D L G V D N N L	Segment 5
<div>[R] [A] [L]</div> asa gag gaa ctg tcc rcc wtg gtg gat atg gga aac tat gac ctc ggc gtc gac aat aac ctc	

FIGURE 12 (Cont)

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ENV OVERLAPPING SEGMENTS

M R V K E T Q M N W P N L W K W G T L I L G L V I I C S A S	Segment 1
atg aga gtg aaa gag aca cag atg aac tgg ccc aat ctg tgg arg tgg ggc aca mtg att ctg gga mtg gtc ats att tgc tcc gcc tcc	
W G T L I L G L V I I C S A S D N L W V T V Y Y G V P V W R	Segment 2
tgg gga acc wtg atc ctc ggc wtg gtg atk atc tgt agc gct agc gas aat ctg tgg gtg aca gtg tat tac gga gtg cct gtg tgg agg	
D N L W V T V Y Y G V P V W R D A D T T L F C A S D A K A H	Segment 3
gam aac ctc tgg gtc acc gtc tac tat ggc gtc ccc gtc tgg aga gas gct rmc aca acc ctc ttc tgt gcc tcc gac gct aag gct yac	
D A D T T L F C A S D A K A H E T E V H N V W A T H A C V P	Segment 4
gam gcc rmt acc aca ctg ttt tgc gct agc gat gcc aaa gcc yat gas aca gag gtc cac aat gtg tgg gcc aca cac gct tgc gtc ccc	
E T E V H N V W A T H A C V P T D P N P Q E I H L E N V T E	Segment 5
gam acc gaa gtg cat aac gtc tgg gct acc cat gcc tgt gtg cct acc gat ccc aat ccc caa gag rtt swc ctc gag aat gtg aca gag	
T D P N P Q E I H L E N V T E N F N M W K N N M V E Q M Q E	Segment 6
aca gac cct aac cct cag gaa rtc swt ctg gaa aac gtc acc gaa aac ttt aac atg tgg aaa aac rat atg gtc gas caa atg caw gag	

FIGURE 12 (Cont)

Segment 7

N F N M W K N N M V E Q M Q E D V I S L W D Q S L K P C V K
D D H I
aat ttc aat atg tgg aag aat rac atg gtg gam cag atg cam gaa gac rtt atc tcc ctg tgg gac oaa agc ctc aag cct tgc gtc aag

Segment 8

D V I S L W D Q S L K P C V K L T P L C V T L N C T N A N L
I
gat rtc att agc ctc tgg gat cag toc ctg aaa ccc tgt gtg aaa ctg aca ccc ctc tgc gtc acc ctc aac tgt acc aat gcc aat ctg

Segment 9

L T P L C V T L N C T N A N L I N V N
ctc acc cct ctg tgt gtg aca ctg aat tgc aca aac gct aac ctc atc aat gtg aat

FIGURE 12 (Cont)

A
E
E
E
I
I
I
I
R
S
E
N
L
T
N
N
A
K
T
I
I
V
H
L
N
E
S
V
E
I
N

Segment 6

gct gag gaa gat rtt rtc att agg tcc gag aat ytc aca rac aat gyc aaa acc att atc gtc cam ctc aac raa agc gtc gwg att aac

V
D
F
Q
K
V

A
K
T
I
I
V
H
L
N
E
S
V
E
I
N
C
T
R
P
N
N
T
R
K

Segment 7

V
gyl aag aca atc atc att gtg caw ctg aat rag tcc gtg gwa atc aat tgc aca agg cct arc aat aac aca agg ama

K
Q
S
T

FIGURE 12 (Cont)

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GAP IN SEGMENTS DUE TO HYPERVARIABLE REGIONS 3,4 AND 5

T F R P G G D I K D N W R S E L Y K Y K V V K I E P L G V I N M R ayc ttt agg cct ggc gga ggc rat ats ara gac aat tgg aga agc gaa ctg tat aag gtc gtg rag att rag cct ctg gga rtc	Segment 1
E L Y K Y K V V K I E P L G V A P T R A K R R V V E R E K R E K I K Q gag ctg tac aaa tac aaa gtc gtc raa atc raa ccc ctc ggc rtt gcc cct acc ara gcc aaa agg aga gtc sag aga gag aaa agg	Segment 2
A P T R A K R R V V E R E K R A V G I G A M I F G F L G A A K Q L F L gct ccc aca arg gct aag aga agg gtc gtc saa agg gaa aag aga gcc gtc ggc mtt ggc gct atg wtt ytc gga ttc ctc ggc gct gcc	Segment 3
A V G I G A M I F G F L G A A G S T M G A A S I T L T V Q A L F L M gct gtg gga mtc gga gcc atg wtc ytt ggc ttt ctg gga gcc gct ggc tcc acc atg ggc gct gcc tcc ats aca ctg aca gtg caa gcc	Segment 4
G S T M G A A S I T L T V Q A R Q L L S G I V Q Q Q S N L L M L N gga agc aca atg gga gcc gct agc atk acc ctc acc gtc cag gct agg cwa ctg ctc agc gga atc gtc cag caa cag arc aat ctg ctc	Segment 5
R Q L L S G I V Q Q Q S N L L R A I E A Q Q H L L Q L T V W L N M aga cwg ctg tcc ggc att gtg caa cag caa art aac ctc ctg agg gct atc gaa gcc caa cag cat mtg ctc cag acc gtc tgg	Segment 6

FIGURE 12 (Cont)

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R A I E A Q Q H L L Q L L T V W G I K Q L Q A R V L A V E R Y	Segment 7
aga gcc att gag gct cag caa cac wtg ctg caa ctg aca gtg tgg ggc att aag caa ctg caa gcc aga gtg ctc gcc rtt gag aga tac	I
G I K Q L Q A R V L A V E R Y L K D Q K F L G L W G C S G K	Segment 8
gga atc aaa cag ctc cag gct agg gtc ctg gct rtc gaa agg tat ctg aaa gac caa mag ytt ctg gga mtc tgg ggc tgt agc gga aag	I
L K D Q K F L G L W G C S G K I I C T T A V P W N S S W S N	Segment 9
ctc aag gat cag maa ytc ctc ggc mtc tgg gga tgc tcc ggc aaa mtc att tgc aca acc rmt gtg cct tgg aac agc wcc tgg tcc aac	I
I I C T T A V P W N S S W S N K S L E E I W N N M T W M E W	Segment 10
mtt atc tgt acc aca rmc gtc ccc tgg aat tcc asc tgg agc aat aag tcc ytc gaa gag att tgg rat aac atg acc tgg ats saa tgg	I Q
K S L E E I W N N M T W M E W E R E I S N Y T N Q I Y E I L	Segment 11
aaa agc ytt gag gaa atc tgg rac aat atg aca tgg atk sag tgg gag aga gag att agc aat tac aca arc cwa atc tat rag att ctg	I Q
E R E I S N Y T N Q I Y E I L T E S Q N Q Q D R N E Q E L L	Segment 12
gaa agg gaa atc tcc aac tat acc art cwg att tac raa atc ctc acc gaa agc caa aac caa cag gat agg aat gag maa gas ctc ctg	K D

FIGURE 12 (Cont)

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T E S Q N Q Q D R N E Q E L L E L D K W A S L W N W F D I T
 aca gag tcc cag aat cag caa gac aga aac gaa mag gam ctg ctc gmg ctc gac aaa tgg gct agc ctc tgg aat tgg ttt rac att asc
 Segment 13
 K D A N S
 E L D K W A S L W N W F D I T N W L W Y I K I F I M I V G G
 Segment 14
 A N S K
 gma ctg gat aag tgg gcc tcc ctg tgg aac tgg ttc rat atc wcc aas tgg ctg tgg tac att aag att ttc att atg att gtg gga ggc
 N W L W Y I K I F I M I V G G L I G L R I V F A V L S I V N
 Segment 15
 K V I
 aam tgg ctc tgg tat atc aaa atc ttt atc atg atc gtc ggc gga ctg rtt ggc ctc agg att rtc ttt gcc gtc ctg tcc atc rtt aac
 L I G L R I V F A V L S I V N R V R Q G Y S P L S F Q T L L
 Segment 16
 V I T
 ctc rtc gga ctg aga atc rtt ttc gct gtg ctc agc att rtc aat agg gtc agg caa ggc tat agc cct ctg tcc ttc caa acc ctc myc
 R V R Q G Y S P L S F Q T L L P A P R G P D R P E G I E E E
 Segment 17
 T L G R
 aga gtg aga cag gga tac tcc ctc agc ttt cag aca ctg myg ccc gct ccc aga ggc cct gac aga cgc gra sgc att gag gaa gag
 P A P R G P D R P E G I E E E G G E Q D R D R S V R L V S G
 Segment 18
 L G R R G G N
 cct gcc cct agg gga ccc gat agg cyg grg rga atc gaa gag gaa ggc gga gag cra grc aga grc aga agc gtc agg ctc gtg art ggc

FIGURE 12 (Cont)

I
A
V
A
E
G
T
D
R
V
I
E
V
A
Q
R
A
G
R
A
I
L
H
I
P
R
R
I
R
Q

att gcc gtc gcc gra kgg aca gac aga rtc att gag gtc gyc caa agg gct kgg aga gcc att ctg mat atc cct asa aga atc aga cag

Segment 25

R
A
G
R
A
I
L
H
I
P
R
R
I
R
Q
G
L
E
R
A
L
L

aga gcc kgg agg gct atc ctc mac att ccc asg agg att agg caa ggc ytt gag aga gcc ctc ctg

Segment 26

FIGURE 12 (Cont)

L K E K G G L E G L V Y S K K R Q E I L D L W V Y H T Q G F Segment 7
ctc aag gaa aag gga ggc ctc gas gga ctg rtt tac tcc maa aag agg caa gas att ctg gat ctg tgg gtg tat mac aca cag gga twc
R Q E I L D L W V Y H T Q G F F P D W H N Y T P G P G I R Y Segment 8
D N Y Q T V
aga cag gaw atc ctc gat ctc tgg gtc tac mat acc caa ggc twt ttc cct gac tgg cas aat tac aca ccc gga ccc gga ryc aga tac
F P D W H N Y T P G P G I R Y P L T F G W C F K L V P V D P Segment 9
Q T V
ttt ccc gat tgg caw aac tat acc cct ggc cct ggc rya agg tat ccc ctc acc ttt ggc tgg tgc ttt aag ctc gtg cct gtg gat ccc
P L T F G W C F K L V P V D P R E V E I N K G E N N C L L Segment 10
S A E
cct ctg aca ttc gga tgg tgt ttc aaa ctg gtc ccc gtc gac cct ags gaa gta gaa gag ryc aac raa ggc gaa aac aat tgc ctc ctg
R E V E I N K G E N N C L L H P M S Q H G M E D E R E V Segment 11
S A E I C L D
agw gag gtc gag gaa ryc aat rag gga gag aat aac tgt ctg ctc cac cct ats rgt cwg cat ggc atg gaa gac gaa aga gag gtc

FIGURE 12 (Cont)

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Segment 12

H P M S Q H G M E D E E R E V L I W K F D S R L A R R H I A

I C L

cat ccc ats rgc cwa cac gga atg gag gat gag'gaw agg gaa gtg ctg awa tgg aaa ttc gat agc crt ctg gct ckc agg cat ats got

Segment 13

L I W K F D S R L A R R H I A R E L R P E F Y K D C

K H L M

ctc awa tgg aag ttt gac tcc crc ctc gcc ckg aga cat ats gcc agg gaa ctg crt ccc gaa twc tac aaa gac tgc

FIGURE 12 (Cont)

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The Genetic Code- First and Second Most Frequently Used Codons

A	R	N	D	C	E	G	H	I
Ala	Arg	Asn	Asp	Cys	Gln	Gly	His	Ile
GGC/GCT	AGG/AGA	AAC/AAT	GAC/GAT	TGC/TCT	CAG/CAA	GAA/GAG	GGC/GGA	ATC/ATT

The Genetic Code- First and Second Most Frequently Used Degenerate Codons For Two or More Amino Acids

TWO BASES AT A SINGLE POSITION

AD	GMC/GMT	RM	AKT/	ND	RAC/RAT	DN	RAC/RAT	CW	TGS/TGK	OR	CRG/CRA	ED	GAS/GAM	CW	KGG/	HN	MAC/MAT	IM	ATS/ATK
AE	GMG/GWA	RW	WGG/YGG	NH	MAC/MAT	DA	MAC/MAT	CR	YGC/YGT	QE	SAG/SAA	EQ	SAG/SAA	GD	GRC/GRT	HD	SAC/SAT	IN	AWC/AWT
AG	GSC/GST	RC	YGC/YGT	NI	AWC/AWT	DE	AWC/AWT	CG	KGC/KGT	QH	CAM/CAW	EA	GMG/GWA	GC	KGC/KGT	HQ	CAM/CAW	IF	WTC/WTI
AP	SCC/SCT	RQ	CRG/CRA	NK	AAS/AAM	DG	AAS/AAM	CF	TKC/TKT	QL	CWG/CWA	EG	GRG/GRA	GE	GRG/GRA	HR	CRC/CRT	IR	AKA/
AS	KCC/KCT	RH	CRC/CRT	NS	ARC/ART	DH	ARC/ART	CS	WGC/WGT	QK	MAG/MAA	EK	RAG/RAA	GA	SGC/SGT	HL	CWC/CWT	IL	MTG/MTT
AT	RCC/RCT	RK	ARG/ARA	NT	AMC/AMT	DY	AMC/AMT	CY	TRC/TRT	QP	CMG/CWA	EV	GWG/GWA	GR	SGC/SGT	HP	CWC/CWT	IS	AKC/AYT
AV	GVC/GVT	RI	AKA/	NY	WAC/WAT	DV	WAC/WAT							GS	RGC/RGT	HY	YAC/YAT	IV	ATC/ATT
		RG	SGC/RGA											GV	GKG/GKC			IX	AWA/
		RP	CSC/CST																
		RT	ASA/ASG																
		RL	CKG/CKC																
		RS	MGC/MGT																

Single letter code

R = A or G
Y = C or T
K = G or T
S = C or G
W = A or T
H = A or C or T
B = C or G or T
V = A or C or G
D = A or G or T
N = A or C or G or T

FIGURE 13

The Genetic Code- First and Second Most Frequently Used Codons

K	M	F	P	S	T	W	Y	V	L										
Lys	AAG/AAA	Met	ATG/	Phe	TTC/TTT	Pro	CCC/CCT	Ser	AGC/TCC	Thr	ACC/ACA	Trp	TGG/	Tyr	TAC/TAT	Val	GTG/GTC	Leu	CTG/CTC

The Genetic Code- First and Second Most Frequently Used Degenerate Codons For Two or More Amino Acids

TWO BASES AT A SINGLE POSITION

KM	AWG/	MR	AKT/	FC	TKC/TKT	PQ	CMG/CMA	SW	TSG/	TM	AYG/	WR	WGG/YGG	YN	WAC/WAT	VM	RTG/	IM	MYG/WTG
KN	AAS/AAM	MI	ATS/ATK	FI	WTC/WTI	PH	CMC/CMT	SN	ARC/APT	TN	AMC/AMT	WG	KGG/	YD	KAC/KAT	VD	GWC/GWT	LW	TKG/
KQ	MAG/MAA	ML	MTG/WTG	FL	YTC/YTT	PA	SCC/SCT	SL	TYG/TYA	TK	AMG/AMA	WS	TSG/	YC	TRC/TRT	VE	GWG/GWA	LS	TYG/TYA
KE	RAG/RAA	MK	AWG/	FS	TYC/TTT	PR	CSC/CST	SC	WGC/WGT	TI	AAC/AAI	WL	TKG/	YH	YAC/YAT	VF	KTC/KTT	LQ	CWG/CWA
KR	ARG/ARA	MT	AXG/	FY	TWC/TWT	PL	CYC/CYG	SF	TYC/TTT	TA	RCC/RCT	WC	TGS/TGK	YF	TWC/TWT	VI	RTC/RFT	LH	CWC/CWT
KT	AWG/AMA	MV	RTG/	FV	KTC/KTT	PS	YCC/YCT	SY	TMC/TMT	TR	ASA/ASG			YS	TMC/TWT	VA	GYC/GYT	LF	YTC/YTT
KI	AWA					PT	MCC/MCT	SI	AKC/AKT	TS	ASC/WCC					VG	GKG/GKC	LI	MTC/MTT
								SA	KCC/KCT							VL	STG/STC	LP	CYC/CYG
								SG	RGC/RGT									LV	STG/STC
								SP	YCC/YCT									LR	CKG/CKC
								SR	MGC/MGT										

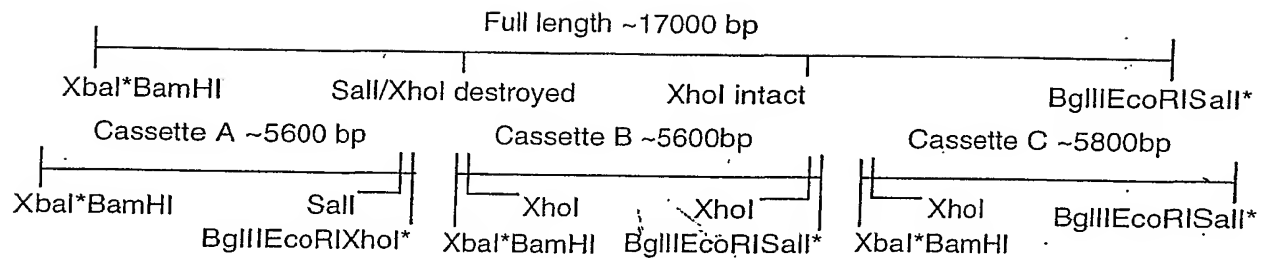
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Single letter code

R = A or G
Y = C or T
K = G or T
S = C or G
W = A or T
H = A or C or T
B = C or G or T
V = A or C or G
D = A or G or T
N = A or C or G or T

FIGURE 13 (cont)

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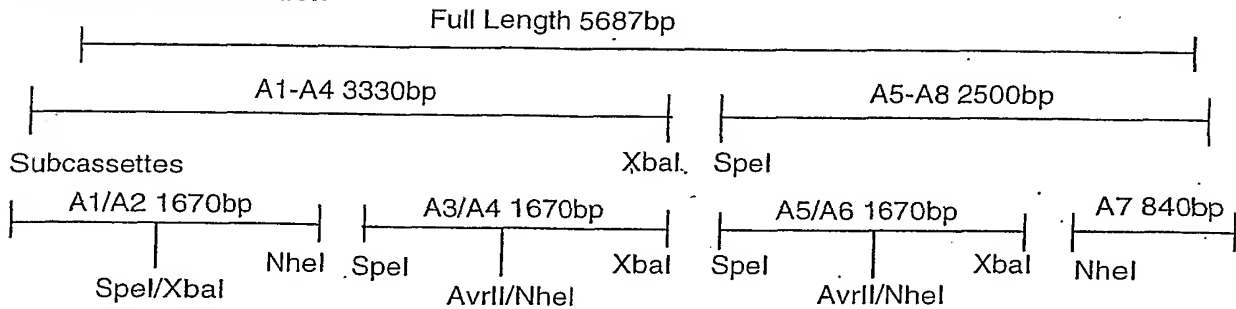
Full length construction after cloning the cassettes into pBS.
 Sites marked with a "*" are in the pBS MCS

Cassette Extras (Can be removed from cassette ends)

A (37bp)	BamHI/Kozak Start	Sall	Stop	BglII	EcoRI	
5'	gc ggatccacc atg.....gtcgac	tga	agatct	gaattc	gc 3'
B (43bp)	BamHI/Kozak Start XhoI	XhoI	Stop	BglII	EcoRI	
5'	gc ggatccacc atg ctcgag...	...ctcgag	tga	agatgt	gaattc	gc 3'
C (37bp)	BamHI/Kozak Start XhoI		Stop	BglII	EcoRI	
5'	gc ggatccacc atg ctcgag...tga		agatct	gaattc	gc 3'

FIGURE 14

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Cassette Construction**Subcassette Extras (Can be removed from cassette ends)**

SC1 (A 28bp, B/C 34bp)	As for 5' of Cassettes	SpeI EcoRI	
SC2 (28bp)	BamHI XbaIactagt gaattc gc 3'	
5' gc ggatcc tctaga.....		NheI EcoRI	
SC3 (28bp)	BamHI SpeIgctagc gaattc gc 3'	
5' gc ggatcc actagt.....		AvrII EcoRI	
SC4 (28bp)	BamHI NheIcctagg gaattc gc 3'	
5' gc ggatcc gctagc.....		XbaI EcoRI	
SC5 (28bp)	BamHI SpeItctaga gaattc gc 3'	
5' gc ggatcc actagt.....		AvrII EcoRI	
SC6 (28bp)	BamHI NheIccatgg gaattc gc 3'	
5' gc ggatcc gctagc.....		XbaI EcoRI	
	tctaga gaattc gc 3'	
For Cassettes A and B only			
SC7 (37bp)	BamHI NheI		
5' gc ggatcc gctagc.....			As for 3' of Cassettes A/B
For Cassette C only			
SC7 (28bp)	BamHI NheI	SpeI EcoRI	
5' gc ggatcc gctagc.....	actagt gaattc gc 3'	
SC8 (31bp)	BamHI XbaI		
5' gc ggatcc tctaga.....			As for 3' of Cassette C

FIGURE 14 (Cont)

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HIV SAVINE CONSTRUCTION

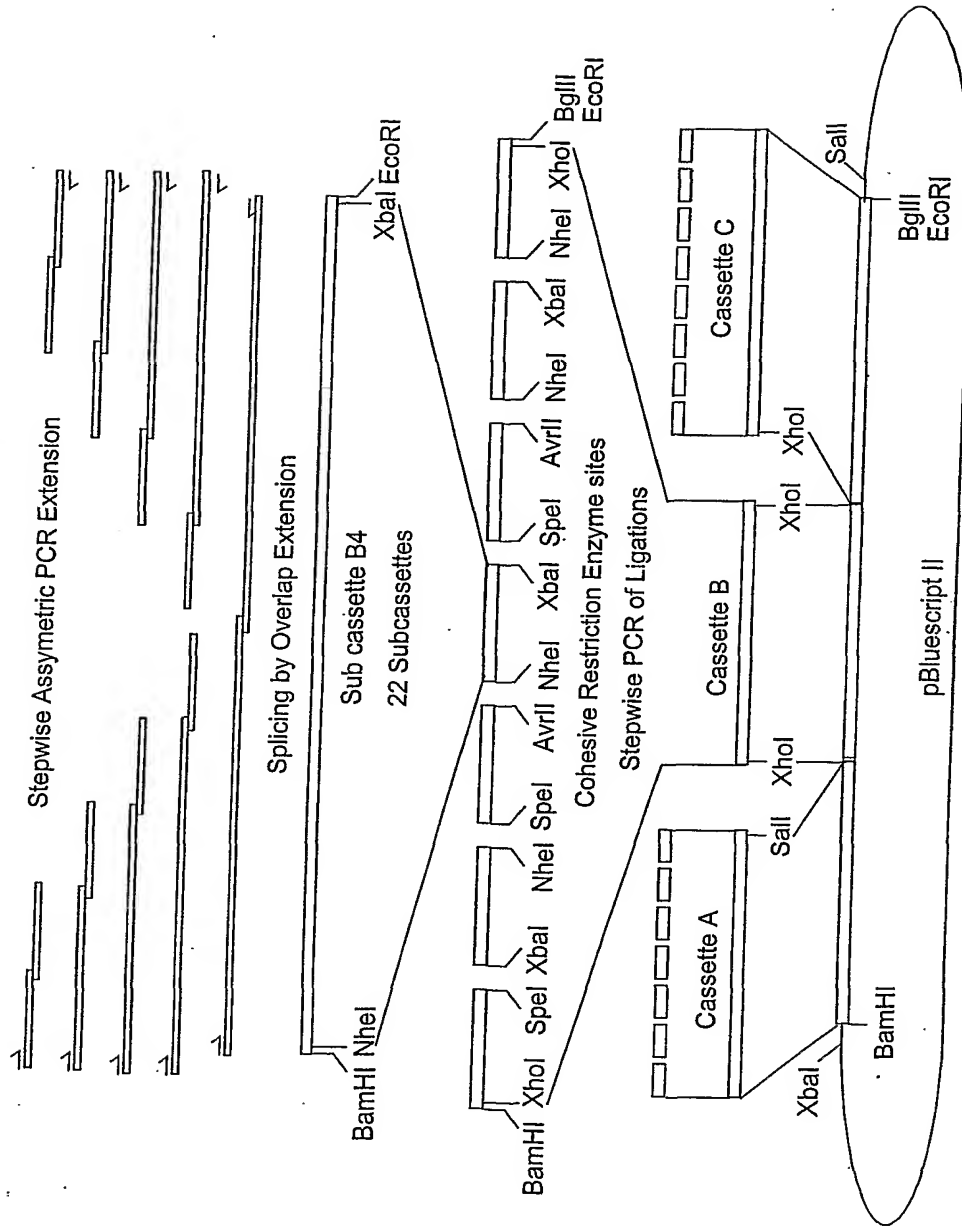


FIGURE 14 (Cont)

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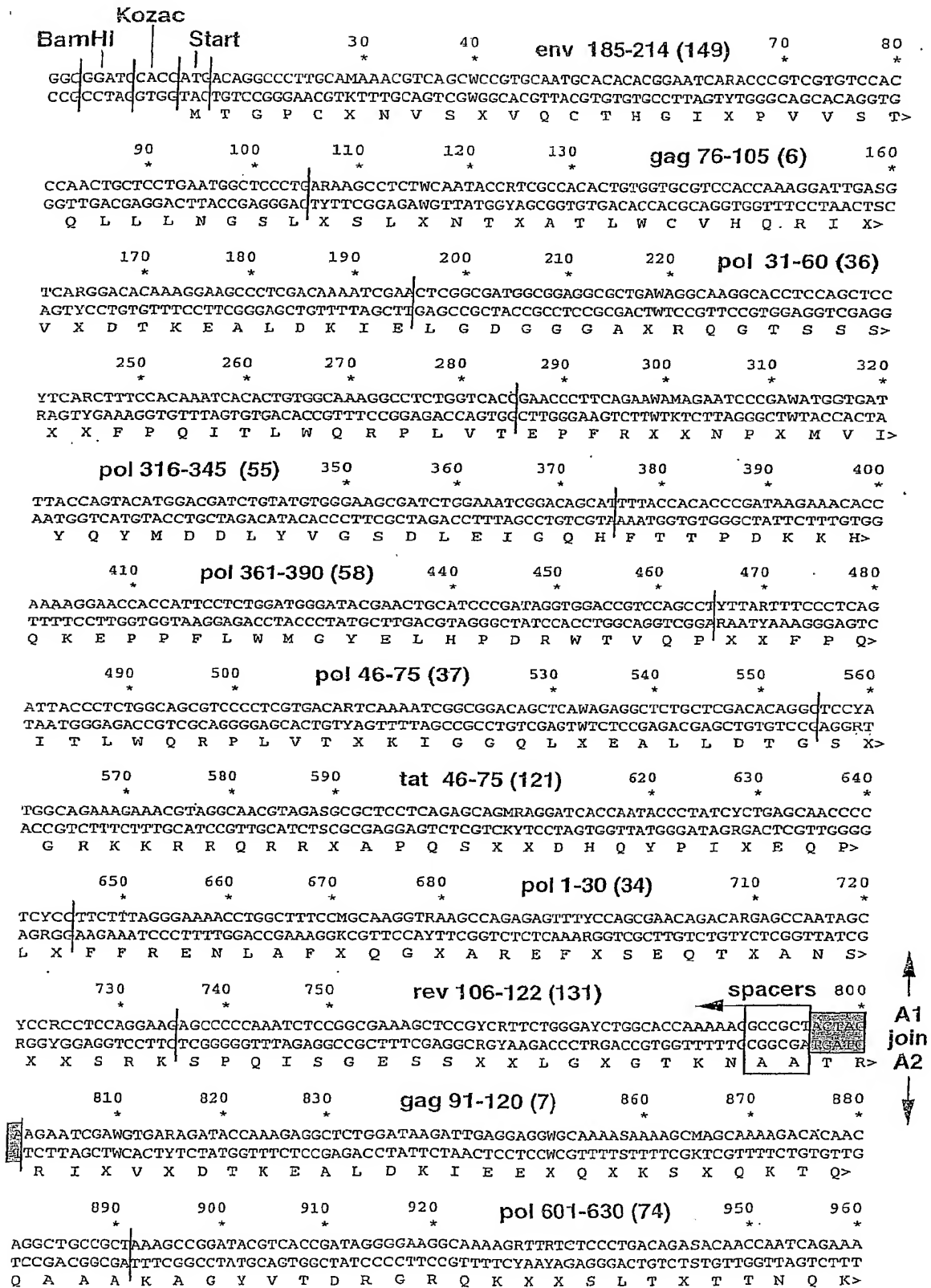


FIGURE 15 (Cont)
SUBSTITUTE SHEET (RULE 26)

1040

* * * * *

ACCGAAGTGCAGGCCATTTCAMGAGCCCTATACCACACTGTTTGGCGCCAGCGATGCCAAAGCCYATGASACAGAGGTCCA
TGCGCTTAGCCTWCGTAAGTKCTKCGGYKATGGTGTGACAAAACGCGGTGCGTACGGTTTCGGRTACTSTGTCTCCAGGT
T E L X A I X X A X T T L F C A S D A K A X X T E V H>

1050 1060 1070 1080 1090 pol 76-105 (39) 1120

* * * * *

CAATGTGTGGGCCACACACGCTTGCCTCCCCGCTGACGATACAGTGCCTGGAGSATSAACTCCCCGGAARATGGAAGC
GTTACACACCCGGTGTGTGCGAACGCGGGCGACTGCTATGTACAGACCTCTSTASTTGGAGGGGCTTYTACCTTCG
N V W A T H A C V P A D D T V L E X X N L P G X W K>

1130 1140 1150 1160 1170 1180 1190 1200

* * * * *

CTAAGATGATTGGCGGAATCGCGGATTCATTAAAGGTGAGAARGATCGGACCCGAAACCCCTTACAATAACCCARTCTTC
GATTCTACTAACC CGCTTAGCGCCTAAGTAATTCACCTCTTCTAGCCTGGGCTTTTGGGAATGTTATGGGGTYAGAAG
P K M I G G I G G F I K V R X I G P E N P Y N T P X F>

pol 196-225 (47) 1230 1240 1250 1260 1270 1280

* * * * *

GCTATCAAGAAAAAGGACTCCACCAATGGAGAAAGCTCGTGGATTTCAGARTTAGGATTATCAAWATCCTCTACCAAAG
CGATAGTTCTTTTTCTGAGGTGGTTACCTCTTTTCGAGCACCTAAAGTCTYAATCCTAATAGTTWTAGGAGATGGTTTC
A I K K D S T K W R K L V D F R X R I I X I L Y Q S>

1290 rev 16-45 (125) 1320 1330 1340 1350 1360

* * * * *

CAATCCCTATCCTAGCTCCGAAGGCWCCAGGCAARCCAGAARGAATAGGAGAAGGAGATGGGGAGGCGAACRGGRTAGGG
GTTAGGGATAGGATCGAGGCTTCGGWGTCGCTTGGTCTTCTATCCTCTTCTCTACCCCTCCGCTTGYYCYATCCC
N P Y P S S E G X R Q X R X N R R R R W G G E X X R>

1370 1380 env 525-554 (171) 1410 1420 1430 1440

* * * * *

ATAGGTCCGCTGAGACTGGTCARCGGATTCTYAGCCCTCGCCTGGGACGATCTGAGAARCCTCTGCCTCTTCGAMAACCTC
TATCCAGGCACTCTGACCACTYGCTAAGARTCGGGAGCGGACCCTGCTAGACTCTTYGGAGACGGAGAAGCTKTGTGGAG
D R S V R L V X G F X A L A W D D L R X L C L F X N L>

1450 1460 1470 env 31-60 (139) 1500 1510 1520

* * * * *

TGGGTACCGTCTACTATGGCGTCCCGCTCTGGAGAGAGCTRMCAACCCCTCTCTGTGCCTCCGACGCTAAGGCCTYA
ACCCAGTGGCAGATGATACCGCAGGGGCAGACCTCTCTSCGAYKGTTGGGAGAAGACACGGAGGCTGCGATTCCGART
W V T V Y Y G V P V W R X A X T T L F C A S D A K A X>

spacers 1550 1560 rev 1-30 (124) 1590 1600

* * * * *

CCTGCCATGGCTGGCAGAAGCGCRRACAGACGAAGAGCTCCTGARGGCTRTCAGATCATTAASATTCTGTATCAGT
CGACGGTACCGACCGTCTTCGCGGYGTGTCTGCTTCTCGAGGACTYCCGAYAGTCTTAGTAATTSTAAGACATAGTCA
A A M A G R S G X T D E E L L X A X R I I X I L Y Q>

1610 1620 1630 1640 1650 vif 16-45 (101) 1680

* * * * *

CCAACCCCTTACCCTTCCGCTGATGARAATCAGAACCTGGAASAGCCTGGTCAAGCATCACAATGYACATCTCCAAGAAA
GGTTGGGAATGGGAAGCGCTGATGCTTACTYTtagtcttgacctstcggaccagtTCGTAGTGTACRTGTAGAGGTCTTTT
S N P Y P S A S M X I R T W X S L V K H H M X I S K K>

1690 1700 1710 1720 1730 1740 1750 1760

* * * * *

GCCAAGGCTGGTCTATAGGCATCACTWTGASAGTCCGAGSTCGTGARTCAGATTATCGAAVAGCTCATCAAAAAGGA
CGGTTWCCGACCAAGATATCCGTAGTGAWACTSTCAGGCTCSAGCTYAGTCTAATAGCTBTBAGTAGTGTTCCT
A X G W F Y R H H X X E S E X V X Q I I E X L I K K E>

pol 661-690 (78) 1790 1800 1810 1820 1830 1840

* * * * *

AARGGTCTACCTAKCATGGGTACCAGCCACAAGGGAATCGGAACAACCAAGAGCTCCAGAAMCAGATTMYCAAATCC
TTYCCAGATGGATMGATACCATGTCGGGTGTTCCCTTAGCTGTTTGGTTTCTCGAGGCTTKGTCTAAKRGTTTTAGG
X V Y L X W V P A H K G I G Q T K E L Q X Q I X K I>

1850 pol 916-945 (95) 1880 1890 1900 1910 1920

* * * * *

AAAACCTTTAGGGTCTACTATAGGGATACGAGACCCCTMTCTGGAAGGGACCCAAAAGCYTTGAGGAAAATCTGGRACAT
TTTTGAAATCCCAGATGATATCCCTATCGTCTCTGGGAKAGACCTTCCCTGGCTTTTCGRAACTCTTAGACCTGTGTA
Q N F R V Y Y R D S R D P X W K G P K S X E E I W X N>

↑
A2
join
A3
↓

FIGURE 15 (Cont)
SUBSTITUTE SHEET (RULE 26)

1930 2000
* *
ATGACATGGATKSAGTGGGAGAGAGAGATTAGCAATTACACAARCCWAATCTATRAGATTCTG|ARACCCGGAACCCACAGC
TACTGTACCTAMSTACCCTCTCTCTCTAATCTTAATGTGTTTGGTTAGATAYTCTAAGAC|TGTGGGCTTGGGTGTCTG
M T W X X W E R E I S N Y T X X I Y X I L X P E P T A>
1960 1970 1980 1990 2000
* * * * *
1930 2020 gag 451-480 (31) 2050 2060 2070 2080
* * * * *
CCCTCCCGCTGAGARTTTCRGATTTCGGTGAGGAAATACACCCCTCCMAAAGCAAGAGCMAAAGGATAGGAGCAATACG
GGCGGCGGACTCTYAAAGYCTAAGCCACTCCTTTGATGTGGGAGGGKTTTCGTTCTCGKTTTCCTATTCCTCTGTATCG
P P A E X F X F G E E T T P S X K Q E X K D K E Q Y>
2090 2100 2110 pol 106-135 (41) 2140 2150 2160
* * * * *
ATCAGATMTTATTGAGATTTCGGGCAAGAAAGCTATTGGTACAGTGTCTCGTGGGACCTACCCCTGTGAATATCATTGGC
TAGTCTAATAAATACTCTAAACGCCGTCTTTTCGATAACCATGTACAGAGCACCCTGGATGGGGACACTTATAGTAACCG
D Q I X I E I C G K K A I G T V L V G P T P V N I I G>
2170 2180 2190 2200 vpr 46-75 (115) 2230 2240
* * * * *
AGNATTTACGAAACCTATGGCGATACCTGGGAGGGCGTCGAGGCTCTGATCAGAACTCCAGCAACTGMTGTTTTCCTCA
TCTTAAATGCTTTGGATACCGCTATGGACCCCTCCCGACCTCCGAGACTAGTCTTTRGGAGGTGCTTGACACAAAYAGGT
R I Y E T Y G D T W E G V E A L I R X L Q Q L X F X H>
2250 2260 2270 2280 2290 tat 31-61 (120) 2320
* * * * *
TTTCAGAATCGGATGTTTTCATTGCGCAASTGTGTTTTCTCACCAGAGTCTCGGCATTAGCYACGGAAGGAAAAAGAGAA
AAAGTCTTACGCTTACAAGAGTAACGGTTSACACAAAAGAGTGGTTTCAGAGCGCTAATCGRTGCCTTCCTTTTCTCTT
F R I G C X H C Q X C F L T K G L G I S X G R K K R>
2330 2340 spacers 2370 2380 tat 1-30 (118)
* * * * *
RACAGAGAAGGSGAGCTCCCCAGCTGCGCTATGGACCCCGTGGACCCCAASCTGGAGCCTTGGAAWACCCTGGCTCCCA
YTGCTCTTCCSCTCGAGGGGTTTCGACCGTACCTGGGGCACTGGGGTTSAGCTCCGAACCTTWTGTTGGGACCGAGGGGTC
X Q R R X A P Q A A M D P V D P X L E P W X H P G S Q>
2410 2420 2430 2440 2450 2460 2470 2480
* * * * *
CCTAMGACAGCCTGTWMCATGCTATTGCAAAAAGTGGCTTTCAGAGACACCCCTAGCCMGAAACAGGAACMGAA
GGATKCTGTGCGACAWKGTTCAGATAACGTTTTCACCTGCTTCTGTTGGGGATCGGKCTTTGTCTTGTGKCTT
P X T A C X K C Y C K K C P S E E T T P S X K Q E X K>
gag 466-495 (32) 2510 2520 2530 2540 2550 2560
* * * * *
AGACAAAGAACWCTACCCCCCTTYAGCCAGCCTCAAGTCCCTGTTTGGCAATGACAATTTCAATATGTGGAAGAATRACA
TCTGTTTCTTGGWATGGGGGGAARTCGGTTCGGAGTTCAGGGACAAACCGTTACTGTTAAAGTTATACACCTTCTTAYTGT
D K E X Y P P X A S L K S L F G N D N F N M W K N X>
2570 env 91-120 (143) 2600 2610 2620 2630 2640
* * * * *
TGGTGGAMCAGATGCAMGAAGACRTTATCTCACTATGGGACCAAAAGCCTCAAGCCTTGCCTCAAGCTCGACGTCGGCGAT
ACCACCTKGTCTACGKTCTTCTGYAATAGAGTGATAACCTGTTTCGGAGTTCGGAACGAGTTCGAGCTGCAGCCGCTA
M V X Q M X E D X I S L W D Q S L K P C V K L D V G D>
2650 2660 pol 256-285 (51) 2690 2700 2710 2720
* * * * *
GCCTATTCTCCGTGCCTCTGGATRAARRCTTCAGAAAGTATACCGCTTTTCAATCCCTAGCAYAAACAATGAGCAACT
CGGATAAAGAGGCACGGAGACCTAYTTTYGAAGTCTTTCATATGGCGAAAGTGTAGGGATCGTRTTTGTACTCTGTTGA
A Y F S V P L D K X F R K Y T A F T I P S X N N E Q L>
2730 2740 2750 pol 751-780 (84) 2780 2790 2800
* * * * *
GAAAGGCGAAGCCATSCATGGCCAAAGTGRATTGTCTACCAGGCATTGGGCACTGGATTGCACACACCTGGAGGGAAAGR
CTTTCGGTTCGGTASGTACCGGTTTCACATACGAGTGGTTCGTAACCGTTGACCTAAGCTGTGTGGACCTCCCTTCY
K G E A X H G Q V X C S P G I W Q L D C T H L E G K>
2810 2820 2830 2840 pol 166-195 (45) 2870 2880
* * * * *
TTATCCTAAGGTCAAGCAATGGCCCTGACAGAGGAAAGATTAAGGCTCTGACTGCGATTGTCAMAGAGATGGAGVAA
AATACGGATTCAGTTCGTTACCGGACCTGTCTCCTTTCTAATTCGAGAGCTGACKCTAAACGKTCTCTACCTCBTT
X I P K V K O W P L T E E K I K A L T X I C X E M E X>

↑
A3
join
A4
↓

FIGURE 15 (Cont)
SUBSTITUTE SHEET (RULE 26)

2890 2900 2910 pol 331-360 (56) 2940 2950 2960

GAGGGAAACATTAGCATGGAATGACCTCTACGTCCGCTCCGACTCGGAGATTGGCCAACATAGGRCAAAAATCGAAGAGCT
CTCCCCTTTCTAATCCTTACCTACTGGAGATGCAGCCGAGGCTGGACCTTAACCGGTTGTATCCYGGTTTTAGCTTCTCGA
E G K I S M D D L Y V G S D L E I G Q H R X K I E E L>

2970 2980 2990 3000 pol 616-645 (75) 3030 3040

CAGGSMACACCTCCTGARATGGGGCTCACCGAMACCACAACCAAAGACTGAGCTCCAMGCTATCCAWCTGGCTCTGCG
GTCCSKTGTGGAGGACTYTACCCCTGAGTGGCTKTGGTGTTGGTTTTCTGACTCGAGTKCAGTAGGTTWGACCGAGACG
R X H L L X W G L T X T T N Q K T E L X A I X L A L>

3050 3060 3070 3080 3090 pol 796-825 (87) 3120

AAGACTCCGGCTYAGAGGTCAACATTGTGACAGACATTCCCGCTGAGACTGGTCAAGAGACCGCCTATTTCTMTCTGAAA
TTCTGAGGCCGARTCTCCAGTTGTAACACTGTCTGTAAGGGCGACTCTGACCAGTTCTCTGGCGGATAAAGKAAGACTTT
Q D S G X E V N I V T D I P A E T G Q E T A Y F X L K>

3130 3140 3150 3160 3170 3180 3190 3200

CTGGCTGGCAGATGGCCTGTGARARYCATTACACAGACAATGGCAGGACAAAGATTGAGGAACCTGAGASMGCATCTGCT
GACCGACCGTCTACCGGACACTYTYRGTAAGTGTGTCTGTTACCGTCCTGTTTCTAACTCCTTGACTCTSKCGTAGACGA
L A G R W P V X X I H T D N G R T K I E E L R X H L L>

pol 346-375 (57) 3230 3240 3250 3260 3270 3280

CARATGGGGCTTCACAACCCCTGCACAAAAGCATCAGAAGAGCCTCCCTTTCTCTGAGTGTCAAGAACTGACAGAGG
GTYTACCCCGAAGTGTGGGGACTGTTTTTCTAGTCTTTCTCGGAGGGAAAGAGACAGTGTCTCTGACTGTCTCTCC
X W G F T T P D K K H Q K E P P F L S S V K K L T E>

3290 vif 166-192 (111) 3320 3330 spacers 3360

ATARGTGGAACRAACCCAGAAAAAYCAAGGGACRCAGAGRAATCACACAATGAATGGCCATGCTGCCACAGAGTCCCAG
TATYACCTTGTYTGGGGTCTTTTRGTTCCCTGYGTCTCYTTAGTGTGTTACTTACCGGTACGACGGTGTCTCAGGGT
D X W N X P Q K X K G X R X N H T M N G H A A A T E S Q>

3370 3380 env 435-464 (165) 3410 3420 3430 3440

AATCAGCAAGACAGAAACGAAMAGGAMCTGCTGGMGCTCGACAAATGGGCAAGCCTCTGGAATTGGTTTRACATTASC
TTAGTCGTTCTGTCTTTGCTTTKCTTGACGACCKCGAGCTGTTTACCCGTTTCGGAGACCTTAACCAAAYTGAATSGCT
N Q Q D R N E X X L L X L D K W A S L W N W F X I X D>

3450 3460 3470 gag 121-150 (9) 3500 3510 3520

CACCGGAARTAGCTCCMAAGTGTCCAGAAATTACCCTATCGTCCAGAATSYCCAAGGCCAAATGGTCCACCAASCMTCT
GTGGCCTTYATCGAGGKTTACAGGGTCTTAATGGGATAGCAGGCTTTASRGGTTCCGGTTTACCAGGTGGTTSSGKAGA
T G X S S X V S Q N Y P I V Q N X Q G Q M V H Q X X>

3530 3540 3550 3560 env 480-509 (168) 3590 3600

CCCCCAGATCTCRTCGGACTGAGAATCRTTTTTCGCTGTGCTCAGCATTTTCAATAGGGTCAGGCAAGGCTATAGCCCTCTG
GGGGGCTTGAGYAGCTGACTCTTAGYAAAAAGCAGACAGAGTCGTAAYAGTTATCCAGTCCGTTCCGATATCGGGAGAC
S P R L X G L R I X F A V L S I X N R V R Q G Y S P L>

3610 3620 3630 3640 3650 vif 106-135 (107) 3680

TCCTTCCAAACCCCTCMYCTCATCCATCTGYAWTACTTTGACTGTTTCKCTGACTCCRCCATTAGGAGAGCCATCCTGGG
AGGAAGGTTTGGGAGKRGGAGTAGGTAGACRTWATGAAACTGACAAAGMAGACTGAGGYGGTAATCCTCTCGGTAGGACCC
S F Q T L X L I H L X Y F D C F X D S X I R R A I L G>

3690 3700 3710 3720 3730 3740 3750 3760

ACASAKAGTGAGMAGGAGATGCGAAATAGCTGTGGGAMTCGGAGCCATGWTCYTTGGCTTTCTGGGTGCCGCTGGCTCCA
TGTSTMTCACTKTCCTCTACGCTTATCGACACCTKAGCCTCGGTACWAGRAACCAGAAAGACCCACGGCAGCCGAGGT
X X V X R R C E Y A V G X G A M X X G F L G A A G S>

env 300-329 (156) 3790 3800 3810 3820 3830 3840

CCATGGGCGCTGCTCCATSACACTGACAGTGAAGCCTATGACCCTAGCAAGACCTCRTTGCTGAGATTGAGAAACAG
GGTACCCGCGAGGAGGTASTGTGACTGTCACGTTCCGATACTGGGATGTTTCTGGAGYAACGACTCTAAGTCTTTGTC
T M G A A S X T L T V O A Y D P S K D L X A E I Q K Q>

A4
join
A5

FIGURE 15 (Cont)
SUBSTITUTE SHEET (RULE 26)

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pol 466-495 (65) 3870 3880 3890 3900 3910 3920
GGTCAGGRTCACTGGACATWTCAGATTTWCCAAAGAGCCTTTCAAAAAGGAAACCGTCCTGGTCGGCCCTACACCCGTCAA
CCAGTCCYAGTCACCTGTAWAGTCTAAAWGGTTCTCGGAAAGTTTTCCTTGGCAGGACCAGCCGGGATGTGGGCAGTT
G Q X Q W T X Q I X Q E P F K N G T V L V G P T P V N>

3930 pol 121-150 (42) 3960 3970 3980 3990 4000
CATCATCGGAAGGAACMTGCTGACACAGMTTGGCYGCACCTCAACTTTCCCATTTAGCAAGGCAGCCCTGCTATCTTTTC
GTAGTAGCCTTCTTGTGACGACTGTGTCKAACCGRCCTGGGAGTTGAAAGGGTAATCCTTTCCGTCGGGACGATAGAAAG
I I G R N X L T Q X G X T L N F P I S K G S P A I F>

4010 4020 pol 301-330 (54) 4050 4060 4070 4080
AGTCCAGCATGMCAMAGATTTCTGGAGCCTTTTAGGAWAMAAAACCTGASATGGTCATCTATCAGTATGCTCTCTG
TCAGGTCGTACKGTCTTAAGACCTCGGAAAATCCTWTKTCTTGGGACTSTACCAGTAGATAGTCATAGCTCTGGGAGAC
Q S S M X X I L E P F R X X N P X M V I Y Q Y P S P L>

4090 4100 4110 nef 136-165 (188) 4140 4150 4160
ACATTCGGATGGTGTCTTCAAACTGGTCCCCGTGGACCCAGSGAAGTGGAGAGRYCAACRAGGGCGAAAACAATTGCGCT
TGTAAGCCTACCACAAAGTTTGACCAGGGGCACCTGGGGTCSCTTCACCTTCTCYRGTGTGTCCTCTTTGTAAACGGA
T F G W C F K L V P V D P X E V E E X N X G E N N C L>

4170 4180 4190 4200 pol 271-300 (52) 4230 4240
CCTCTTTAGGAAATACACAGCCTTTACCATTCCCTCCAYCAATAACGAAACCCCTGGCATTAGGTATCAGTATAACGTCC
GGACAAATCCTTTATGTCTCGGAAATGGTAAGGGAGGTGTATTGCTTTGGGACCGTAATCCATAGTCATATTGCAGG
L F R K Y T A F T I P S X N N E T P G I R Y Q Y N V>

4250 4260 4270 4280 4290 env 315-344 (157) 4320
TGCCTCAGGGATGGGGAAGCACAAATGGGAGCCGCCAGCATKACCCCTACCGTCCAGGCTAGGCWACTGCTCAGCGGAATC
ACGGAGTCCCTACCTTCGTGTACCCCTCGGCGGTGTGTAMTGGGAGTGGCAGGTCCGATCCGWTGACGAGTCGCTTAG
L P Q G W G S T M G A A S X T L T V Q A R X L L S G I>

4330 4340 4350 4360 4370 pol 451-480 (64) 4400
GTCCAGCAACAGARCAATCTGCTCGMGGAGAATAGGGAAATCCTCARAGAGCCTGTGCATGGCGTCTACTACGATCCCTC
CAGGTCGTTGTCTYGTAGACGACCKCCTCTTATCCCTTTAGGAGTYTCTCGGACAGTACCGCAGATGATGTAGGGAG
V Q Q Q X N L L X E N R E I L X E P V H G V Y Y D P S>

4410 4420 4430 4440 4450 vpu 61-81 (136) 4480
CAAGGATCTGRTCGCTGAARTCCAAAAGCAAGGASAGAGGAAGTGTCCRCCTGGTGGATATGGGAAACTACGACCTCG
GTTCTTAGACYAGCGACTTYAGGTTTTCGTTCCCTSTCTCCTTGACAGGYGGWACCACCTATACCTTTGATGCTGGAGC
K D L X A E X Q K Q G X E E L S X X V D M G N Y D L>

spacers 4510 4520 4530 vpr 61-90 (116) 4560
GAGTGGACAATAAATCGCCGCTATTAGAAYCCTGCAACAGCTMTGTTCTTCACTTTAGGATTGGCTGCCRGCACTCC
CTCACCTGTTATTGGACCGGCGTAATCTTRGGACGTTGTGAGKACAAGYAAGTGAATCCTAACCGACGGYCGTGAGG
G V D N N L A A I R X L Q Q L X F X H F R I G C X H S>

4570 4580 4590 4600 4610 gag 406-435 (28) 4640
AGGATTGGCATCMYCCGTCAGAGAAGGGSCAGAGCTCCAGGAAAAAGGGATGCTGGAAGTGTGGCARAGAGGGACACCA
TCCTAACCGTAGKGGCAGTCTCTTCCCSGTCTCGAGGGTCCCTTTTCCCTACGACCTTCACACCGTYTCTCCCTGTGGT
R I G I X R Q R R X R A P R K K G C W K C G X E G H Q>

4650 4660 4670 4680 4690 4700 4710 4720
GATGAAGGATTGCACTGAGAGACAGGCTAACTTTCTGGGAAAGGAWGCCAGACTGRTTATCARAACCTATTGGGGACTGC
CTACTTCTTAACGTGACTCTCTGTCGATTGAAAGACCCCTTTCTWCGGTCTGACYAATAGTYTTGGATAACCCCTGACG
M K D C T E R Q A N F L G K X A R L X I X T Y W G L>

vif 61-90 (104) 4750 4760 4770 4780 4790 4800
ATACCGGTGAGAGAGACTGGCASCCTCGGCCAWGGCGTCAGCATTGAGTGGAGGAYAAAGGGAAAGGGCTGAGGATAGCGGC
TATGGCCACTCTCTGACCGTSGAGCCGGTWCCGAGTCGTAACACCTCTTCTTCCCTTTCCCGACTCCTATTCGCCG
H T G E R D W X L G X G V S I E W R X R E R A E D S G>

A5
join
A6FIGURE 15 (Cont)
SUBSTITUTE SHEET (RULE 26)

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vpu 46-75 (135) 4830 4840 4850 4860 4870 4880
AACGAAAGCGAAGGCGACASAGAAGAGCTCAGCRCATWGGTGGACATGGGCAATTACGATCTGCTAGGCTGCCCCCAG
TTGCTTTTCGCTTCCGCTGTSTCTTCTCAGTCGYGTWACCACCTGTACCCGTTAATGCTAGACATCCGGACGGGGGTC
N E S E G D X E E L S X X V D M G N Y D L S S P A P R>

4890 env 510-539 (170) 4920 4930 4940 4950 4960
GGGACCCGATAGGCGYGGRRGAATCGAAGAGGAAGGCGGAGACRAGRCAGAGRCAGAAGCGTCAGGCTCGTGARTGGCA
CCCTGGGCTATCCGRCCYCYCTTAGCTTCTCCTTCCGCCCTCTCGYTCYGTCTCYGTCTTCGAGTCCGAGCACTYACCGT
G P D R X X X I E E E G G E X X R X R S V R L V X G>

4970 4980 nef 151-180 (189) 5010 5020 5030 5040
GWGAGGTCGAGGAARYCAATRAGGGAGAGAATAACTGTCTGCTCCACCCATSRGTCWACATGGCATGGAAGACGAAGAS
CWCTCCAGCTCCTTYRGTTAYTCCCTCTCTTATTGACAGACGAGGTGGGATASVCAGWTGTACCGTACCTTCTGCTTCTTS
X E V E E X N X G E N N C L L H P X X X H G M E D E X>

5050 5060 5070 pol 961-990 (98) 5100 5110 5120
AGAGAGGTCAATAGCGATATCAAAGTGGTCCCCAGAAAGGAAAGCCAAATCATTAGGGATTACGGAAAGCAAATGGCTGG
TCTCTCCAGTTATCGCTATAGTTTACCAGGGGCTTCTCTTCGGTTTTAGTAATCCCTAATGCCTTTCGTTTACCAGCC
R E V N S D I K V V P R R K A K I I R D Y G K Q M A G>

5130 5140 5150 5160 pol 16-45 (35) 5190 5200
CGMTGACTGTGTGGCCRGCTTCYCTTCCGAGCAAACARGGGCTAACTCCYCTRCAAGCAGAAAGCTGGGAGACGGAGGGCG
GCKACTGACACACCGGYCAGAGGAAGGCTCGTTTGTGCCGATTGAGRGAYGTTCTGCTTTTCGACCTCTGCCTCCGC
X D C V A X F X S E Q T X A N S X X S R K L G D G G>

5210 5220 5230 5240 5250 gag 390-420 (27) 5280
GAGCCGASAGACAGGGAACAAGCTCCAGCTGTTTCAATTGCGGCAAGAGGGACACMTTGCCARAAACTGTAGGGCCCCCT
CTCGGCTSTCTGCTCCCTTGTTCGAGGTCCACAAAGTTAACGCCGTTTCTCCCTGTGKAACGGTYTTTGACATCCCGGGGA
G A X R Q G T S S S C F N C G K E G H X A X N C R A P>

5290 5300 5310 5320 5330 5340 5350 5360
CGCAAGAAAGGTTGTGGAAATGCGGAARGGAAGGCCATCAATGAAAGACTGTACCGAAAGGCAAGCCAATTTCTCGG
GCGTTCTTTCCAACACCTTTACGCCTTYCCTCCGGTGTGTTACTTTCTGACATGGCTTTCCGTTTCGGTTAAAGGAGCC
R K K G C W K C G X E G H Q M K D C T E R Q A N F L G>

gag 421-450 (29) 5390 5400 5410 5420 5430 5440
CAAAATCTGGCCCTCCMRCAAAGGCAGACCCGAAACTTTCYCCAAAGCAAMTGGCTCTGGTATATCAAAATCTTTATCA
GTTTATAGACCGGGAGGKYGTTCGCTCTGGGCCCTTTGAAAGRGGTTTCTTACCGAGACCATATAGTTTATAGAAATAGT
K I W P S X K G R P G N F X Q S X W L W Y I K I F I>

5450 env 465-494 (167) 5480 5490 5500 5510 5520
TGATCGTCGGTGGACTGRTTGGCCCTCAGGATTRTCTTTGCGCTCCTGTCCATCRITTAAGGAGCCGYGAGCCCRAGACCTC
ACTAGCAGCCACCTGACYAACCAGGAGTCTTAAYAGAAACGGCAGGACAGGTAGYAATTCCCTCGGCRCTCGGYTCTGGAG
M I V G G L X G L R I X F A V L S I X N G A X S X D L>

5530 5540 nef 31-60 (181) 5570 5580 spacers
GATAAACATGGCGCTMTTACAAGCTCCAATACCSTGCCAATAACSTGACTGTGYCTGGCTGRAGGCTGCTGCCATGAC
CTATTTGTACCCGAKAATGTTTCGAGGTTATGGSGACGGTTATTGSGACTGACACRGACCCGACTCCGACGAGTACTG
D K H G A X T S S N T X A N N X D C X W L X A A A M T>

5610 5620 5630 vpu 1-30 (132) 5660 5670 5680
ACCCCTGGAGATCATCGCTATCGTCGCCYTTATCGTCGCCCTCATMTAGCCATTGTGGTCTGGACAATCGYCTWCATGT
TGGGACCTCTAGTAGCGATAGCAGCGGRAATAGCAGCGGGAGTAGKATCGGTAACACCAGACCTGTAGCRGAWGTAA
P L E I I A I V A X I V A L I X A I V V W T I X X I>

5690 5700 5710 5720 pol 136-165 (43) 5750 5760
AGTATCTGCAAGCAATMTGCTCACCCAAMTGGAYGCACACTGAATTTCCCTATCTCCCCATTGASACAGTGCCTGTGAAA
TCATAGAGCTTTAKACGAGTGGGTTKAGCCTRCGTGTGACTTAAAGGGATAGAGGGGGTAAGTSTGTCACGGACACTTT
E Y V E N X L T Q X G X T L N F P I S P I X T V P V K>

A6
join
A7A7
join
B1FIGURE 15 (Cont)
SUBSTITUTE SHEET (RULE 26)

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5770 spacers 5800 5810 env 255-284 (153) 5840
* * * * *
CTGAAACCCGGAATGGATGGCGCCGCCAYCTTTAGGCCTGGCGGAGGCRATAT SARAGACAATGGAGAAGCGAAGCTGTA
GACTTTGGGCCTTACCTACCGCGGCGGTRGAAATCCGGACCGCCTCCGYTATASTYTCTGTTAACCTCTTCGCTTGACAT
L K P G M D G A A X F R P G G G X X X D N W R S E L Y>

5850 5860 5870 5880 5890 5900 5910 5920
* * * * * * * *
TAAGTATAAGGTCGTGRAGATTRAGCCTCTGGGARTACATGGATTCCCGAATGGGAGTTCGTCAACACACCCCCACTGG
ATTTCATATCCAGCACYCTCTAAYTCGGAGACCCTYAGTGTACCTAAGGGCTTACCCTCAAGCAGTTGTGTGGGGGTGACC
K Y K V V X I X P L G X T W I P E W E F V N T P P L>

pol 556-585 (71) 5950 5960 5970 5980 5990 6000
* * * * * *
TCAAGCTATGGTATCAGCTGGAGAAAGASCCTATCGYTGGCGYTGAGCCTCAGGATCTCAACAYGATGCTGAATAYTGTA
AGTTCGATACCATAGTCGACCTCTTTCTSGGATAGCRACCGCRACCTGGAGTCTAGAGTTGTCTACGACTTATACAT
V K L W Y Q L E K X P I X G X E P Q D L N X M L N X V>

6010 gag 181-210 (13) 6040 6050 6060 6070 6080
* * * * * *
GGAGGCCATCAGGCCGCTATGCAAATGCTGAAAGASACAATCAATGAGGAAGCCGCTGTCTCTTTCTGGATGGCATTRA
CCTCCGGTAGTCCGGCGATACGTTTACGACTTTCTSTGTTAGTTACTCTTCGGCGACAGGACAAAGACCTACCGTAAYT
G G H Q A A M Q M L K X T I N E E A A V L F L D G I X>

6090 6100 pol 706-735 (81) 6130 6140 6150 6160
* * * * * *
CAAAGCTCAAGAGGAACATGAGARGTATCACTCCAAGTGGAGGACAAATGGCCARCGAMTTTAACTCTMTGAAGCATMTCG
GTTTCGAGTTCTCCTTGACTCTYCATAGTGAGGTTGACCTCCTGTACCCTGCTGCTKAAATTAGACACTTCGTAKAGC
K A Q E E H E X Y H S N W R T M A X X F N L X K H X>

6170 6180 6190 gag 31-60 (3) 6220 6230 6240
* * * * * *
TCTGGCCCTTAGGGAGCTGGAGAGATTCGCTCTGAATCCCRGCTGCTGGAGACAKCCGAAGGCTGTMAAGCAAATGCT
AGACCCGGAGATCCCTCGACCTCTCTAAGCGAGACTTAGGGYCGGACGACCTCTGTMGCTTCCGACAKTGTCTTAACGA
V W A S R E L E R F A L N P X L L E T X E G C X Q I A>

6250 6260 6270 6280 env 215-244 (151) 6310 6320
* * * * * *
GAGGAAGAGATTATCATTAGTCCGAGAATYTCACARACAATGYCAAAACCATTATCGTCCAMCTCAACRAAGCGTCGW
CTCCTTCTCTAATAGTAATCCAGGCTCTTARAGTGTGTGTACRGTCTTGGTAATAGCAGGTGKAGCTTGYTTTCGAGCW
E E E I I I R S E N X T X N X K T I I V X L N X S V X>

6330 6340 6350 6360 6370 gag 1-30 (1) 6400
* * * * * *
GATTAAGATGGGCGCTAGGGCTAGTGTCTCAGMGGCGGCRAGCTGGAGCGCTGGGAAAAGATTAGGCTCAGGCCCTGGCG
CTAATTTACCCCGATCCCGATCACAGGAGTCKCCGCCGYTCGACCTGCGGACCCCTTTCTAATCCGAGTCCGACCGC
I N M G A R A S V L X G G X L D A W E K I R L R P G>

6410 6420 6430 6440 6450 nef 91-120 (185) 6480
* * * * * *
GAAAGAAAAGTATAGGCTCAAGGAGAAGGGAGGCCTGGASGGACTGRTTTACTCCMAAAAGAGGCAAGASATTTGGAT
CTTTCTTTTTCATATCCGAGTTCTCTTCCCTCCGGACCTSCCTGACYAAATGAGGKTTTCTCCGTTCTSTAAGACCTA
G K K K Y R L K E K G G L X G L X Y S X K R Q X I L D>

6490 6500 6510 6520 6530 6540 6550 6560
* * * * * * *
CTGTGGGTGTATMACACACAGGGATTCAGTACCTGGGGAACCWGTGATCCTCGGCWTTGGTGATKATCTGTAGCGCCAGCGA
GACACCCACATAKTGTGTGTCCCTAAGTACCTACCCCTTGGWACTAGGAGCCGWACCACTAMTAGACATCGCGGTGCGT
L W V Y X T Q G F T R W G T X I L G X V X I C S A S X>

env 16-45 (138) 6590 6600 6610 6620 6630 6640
* * * * * *
SAATCTGTGGGTGACAGTGTATTTACGGAGTGCCTGTGTGGAGGAGACWGCTCCTGTCCGGCATGTGTGCACAGCAAART
STTAGACACCCACTGTACATAATGCCTCACGGACACACCTCCTCTGWCGAGGACAGCGCGTAACACGTTGTCTGTTTAT
N L W V T V Y Y G V P V W R R X L L S G I V Q Q Q X>

6650 env 330-359 (158) 6680 6690 6700 6710 6720
* * * * * *
ACCTCCTGAGGGCTATCGAAGCCCAACAGCATCTGCTCCAGCTCACCCTGCTGCTCAGGCATTTCCCCAGGCCTTGGCTC
TGGAGGACTCCCGATAGCTTCGGGTGTCTGCTAGACGAGGTGAGTGGCAGACCTCAGTCCGTAAAGGGGTCCGGAACCGAG
N L L R A I E A Q Q H L L Q L T V W V R H F P R P W L>

B1
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B2FIGURE 15 (Cont)
SUBSTITUTE SHEET (RULE 26)

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vpr 31-60 (114) 6750 6760 6770 6780 6790 6800
CACRRCTGGGACAGYACATCTATGAGACATACGGAGACACATGGKMGAGTGGAAGCCCTC|AMAGCCCTCATCAMACC
GTGYGGACCCTGTCRTGTAGATACTCTGTATGCCTCTGTGTACCMKCCCTCACCTTCGGGAGTKTCGGGAGTAGTKTGG
H X L G Q X I Y E T Y G D T W X G V E A L X A L I X P>

6810 6840 6850 6860 6870 6880
* * * * *
CAAAAAGATTARGCCTCCCTCCCATCCGTGAAAAAGCTCACCGAAGACARATGGAATRAGCCTCAAAAGAYA|TATAGCG
GTTTTTCTAATYCGGAGGGGAGGGTAGGCAC|TTTTCGAGTGGCTTCTGTACCTTAYTCGGAGTTTCTRTATATCGG
K K I X P P L P S V K K L T E D X W N X P Q K X Y S>

6890 6900 6930 6940 6950 6960
* * * * *
CTGGCGAAGGATTTRTCGATATCA|TGCACWCCGACATTCAGACTAAGGAAGTGCAAAASCAAATCMYAAAGATTTCAGAAT
GACCGCTTTCCTAAYAGCTATAGTAACGTWGGCTGTAACTCTGATTCCCTTGACGTTTSGTTTAKRTTCTAAGTCTTA
A G E R I X D I I A X D I Q T K E L Q X Q I X K I Q N>

6970 6980 6990 7020 7030 7040
* * * * *
TT|GCTGTGTTTATCCATAACTTTAAGAGGAAGGGAGGCATTGGCGGCTACTCCGCCGAGAGAGAATC|RTTGACATTAT
AAGCGACACAAATAGGTATTGAAATTCTCCTCCCTCCGTAACCGCCGATGAGGCGGCTCTCTCTTAGYAAC|TGAATA
F A V F I H N F K R K G G I G G Y S A G E R I X D I I>

7050 7060 7070 7080 7110 7120
* * * * *
CGCCASCGATATC|RTTCCCGTGGGCGAWATCTATAAGAGATGGATCATTCTGGGACTCAACAAAATCGTGAGAA|TGTATY
CGGTS|GCTATAGYAAGGGCACCCTGCTWAGATATCTCTACCTAGTAAGACCTGAGTTGTTT|TAGCCTTACATAR
A X D I X P V G X I Y K R W I I L G L N K I V R M Y>

7130 7140 7150 7160 7170 7200
* * * * *
MACCCGTCAGCATTCTGGATATC|AGAGTGAGACAGGGATACTCCCCCTCAGCTTTCAGACACTGMYGCCCGCTCC|CAGA
KTGGGCAGTCGTAAGACCTATAGTCTCACTCTGTCCTTATGAGGGGGAGTCGAAAGTCTGTGACR|CGGGCAGGGTCT
X P V S I L D I R V R Q G Y S P L S F Q T L X P A P R>

7210 7220 7230 7240 7250 7260 7270 7280
* * * * *
GGCCCTGACAGACYCGRASGCATTGAGGAAGAGTCCAGSCAGGACCATCAGTATCCCATTYCCGAACAGCCTCTGYCTCA
CCGGGACTGTCTGRGCTSCGTAACCTCTC|CAGGTCGTCCTGGTAGTCATAGGGTAARGGCTTGT|CGGAGACRGAGT
G P D R X X X I E E E S X Q D H Q Y P I X E Q P L X Q>

tat 61-90 (122) 7310 7320 7330 7340 7350 7360
* * * * *
GMCAAGGGGAGRCAATCCACAGRCCCTRAGGAAGCAAAAG|GGAGTGGTCGAGTCCATGAATAAGGA|ACTGA
CKGTTCCCTCTCYGTTAGGGTGTCTYGGGAYTCTTTTCTGTTT|CCTCACCAGCTCAGGTACTTATTCCTTGACT
X R G X N P T X P X E S K K A S G V V E S M N K E L>

7370 7400 7410 7420 7430 7440
* * * * *
AAAAGATTATCGGACAGGTCAGGGAMCAGGCTGAGCACCTGAAAACCGCTGTGCAAAATGGCTGCCATGCAGATGCTCAAG
TTTTCTAATAGCCTGTCCAGTCCCTKGTCCGACTCGTGGACTTTTGGCGACACGTTTAC|GACGGTACGTC|TACGAGTTC
K K I I G Q V R X Q A E H L K T A V Q M A A M Q M L K>

7450 7460 7490 7500 7510 7520
* * * * *
GAWACCATTAAACGAAGAGGCTGCCGAGTGGGACAGARTCCATCCGTC|CATGCCGACCRTTSCCCTCTCACCGMGAT
CTWTGGTAATTGCTTCTCCGACGGCTCACCTGTCTYAGGTAGGGCAGGTACGGCTGGGYAASGGGGAGAGTGGCKCTA
X T I N E E A A E W D R X H P V H A G P X X P L T X I>

7530 7540 7550 7580 7590 7600
* * * * *
TTGTAMAGAAATGGA|VAAGAAGGCAAAATCTCCARGATTGGCCCTGAGAATCCCTATAACACACCCRTCTTTGCCATT
AACATKTCTTTACCTTBTCTTCCGTTT|TAGAGTYCTAACCGGACTCTTAGGGATATTGTGGGYAGAAACGGTAAG
C X E M E X E G K I S X I G P E N P Y N T P X F A I>

7610 7620 7630 7640 7670 7680
* * * * *
AAGTGAGAGASCAAGCCGAACACCTCAAGACAGCCGTCAGATGGCAGTCTTCATTCA|CAATTTCAAAGGARAGGCGGA
TTCACTCTCTSGTTCGGCTTGTGGAGTCTGTGCGCAGGTCTACCGTCAGAAGTAAGTGT|TAAAGTTTCTCTYTCGGCCT
Q V R X Q A E H L K T A V Q M A V F I H N F K R X G G>

B2
join
B3FIGURE 15 (Cont)
SUBSTITUTE SHEET (RULE 26)

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7690 7700 7710 pol 211-240 (48) 7740 7750 7760
ATCGGAGG|AAAAAGAAAGATAGCACAAAGTGGAGGAACTGGTAGACTTTAGGGAGCTCAACAAACGTACACAGGATTT
TAGCCTCCCTTTTCTTTCTATCGTGTTCACCTCCTTTGACCATCTGAAATCCCTCGAGTTGTTTGCATGTGTCTTAAA
I G G K K K D S T K W R K L V D F R E L N K R T Q D F>

7770 7780 7790 7800 env 540-569 (172) 7830 7840
CTGGGAGGTCCAGCTCGGCTTTTGGCTCTGGCTTGGGATGACCTCAGGAGCCTGTGTCTGTTTCAGCTATCACAGACTGA
GACCTCCAGGTTCGAGCCGAAAARCCGAGACCGAACCTACTGGAGTCTCGGACACAGACAAGTCGATAGTGTCTGACT
W E V Q L G F X A L A W D D L R S L C L F S Y H R L>

7850 7860 7870 7880 7890 vpr 76-96 (117) 7920
GAGACYTTATCCTCATCGYTGCCAGAACTTGCCRACATAGCAGAATCGGCATCACTAGGCAACGTAGAGSTAGGAACGGC
CTCTGRAATAGGAGTAGCRACGGTCTTRCACGGYTGATCGTCTTAGCCGTAGTGATCCGTTCATCTCSATCCTTGCCG
R D X I L I X A R X C X H S R I G I T R Q R R X R N G>

spacers 7950 7960 7970 env 155-184 (147) 8000
KCCTCCAGGTCGCTGCC|CCCAAARTCWCTTCGAMCCCATTCCTATTCATTTGCGCTCCCGCTGGCTWCCTATCCT
MGGAGGTCCAGCGCAGCGGGGTTTYAGWGAAGCTKGGGTAAGGTAAAGTGATAACGCGAGGGCGACCGAWGCGATAGGA
X S R S A A P K X X F X P I P I H Y C A P A G X A I L>

8010 8020 8030 8040 8050 vif 76-105 (105) 8080
CAAGTGTAACRATAAGAMTTCAATGGCGAAARGATTGGCAWCTGGGACASGGAGTGTCCATCGAATGGAGAMWGA
GTTTACATTGATATTCTKKAAGTTACCGCTTTTCCTAACCGTGWACCTGTSCCTCACAGGTAGCTTACCTCTKWTCTTT
K C N X K X F N G E X D W X L G X G V S I E W R X K>

8090 8100 8110 8120 8130 gag 481-499 (33) 8160
GSTATAGCACAGGTGGACCTGRCCTCGCCGATCAGCTTAGCTCTATCCTCCCTYAGCTTCCCTGAAAAGCCTCTTC
CSATATCGTGTGTCCACCTGGGACGCGGCTAGTGGATGAGATAGGAGGGARTCGAAGGGACTTTTCGGAGAAG
X Y S T Q V D P X L A D Q P S L Y P P X A S L K S L F>

8170 spacers 8200 8210 vif 121-150 (108) 8240
GGAAACGATCCCTYATCCCAAGCGCTAGAAAGGCTATCTCGCCAWAKAGTCAGSAGAAGGTGTGAGTATCMGKCCGG
CCTTTGCTAGGGARTAGGGTTCGCGGATCTTCCCGATAGGAGCCGGTWTMTCACTCTCTCCACACTCATAGKMGCC
G N D P X S Q A A R R A I L G X X V X R R C E Y X X G>

8250 8260 8270 8280 8290 8300 8310 8320
ACACAATAAGGTGCGCTCCCTGCAATACCTGCACTAGCCAAACCCAMAACCGCTGCGWMAAGTGTACTGTAAGAAAT
TGTGTATTTCAGCCGAGGGACGTTATGGAGCGTGA|TCGGTTGGGTTKTTGGCGAACGKGTTCACAATGACATTCTTTA
H N K V G S L Q Y L A L S Q P X T A C X K K C Y C K K>

tat 16-45 (119) 8350 8360 8370 pol 976-995 (99) 8400
GTTGCTWCCACTGTCTAGSTCTGCTTCCTGAMGAAGGGACTGGGAAT|AGGGATTACGGAAGCAAATGGCTGGCGMTGAC
CAACGAWGGTGACAGTCSAGACGAAGGACTKCTTCCTGACCTTACCTTACCTAATGCCCTTCGTTTACCGACCGCKACTG
C C X H C Q X C F L X K G L G I R D Y G K Q M A G X D>

8410 spacers 8440 8450 pol 721-750 (82) 8480
TGTTGTGGCCRGCAAGGCAAGACGAAGACGCAGCCAAAGTACCATAGCAATTGGAGAACCATGGCCARTGASTTTAACCTCCC
ACACACCGGCGTCCGTTCTGCTTCTCGTCGGTTTCATGATCGTTAACCTTTGGTACCGGTACTSAAATTGGAGGG
C V A X R Q D E D A A K Y H S N W R T M A X X F N L P>

8490 8500 8510 8520 8530 8540 8550 8560
CCCTATCGTCSCTAAGGAAATCGTCGCAWRTTGGGATAAGTGT|AACGAATGGRCACCTGGAACCTGCTGGAGGAACCTGAAAM
GGGATAGCAGSATTCTTTAGCAGCGTGYAACGCTATTACATTGCTTACCYGTGACCTTGACGACCTCCTTGACTTTK
P I V X K E I V A X C D K C N E W X L E L L E E L K>

vpr 16-45 (113) 8590 8600 8610 8620 8630 8640
AWGAAGCCGTGAGACACTTTCCAGACCTGGCTGCATGGCTCGGTCAACAC|GATRTCATTAGCCTCTGGGATCAGTCC
TWTTCGGCACTCTGTGAAAGGGTCTGGGACCGACGTACCGGAGCCAGTTGCTCTAYAGTAATCGGAGACCTTAGTCAGG
X E A V R H F P R P W L H G L G Q H D X I S L W D Q S>

B3
join
B4FIGURE 15 (Cont)
SUBSTITUTE SHEET (RULE 26)

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8650 * env 106-144 (144) * 8680 * 8690 * 8700 * 8710 * 8720 *
CTGAAACCCCTGTGTGAAACTGACACCCCTCTGCGTCACCCCTCAACTGTACCAATGCCAATCTG|MWGAAGAGMTACTCCAC
GACTTTGGGGACACACTTTGACTGTGGGGAGACGAGTGGGAGTTGACATGGTTACGGTTAGAC|KWCCTCTCTKATGAGGTG
L K P C V K L T P L C V T L N C T N A N L X K X Y S T>
8730 * 8740 * vif 91-120 (106) * 8770 * 8780 * 8790 * 8800 *
CCAAGTGGACCCCGTCTGGCTGACCAWCTGATTCACCTCCACTATTTGATTGCTTTPKCCGATAGCRC|CAATCCATCCCA
GGTTCACCTGGGGCYAGACCGACTGGTWGACTAAGTGGAGGTGATAAAGCTAACGAAAMGGCTATCGYGT|TAGGTAGGGT
Q V D P X L A D X L I H L H Y F D C F X D S X I H P>
8810 * 8820 * 8830 * nef 166-195 (190) * 8860 * 8870 * 8880 *
TSRGGCWACACGGAATGGAGGATGAGGAWAGGGAAGTGCTGAWATGGAAATTCGATAGCCRTCTGGCT|CKCAGGCATATS
ASYCGGWTGTGCCTTACCTCCTACTCCTTTCCTTCCCTTACGACTWTACCTTTAAGCTATCGGYAGACCGAGMGT|CCGTATAS
X X X H G M E D E X R E V L X W K F D S X L A X R H X>
8890 * 8900 * 8910 * 8920 * pol 151-180 (44) * 8950 * 8960 *
GCT|TCTAGCCTATCGAWACCGTCCCCGTCAAGCTCAAGCCTGGCATGGACGGACCCAAAGTGAAACAGTGGCCCTC|CAC
CGA|TCTAGCCTATCGAWACCGTCCCCGTCAAGCTCAAGCCTGGCATGGACGGACCCAAAGTGAAACAGTGGCCCTC|CAC
A S S P I X T V P V K L K P G M D G P K V K Q W P L T>
8970 * 8980 * 8990 * 9000 * 9010 * gag 436-465 (30) * 9040 *
CGAAGAGAAAATCAAAGC|ATTTGGCCTAGCMRCAAGGGAAGGCTGGCAATTTCCYGCAGTCCARGCCTGAGCCT|ACCG
GCTTCTCTTTTAGTTTCG|CTAAACCGGATCGKYGTTCCTTCCGGACCGTTAAAGGRCGTGAGGTTCGGACT|CGGATGGC
E E K I K A I W P S X K G R P G N F X Q S X P E P T>
9050 * 9060 * 9070 * 9080 * 9090 * vif 31-60 (102) * 9120 *
CACCCCCAGCCGAGARCTTTRGATTTCGG|ATTAGCAAAAAGGCTAASGGATGGTTTTACAGACACCATTWCGAWAGCCRA
GTGGGGGTTCGGCTCTYGAAYCTAAGCCGTAATCGTTTTCGGATTSCCTACCAAAATGTCTGTGGTAAWGCTWT|CGGYT
A P P A E X F X F G I S K K A X G W F Y R H H X X S X>
9130 * 9140 * 9150 * 9160 * 9170 * 9180 * 9190 * 9200 *
CACCCTAAGGTCAGCTCCGAGGTCCACATTCCCTTCGG|ATGATGACCGCTTGCCAAGGCGTCCGCGGACCCRGTCACAA
GTGGGATTCCAGTCCGAGCTCCAGGTGTAAGGGGAGCCCT|TACTACTGGCGAACGGTTCGCGAGCCGCTGGGYCAGTGT
H P K V S S E V H I P L G M M T A C Q G V G G P X H K>
gag 346-375 (24) 9230 * 9240 * 9250 * 9260 * 9270 * 9280 *
AGCCAGGGTACTGGCAGAGGCTATGTC|CCAGGYGAMCMACGCTAACAT|CCTCCATTGTGSCCAAAGAGATTGTGGCAW
TCGGTCCCATGACCGTCTCCGATACAGGGTCCRCTK|GKTGCGATTGTAAGGAGGGTAACACSGGTTTCTCTAACACCGTW
A R V L A E A M S Q X X X A N I P P I V X K E I V A>
9290 * pol 736-765 (83) * 9320 * 9330 * 9340 * 9350 * 9360 *
RCTGTGACAAAATGCCAGCTCAAGGGTGAGGCTATK|CACGGACAGGTGRACTGTAGCCCT|TCCGAGGGAACAGACAGRCT
YGACACTGTTTACGGTCGAGTTCCCACTCCGATAMGT|GCTGTCCACYTGACATCGGGTAGGCTCCCTWGTTCGTCTCYGA
X C D K C Q L K G E A X H G Q V X C S P S E G X R Q X>
9370 * 9380 * rev 31-60 (126) * 9410 * 9420 * 9430 * 9440 *
AGGARGAACAGACGTAGAGGTGGCGTG|MGAGGCAAGGCAAAATCCRCCKCATCTCCGAGWGGATTCT|GGACAGATRAG
TCCTYCTTGTCTGCATCTTCCACCGCACKCTCCGTT|TCCGTTTAGGYG|MGCTAGAGGCTCWCC|TAAGA|CCTGTCTAYTC
R X N R R R R W R X R Q R Q I X X I S E X I L G Q X R>
9450 * 9460 * 9470 * gag 226-255 (16) * 9500 * 9510 * 9520 *
GGAACCCAGAGGCTCCGACATTGCCGGTACCACAAGC|ACACTGCAAGAGCAAAATCGSATGGATGACAARCAAT|CCCCCTR
CCTTGGGCTCCCGAGGCTGTAACGGCCATGGTGTTC|GCTGACGTTCTCGTTTAGCSTACCTACTGTT|YGTAGGGGGAY
E P R G S D I A G T T S T L Q E Q I X W M T X N P P>
9530 * 9540 * 9550 * 9560 * pol 841-870 (90) * 9590 * 9600 *
RCATTMAGCAAGAGTTTGGCATTCCCTATAACCTC|AGTCCAGGGCGTCTGGAAAGCATGAACAAAGAGCTCAAGAAA
YGTAAKTCGTTCTCAAACCGTAAGGGATATTGGGAGT|CAGGGTCCCGCAGCACCTTTCGTACTTGTTC|TCGAGTTCTTT
X I X Q E F G I P Y N P Q S Q G V V E S M N K E L K K>

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VFIGURE 15 (Cont)
SUBSTITUTE SHEET (RULE 26)

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9610 9620 9630 **nef 106-135 (186)** 9660 9670 9680
* * * * *
ATCATTTGGGAGACAGGAGATCCTCGATCTCTGGGTCTACMATACCCAAGGCTWTTTCCCTGACTGGCASAATTACACACC
TAGTAACCGTCTGTCTCTTAGGAGCTAGAGACCCAGATGKTATGGGTTCGAWAAAGGGACTGACCGTSTTAATGTGTGG
I I G R Q E I L D L W V Y X T Q G X F P D W X N Y T P>
9690 9700 9710 9720 **rev 46-75 (127)** 9750 9760
* * * * *
CGGACCCGARYCAGATACCTAGAGAGMAAGACAGAGACAGATTCTRTKCTATTAGCGAAWGGATTCTCAGCAMCTKCC
GCCTGGGCTYRGTCCTATCGAATCTCTCKTCTGTCTGTCTAAGYAMGATAATCGCTTWCCTAAGAGTCGTGKAMGG
G P G X R Y P S R X R Q R Q I X X I S E X I L S X X>
9770 9780 9790 9800 9810 **gag 301-330 (21)** 9840
* * * * *
TCGGCAGAYCCGCTGAGCCTGTGCCCTGTGCAACTGTWTAAGACTGAGAGCCGAACAGGCTWCCCAAGASGTCAAGAAT
AGCCGCTCTRGCGACTCGGACACGGAGACCTTGACAWATTCTGTGACTCTCGGCTTGTCCGAWGGGTCTSCAGTTCTTA
L G R X A E P V P L Q L X K T L R A E Q A X Q X V K N>
9850 9860 9870 9880 9890 9900 9910 9920
* * * * *
TGGATGACCGASACACTGCTCGTGCAAAACGCTAACCTGACTGTGAGARAGTGTATCTGKCTTGGGTCCCCGCTCATAA
ACCTACTGGCTSTGTGACGAGCAGCTTTTGCGATTGGGACTGACACTCTYTACATAGACMGAAACCCAGGGGCGAGTATT
W M T X T L L V Q N A N P D C E X V Y L X W V P A H K>
pol 676-705 (79) 9950 9960 9970 9980 9990 10000
* * * * *
AGGCATTGGCGGAAACGAACAGGTGGACAAACTGGTCAKCKCTGGCATTAGGAAACAGACCCCTAACCCCTCAGGAARTCS
TCCGTAACCGCTTTGCTTGTCCACCTGTTTGACAGTGMGACCGTAATCCTTTGTCTGGGATTGGGAGTCTTCTYAGS
G I G G N E Q V D K L V X X G I R K T D P N P Q E X>
10010 **env 76-105 (142)** 10040 10050 10060 10070 10080
* * * * *
WTCTGGAAACCGTCAACGAGAACCTTTAACATGTGGAAAAACRATATGGTGGASCAAATGCAWAGGCTGGCTWTGCCATT
WAGACCTTTTGACAGTGGCTCTTGAATTTGTACACCTTTTGTATACCACCTSGTTTACGTWCTCCGACCGAWACGGTAA
X L E N V T E N F N M W K N X M V X Q M X E A G X A I>
10090 10100 **env 170-199 (148)** 10130 10140 10150 10160
* * * * *
CTGAAATGCAATRACAAAAMSTTCAACGGAACCTGGACCTGTAMGAATGTGTCCASCGTCCAGTGTACCCATGGCCWAGA
GACTTTACGTTATGTTTTKSAAGTTGCGCTTGACCTGGGACATKCTTACACAGGTSGCAGGTACATGGGTACCGWTCT
L K C N X K X F N G T G P C X N V S X V Q C T H G X E>
10170 10180 10190 **env 600-629 (176)** 10220 10230 10240
* * * * *
GCTCAAGAWTAGCGCTRTCTCCCTGCTCAACGCTACCGCTATCGCTGTGGCTGRGKGGACCGATAGGRTTATCGAAGTGG
CGAGTTCTWATCGCGAYAGAGGGACGAGTTGCGATGGCGATAGCGACACCGACYCMCTGGCTATCCYAATAGCTTCACC
L K X S A X S L L N A T A I A V A X X T D R X I E V>
10250 10260 10270 10280 **vif 46-75 (103)** 10310 10320
* * * * *
YTCACTCCCRGCATCCCAAAGTGTCCAGCGAAGTGCATATCCCTCTGGGAGAGSGCTAGGCTCRTCATTARGACATACTGG
RAGTLAGGGYCGTAGGGTTTACAGGTCGCTTCACGTATAGGGAGACCCCTCTSCGATCCGAGYAGTAATYCTGTATGACC
X Q S X H P K V S S E V H I P L G X A R L X I X T Y W>
10330 **spacers** 10360 10370 **nef 1-30 (179)** 10400
* * * * *
GGCCTCCASACAGGCGCTGCTATGGGCGGTAAATGGTCCAAGWGCTCCCYCGTGGGATGGCCCGMAGTGAGAGAGAGAAT
CCCGAGGTTGTCCCGACGATACCCGCCATTTACAGGTTCCWCGAGGGGRCAGCCTACCGGGCKTCACTCTCTCTTA
G L X T G A A M G G K W S K X S X V G W P X V R E R I>
10410 10420 10430 10440 10450 **pol 496-525 (67)** 10480
* * * * *
CAGACRGRACASCCCTGCGCTGAGGGAGTCTCAAGACCCGGCAAGTACKCTAGGAWGAGGRGTGCCCATACCAATGACG
GTCTGYCYGTSGGGGACGGCGACTCCCTCAGAGTTCTGGCCCTTCATGMGATCTWCTCCYACGGGTATGGTTACTGC
R X X X P A A E G V L K T G K Y X R X R X A H T N D>
10490 10500 10510 10520 10530 10540 10550 10560
* * * * *
TCARGCACTGACAGMGYTGTCGAAAAGATTGCCACAGAGCTGAGCTGGGAGGCTGAAATACTKKGGAATCTGCTC
AGTYCGTTGACTGTCKCCRACAGTTTCTAACGGTGTCTGAGATGACCTCCSAGACTTTATGAMCMCTTAGACGAG
V X Q L T X X V Q K I A T E S S W E X L K Y X X N L L>

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B7FIGURE 15 (Cont)
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env 585-614 (175) 10590 10600 10610 10620 10630 10640
* * * * *
CWGTACTGGGGCCWGGAACTGAAAAWCTCCGCCRTCAGCCTCCTGAATGCCACAGCATTATSWGCTGCCTGAGAAAGAWAG
GWCATGACCCCGWCCTTGACTTTTGWAGGCGGYAGTCGGAGGACTTACGGTGTGCGTAAASWCGACGGACTTTCTCTWTC
X Y W G X E L K X S A X S L L N A T A I X L P E K X S>

10650 pol 391-420 (60) 10680 10690 10700 10710 10720
* * * * *
CTGGACCGTCAACGATATCCAAAAGCTCGTGGGAAAGCTCAACTGGGCATCCCAGATTACSCCGGAAGAGCCATTGAGG
GACCTGGCAGTTGCTATAGTTTTCGAGCACCCCTTCGAGTTGACCCGTAGGGTCTAAATGSGGCCCTTCTCGGTAACCTC
W T V N D I Q K L V G K L N W A S Q I Y X G R A I E>

10730 10740 env 345-374 (159) 10770 10780 10790 10800
* * * * *
CTCAGCAACACWTGCTGCAACTGACAGTGTGGGGCATTAAAGCAACTGCAAGCCAGAGTGTCTGCCRTTGTAGAGATATCTC
GAGTCGTTGTGWACGACGTTGACTGTACACCCCGTAATTCGTTGACGTTGCGTCTCAGGAGCGGYAACTCTCTATGGAG
A Q Q H X L Q L T V W G I K Q L Q A R V L A X E R Y L>

10810 10820 10830 pol 631-660 (76) 10860 10870 10880
* * * * *
GCCCTCCAGGATAGCGGATYGGAAAGTGAATATCGTCACCGATAGCCAATACGCTCTAGGCATCATTCWGGCTCAGCCTGA
CGGGAGGTCTTATCGCCTARCTTCACCTTATAGCAGTGGCTATCGGTTATCGGAGATCCGTAGTAAGWCCGAGTCCGACT
A L Q D S G X E V N I V T D S Q Y A L G I I X A Q P D>

10890 10900 10910 10920 env 420-449 (164) 10950 10960
* * * * *
CARAAGCGAAAAGGAAATCTCCAATATACCAARTCWGATTACRAGATCCTACCGAATCTCAAAATCAACAGGATAGGA
GTYTTCGCTTTCCCTTTAGAGTTGATATGGTYAGWCTAAATGYTCTAGGAGTGGCTTAGAGTTTGTAGTTGTCTATCTC
X S E R E I S N Y T X X I Y X I L T E S Q N Q Q D R>

10970 10980 10990 11000 11010 env 285-314 (155) 11040
* * * * *
ATGAGMAAGASCTCCTGCTCCACAAAGGCTAAGACAAGGGTCGTGSAAGGGAAAAGCGTGCCGTGCGGCTTGGCGCT
TACTCKTTCTSGAGGACCGAGGGTGTTCGATCTCTTCCAGCACSTTCCCTTTTCGCACGGCAGCCGKAACCCGGA
N E X X L L A P T X A K R R V V X R E K R A V G X G A>

11050 11060 11070 11080 11090 pol 91-120 (40) 11120
* * * * *
ATGWTYYTCGGAATTCCTCGGCGCTGCTAAACCCAAAATGATCGGAGGCATTGGAGGCTTTATCAAAGTCAGGCAGTATGA
TACWAARAGCCTAAGGAGCCGCGACGCTTTGGGTTTACTAGCCTCCGTAACCTCCGAAATAGTTTCACTCCGTCATCT
M X X G F L G A A K P K M I G G I G G F I K V R Q Y D>

11130 11140 11150 11160 11170 11180 11190 11200
* * * * *
CCAAATCMTTATCGAAATCTGTGGAMASAAGGCTATCTCTACCATAGGCTCAGGGATTTCATCTGATCGYCGCTAGGA
GGTTTAGKAATAGCTTTAGACACCTKTSTTCCGATAGAGGATGGTATCCGAGTCCCTAAAGTAAGACTAGCRGCGATCCT
Q I X I E I C G X K A I S Y H R L R D F I L I X A R>

env 555-584 (173) 11230 11240 11250 11260 11270 11280
* * * * *
YTGTTGGAAGTCTCGGCCRTAGCTCCCTGARAGGCCCTCCRGAGAGGCACACTGAATGCCTGGGTGAAAGTGRTTGAGGAA
RACACCTTGACGAGCCGGYATCGAGGGACTYTCGGGAGGYCTCTCCCTGTGACTTACGGACCCACTTTTCACYAACCTCCTT
X V E L L G X S S L X G L X R G T L N A W V K V X E E>

11290 gag 151-180 (11) 11320 11330 11340 11350 11360
* * * * *
AAGGSATTCARTCCCGAAGTGATTCCTATGTTTWCCTCTGTCCGAGGGAGCCACACTGAGCAACACASCCGCTAA
TTCCSTAAGTYAGGGCTTCACTAAGGGTACAAAWGCCGAGACAGGCTCCCTCGGTGTGAGCTTCGTTGTGTSGGCGATT
K X F X P E V I P M F X A L S E G A T L E S N T X A N>

11370 11380 nef 46-75 (182) 11410 11420 11430 11440
* * * * *
CAATSCCGATTGCGYGTGGCTGRAAGCCAGGAAGCGAAGRAGTGGGATTTCTGTGAGACCCCAAGTGCTTACAGCCCK
GTTASGGCTAACGCRACCCGACYTTCGGGTCTCTCTCTCYTACCCTAAAGGACACTCTGGGGTTACGGGATCTCGGM
N X D C X W L X A Q E E E X V G F P V R P Q V P R A>

11450 env 630-651 (178) 11480 11490 spacers 11520
* * * * *
GGAGGGCTATCCTCMACATTCCASGAGGATTAGGCAAGGCYTTGAGAGAGCCCTCCTAGCCGCGAATGGGATAGGRIT
CCTCCCGATAGGAGKTGTAAGGGTSCCTAATCCGTTCCGRAACTCTCTCGGGAGGATCGGCGGCTTACCTATCCYAA
X R A I L X I P X R I R Q G X E R A L L A E W D R X>

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C1FIGURE 15 (Cont)
SUBSTITUTE SHEET (RULE 26)

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11530 11540 gag 211-240 (15) 11570 11580 11590 11600
* * * * *
CACCCCTGTGCACGCTGGCCCTRTCSCTCCCGGCCAAATSAGAGAGCCCAAGGGAAGCGATATCGCTGGCACAACCTCAG
GTGGGACACGTGCGACCGGGAYAGSGAGGGCCGGTTTASTCTCTCGGGTCCCTTCGCTATAGCGACCGTGTGGGAGTC
H P V H A G P X X P G Q X R E P R G S D I A G T T L R>

11610 11620 11630 nef 76-105 (184) 11660 11670 11680
* * * * *
GCCCCATGACATATAAGGSCGCTRTTGACCTCAGCYTGTTTTCTGAAAGAGAAAGGCGGACTGGAWGGCTCCTCTATAGCM
CGGGTACTGTATATCCSGCGAYAAGTGGAGTCGRACAAAGACTTTCTCTTCCGCTGACCTWCCGGAGYAGATATCGK
P M T Y K X A X D L S L F L K E K G G L X G L X Y S>

11710 11720 vpr 1-30 (112) 11750 11760
* * * * *
AGAAAGCTGCTATGGAACAGGCTCCCGAAGACCAARGCYCTCAGAGAGAGCCTTACAATGAGTGGRCCTGGAGCTCCTG
TCTTTCGACGATACCTTGTCCGAGGGCTTCTGGTTCGRGAGTCTCTCTCGGAATGTTACTCACCYGGGACCTCGAGGAC
X K A A M E Q A P E D Q X X Q R E P Y N E W X L E L L>

11770 11780 11790 11800 11810 pol 481-510 (66) 11840
* * * * *
GAAGAGCTCAAGMAMGAGGCTCAAGRCCAATGGACCTWCCAAATCTWTGAGGAACCTTTAAGAATCTGAAAACCGGAAA
CTTCTCGAGTTCTKCTCCGAGTTTCYGGTTACCTGGAWGGTTAGAWAGTCTTGGGAAATCTTAGACTTTTGGCCTTT
E E L K X E A Q X Q W T X Q I X Q E P F K N L K T G K>

11850 11860 11870 11880 11890 11900 11910 11920
* * * * *
GTATKCCAGAAWAGARGCGCTCACACAACTGGATGACAGAWACCTCCTGGTCCAGAATGCCAATCCCGATTGCAAGW
CATAMGGTCTTWTCTTCYCGCGAGTGTGTTTGACCTACTGTCTWTGGGAGGACCAGGTCTTACGGTTAGGGCTAACGTTCTW
Y X R X R X A H T N W M T X T L L V Q N A N P D C K>

11950 11960 11970 11980 11990 12000 gag 316-345 (22)
* * * * *
CCATCCTCARGGCTCTGGGAMCCGAGCCWCACCTGGAAGACCTGAGGTCATCCCTATGTTTCWCAGCCCTCAGCGAAGGC
GGTAGGAGTYCCGAGACCCTKGGCCTCGGWTGACCTTCTGGACTCCAGTAGGGATACAAGWGTGGGAGTCGCTTCCG
X I L X A L G X G A X L E E P E V I P M F X A L S E G>

12010 12040 12050 12060 12070 12080 gag 166-195 (12)
* * * * *
GCTACCCCCAAGACCTGAATAYGATGCTCAACAYCGTCGGCGGACACCAATCCACCTCCAGGAACAGATTGSCCTGGAT
CGATGGGGGGTTCTGGACTTATRCTACGAGTTGTRGCAGCCCGCTGTGGTTAGGTGGGAGGTCTTGTCTAACSGACCTA
A T P Q D L N X M L N X V G G H Q S T L Q E Q I X W M>

12090 12100 12130 12140 12150 12160 gag 241-270 (17)
* * * * *
GACAARTAACCTCCCTCCCTGTGCGGAGASATTTACAAAAGGTGGATTATCCTCGGCCTCAGCTATCCCCCATCCCCG
CTGTTYATTGGGAGGGYAGGGACAGCCTCTSTAAATGTTTTCCACCTAATAGGAGCCGGACCTAGGGGGTAGGGG
T X N P P X P V G X I Y K R W I I L G L T R I P H P>

12170 12180 12190 12220 12230 12240 pol 241-270 (50)
* * * * *
CCGGCCTCAAGAAAAAGAAAGCGTCACCGTCCCTGGATGTGGGAGACGCTTACTTCAGCGTCCCCCTCGACRAARRCAA
GGCCGGAGTTCTTTTCTTTTCGCACTGGCAGGACCTACACCTCTGCGAATGAAGTCGAGGGGGAGCTGYTTYGGTT
A G L K K K K S V T V L D V G D A Y F S V P L D X X Q>

12250 12260 12270 12280 12310 12320 pol 541-570 (70)
* * * * *
ARGGAAACCTGGGAGRCTTGGTGGAYGGAMTACTGGCAGGCTACCTGGATTCTGAGTGGGAGTTTGTGAATACCCCTCC
TYCCTTTGGACCCTCYGAACCCTRCCTKATGACCGTCCGATGGACCTAAGGACTCACCTCAAACACTTATGGGGAGG
X E T W E X W W X X Y W Q A T W I P E W E F V N T P P>

12330 12340 12350 12360 12370 nef 121-150 (187) 12400
* * * * *
CCTCGTCTTTCCCGATTGGCAWAACCTATACCCCTGGCCCTGGCRYAAGGTATCCCTCACCTTTGGATGGTGCTTTAAGC
GGAGCACAAGGGCTAACCGTWTGATATGGGACCGGGACCGYRTTCCATAGGGGAGTGGAAACCTACCACGAAATTCG
L V F P D W X N Y T P G P G X R Y P L T F G W C F K>

12410 12420 12430 12440 12450 pol 571-600 (72) 12480
* * * * *
TCGTGCTGTGGACCCCAACTGTGGTACCAACTGGAAGGAMCCCATGTCGGAGYCGAAACCTTTTACGTGGACCGGA
AGCACGGACACCTGGGCTTGACACCATGGTTGACCTTTCTKGGGTACRGCTTCRGCTTTGGAAAATGCACCTGCCT
L V P V D P K L W Y Q L E K X P I X G X E T F Y V D G>

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C2FIGURE 15 (Cont)
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12490 12500 12510 12520 **gag 136-165 (10)** 12550 12560
 * * * * *
 GCCGCCARCAGAGACAAAGCTCGG|CAAAACSYCCAGGGACAGATGGTGCATCAGSCTMTTAGCCCCAGGACCCTCAA
 CGGCGGTGTCTCTCTGTTTCGAGCCG|GTTTGSRRGTCCTGTCTACCACGTAGTCSGAKAATCGGGTCTCTGGGAGTT
 A A X R E T K L G Q N X Q G Q M V H Q X X S P R T L N>

12570 12580 12590 12600 12610 **env 61-90 (141)** 12640
 * * * * *
 CGCTTGGGTCAAGGTCRTCGAAGAGAAAGSCTTTAR|GAMACCGAAGTGCATAACGTCTGGGTACCCATGCCTGTGTGC
 GCGAACCCAGTTCCAGYAGCTTCTCTTTCGAAATY|GCTKTGGCTTACGTATTGCAGACCCGATGGGTACGGACACACG
 A W V K V X E E K X F X X T E V H N V W A T H A C V>

12650 12660 12670 12680 12690 12700 12710 12720
 * * * * *
 CTACCGATCCCAATCCCAAGAGRTTSWCCTGGAGAATGTGACAGAG|CTCAAGGATCAGMAAYTCCTCGGCMTTTGGGGA
 GATGGCTAGGGTTAGGGGTTCTCYAASWGGACCTTTACACTGTCT|GAGTTCCTAGTCKTTRAGGAGCCGKAAACCCCT
 P T D P N P Q E X X L E N V T E L K D Q X X L G X W G>

env 375-404 (161) 12750 12760 12770 12780 12790 12800
 * * * * *
 TGCTCCGGCAAAMTCATTTCACACAACCRMTGTGCCTTGGAAACAGCWCTGGTCCAA|CMAKCTGGCCATAACAAAGTGGG
 ACGAGGCCGTTTTCAGTAAACGTGTTGGYKACACGGAACCTTTCGCGGAGACCAGGTT|GKTMGACCCGATATTGTTTCACCC
 C S G K X I C T T X V P W N S X W S N X X G H N K V G>

12810 **vif 136-165 (109)** 12840 12850 12860 12870 12880
 * * * * *
 AAGCCTCCAGTATCTGGCTCTGAMGGCTCTGATTAMGCCTAAGAAAAATCARACCCCTCTGCC|TAGCGYTAAGACAATCA
 TTCCGAGGTCATAGACCAGACTKCCGAGACTAATKCGGATTCTTTTAGTYTGGGGGAGACGGATCG|CRATTCTGTAGT
 S L Q Y L A L X A L I X P K K I X P P L P S X K T I>

12890 12900 **env 230-254 (152)** 12930 **spacers** 12960
 * * * * *
 TTGTGCATCTGAATRAGTCCGTTGGWAATCAATTGCACAAGGCCTARCAATAACACAAGGAM|GCCGCGCTAGTGAAGWA
 AACACGTAGACTTAYTCAGGCACCWTTAGTTAACGTGTTCGGATYGTATTGTGTTCCTK|TCGGCGCGGATCACTTCWT
 I V H L N X S V X I N C T R P X N N T R X A A A S E X>

12970 12980 12990 **gag 106-135 (8)** 13020 13030 13040
 * * * * *
 CAGAAWAAGTCCMAACAGAAAACCCAGCAAGCCGCGCCGATACAGGCARCTCCAGCMAGGT|CAGCCAAACTATCCCAT
 GTCTTWTTCAGGKTTGTCTTTTGGGTCGTTCCGCGCGCGCTATGTCCGTYGAGGTCGKTC|CAGTCGGTTTGTATAGGGTA
 Q X K S X Q K T Q Q A A A D T G X S S X V S Q N Y P I>

13050 13060 13070 13080 **pol 826-855 (89)** 13110 13120
 * * * * *
 TGTCTCCAACTTTACCTCCRCRCTGTGAAGCCGCTTGTGGTGGGCCRRTATCMAACAGGAGTTT|GGAATCCCTTACA
 ACACAGGTTGAAATGGAGGYGGYGACACTTTCGGCGCAACACCCGGYATAGKTTGTCTCA|AACCTTAGGGAAATGT
 V S N F T S X X V K A A C W W A X I X Q E F G I P Y>

13130 13140 13150 13160 13170 **pol 586-615 (73)** 13200
 * * * * *
 ATCCCAAAAGCCAAACATTCTATGTGGATGGCGCTGCCARTAGGGAAACCAAACCTGGGAAAGGCT|GGCTATGTGACAGAC
 TAGGGGTTTTCGGTTTGTAAAGATACACCTACCGCGACGGTYATCCCTTTGGTTTGGACCTTT|CCGACCGATACACTGTCTG
 N P Q S Q T F Y V D G A A X R E T K L G K A G Y V T D>

13210 13220 13230 13240 13250 **pol 766-795 (85)** 13280
 * * * * *
 AGAGGCAGACAGAAARTCRTTAG|GGAATCTGGCAGCTCGACTGTACCCATCTGGAAAGGCAAARTCATTTCTGGTAGCCGT
 TCTCCGCTGTCTTTTAYGYAATCC|CCTTAGACCGTCGAGCTGCATGGGTAGACCTTCCGTTTAYAGTAAGACCATCGGCA
 R G R Q K X X S G I W Q L D C T H L E G K X I L V A V>

13290 13300 13310 13320 13330 13340 13350 13360
 * * * * *
 CCACGTCGCTCCGGCTACATTGAGGCTGAGGT|GGCAATGAGCAAGTGATAAGCTCGTGA|KTKCCGGAATCAGAAAGG
 GGTGCAGCGGAGGCCGATGTAACCTCCGACTCCAG|CCGTTACTCTTACCTATTTCGAGCACTMAMGGCCTTAGTCTTTCC
 H V A S G Y I E A E V G N E Q V D K L V X X G I R K>

pol 691-720 (80) 13390 13400 13410 13420 13430 13440
 * * * * *
 TGCTATTCTCGACGGAATCRATAAGGCTCAGGAAGAGCAGAA|GTCAGGGAAAGGATTAGGCRARCCSCTCCCGTCTGCT
 ACGATAAGGAGCTGCCTTAGYTATTCCGAGTCCTTCTCGTGCT|CAGTCCCTTTCTAATCCGYTYGGSGAGGGCGACGA
 V L F L D G I X K A Q E E H E V R E R I R X X X P A A>

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FIGURE 15 (Cont)
 SUBSTITUTE SHEET (RULE 26)

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nef 16-45 (180) 13470 13480 13490 13500 13510 13520
* * * * *
GAAGGCGTCGGCGCTGYCTCCCRGGATCTGGATAAGKACGGAGCCMTCACCTCCACAAGCGGAACCCAACAGTCCCAGGG
CTTCCGACGCGGACRGAGGGYCCTAGACCTATTCMTGCCCTCGGKAGTGGAGGCTGTTCCGCTTGGGTTGTCTAGGGTCCC
E G V G A X S X D L D K X G A X T S T S G T Q S Q G>

13530 rev 91-120 (130) 13560 13570 13580 13590 13600
* * * * *
AACTGAAACTGGCGTCGGCMRCCCTCAGATTTTGGGAGAGTCCAGCGYTRTCTCGGCGYCCGGCTCCATCGTCATCTGGG
TTGACTTTGACCGCAGCCGKYGGGAGTCTAAARCCCTCTCAGGTCGCRA YAGGAGCCGRGGCCAGGTAGCAGTAGACCC
T E T G V G X P Q I X G E S S X X L G X G S I V I W>

13610 13620 pol 526-555 (69) 13650 13660 spacers
* * * * *
GTAAACCCCTAAGTTTARGCTCCCCATTGAGARAGAGACATGGGAARCCCTGGTGAYGGASTATTGGCAAGCCGCTGCT
CATTTTGGGGATTCAAATYCGAGGGGTAAGTCTYTCTGTACCTTYGGACCACCTRCCTSATAACCGTTCCGCCGACGA
G K T P K F X L P I Q X E T W E X W W X X Y W Q A A A>

13690 13700 13710 env 140-169 (146) 13740 13750 13760
* * * * *
TACAGACTGATCARCTGTAACACAAGCGYTATCAMACAGGCTTGCCCTAAGRITASCCTTTGASCCTATCCCTATCCATTA
ATGCTGACTAGTYGACATTGTGTTCGCRATAGTKGTCCGAACGGGATTCTYAATSGAACTSGGATAGGGATAGGTAAT
Y R L I X C N T S X I X Q A C P K X X F X P I P I H Y>

13770 13780 13790 13800 pol 376-405 (59) 13830 13840
* * * * *
CTGTGCCCCCTGATGTTGGATGGGCTATGAGCTCCACCTTGACAGATGGACAGTGCACCCATCSWGCTCCCCGAAAAGG
GACACGGGGGACCTACCCGATACTCGAGGTGGGACTGTCTACCTGTACGTTGGGTAGSWCAGGGGGCTTTTCC
C A P P S W M G Y E L H P D R W T V Q P I X L P E K>

13850 13860 13870 13880 13890 gag 331-360 (23) 13920
* * * * *
ASTCCTGACAGTGAATGACATTGACAAAWCAATTCTGARAGCCCTCGGCMCAGGCGCTWCCCTGGAGGAAATGATGACA
TSAGGACCTGTCACTTACTGTAAGTCTTTWGTAAAGACTYTCGGGAGCCGKGTCCGCGAWGGGACCTCCCTTACTACTGT
X S W T V N D I Q K X I L X A L G X G A X L E E M M T>

13930 13940 13950 13960 13970 13980 13990 14000
* * * * *
GCATGTCAGGGAGTGGGAGGCCCTTRGCCATAAGGCTAGAGTGTATTACAGAGACTCCAGGGACCCCMTTTGGAAAGGCCC
CGTACAGTCCCTCACCCCTCGGGAYCGGTATTCCGATCTCACAATAATGCTCTGAGGTCCCTGGGGKAAACCTTTCCGGG
A C Q G V G G P X H K A R V Y Y R D S R D P X W K G P>

pol 931-960 (96) 14030 14040 14050 14060 14070 14080
* * * * *
TGCCAAACTGCTCTGGAAAGGCGAAGGCGTGTGGTCATCCAAGACRTTAAGATTGGAGGCCAACTGAWAGAAGCCCTCC
ACGGTTTGACGAGACCTTTCCGCTTCCGCGACACCAGTAGGTTCTCTAATCTAACCTCCGTTGACTWCTTCGGGAGG
A K L L W K G E G A V V I Q D X K I G G Q L X E A L>

14090 pol 61-90 (38) 14120 14130 14140 14150 14160
* * * * *
TGGATACAGGAGCCGATGACACCGTCTGGAAGAWATSAATCTGCCTGGCARGTGGGGAATCAAACAGCTCCAGGCTAGG
ACCTATGCTCTCGGCTACTGTGGCAGGACCTTCTWTASTAGACGGACCGTYCACCCCTTAGTTTGTGCGAGGTCCGATCC
L D T G A D D T V L E X X N L P G X W G I K Q L Q A R>

14170 14180 env 360-389 (160) 14210 14220 spacers
* * * * *
GTCCTGGCTRTCGAGAGGTATCTGAAAGATCAAMAGYTTCTGGGAMTCTGGGGCTGTAGCGGAAAGCCTGCTATGAAAAA
CAGGACCGAYAGCTCTCCATAGACTTTCTAGTTKTCRAAGACCTKAGACCCCGACATCGCTTTCCGACGATACCTTTT
V L A X E R Y L K D Q X X L G X W G C S G K A A M E N>

14250 14260 14270 vif 1-30 (100) 14300 14310 14320
* * * * *
CAGATGGCAAGTGMTGATCGTCTGGCAAGTGGACAGGATGARGATTAGGACATGGAAGACCTCGTGAAACACCATATGY
GTCTACCGTTCAKACTAGCAGACCGTTACCTGTCTACTYCTAATCCTGTACCTTWTGCGAGCACTTTGTGGTATACR
R W Q V X I V W Q V D R M X I R T W X S L V K H H M>

14330 14340 14350 14360 env 390-419 (162) 14390 14400
* * * * *
ATMTTATCTGTACCACARMCGTCCCTTGGAACTCCASCTGGAGCAATAAGTCCYTCGAAGAGATTGGRATAACATGACC
TKAATAGACATGGTGTGKGCAGGGGACCTTGAGGTSGACCTCGTTATTTCAGGRAGCTTCTCTAAACCTTATTGTACTGG
X X I C T T X V P W N S X W S N K S X E E I W X N M T>

FIGURE 15 (Cont)
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14410 14420 14430 vpu 16-45 (133) 14460 14470 14480
* * * * *
TGGATKSAATGGCTGATTMTTCGCTATCGTCGTGTGGACCATGCGTWTATCGAATACARGAACTGCTCARGCAAAGGAR
ACCTAMSTTACCGACTAAKAGCGATAGCAGCACACCTGGTAACRCAWATAGCTTATGTYCTTTGACGAGTYCGTTTCCTY
W X X W L I X A I V V W T I X X I E Y X K L L X Q R X>

14490 14500 14510 gag 46-75 (4) 14550 14560
* * * * *
AATCGATAGGCTCATCRAAAGCTCAACCCCTGGCCTCCTGGAACCKCTGAGGGATGTMAACAGATCCTGGRACAGCTCC
TTAGCTATCCGAGTAGYTTTTCGAGTTGGGACCGGAGGACCTTTGGMGACTCCCTACAKTTGTCTAGGACCTGTCTCGAGG
I D R L I X R L N P G L L E T X E G C X Q I L X Q L>

14570 14580 14590 14600 14610 14620 14630 14640
* * * * *
AGYCCGCCCTCMAGACAGGCWCCGAAGAGCTCAGAGAGCTCAGAGAGCTCCTGARACAGAGAARGATTGACAGACTGATTRAG
TCRGGCGGGAGKTCGTCTCGWGGCTTCTCGAGAGAGAGCTCCTTCGAGGACTYGTCTCTTYCTAAGTGTCTGACTAAYTC
Q X A L X T G X E E L S S R K L L X Q R X I D R L I X>

vpu 31-60 (134) 14670 14680 14690 14700 14710 14720
* * * * *
AGAAYCAGAGAGAGAGCCGAAGACTCCGGCAATGAGTCCGAGGGAGACACCCGGAATCAGATACCAATACAATGTGCT
TCTTRGTCTCTCTCGGCTTCTGAGGCGGTTACTCAGGCTCCCTCTCTGTTGGGCTTAGTCTATGTTATGTTACACGA
R X R E R A E D S G N E S E G D T P G I R Y Q Y N V L>

14730 pol 286-315 (53) 14760 14770 14780 14790 14800
* * * * *
CCCCAAGGCTGGAAGGGCTCCCCASCCATTTTCCAAAGCTCCATGMCCMAAATCCTCATGATGCAAGGGGAACTTTA
GGGGGTTCCGACCTTCCCGAGGGGTSGGTAAAAGGTTTCGAGGTACKGGKTTTAGGACTACTACGTTTCCCTTTGAAAT
P Q G W K G S P X I F Q S S M X X I L M M Q R G N F>

14810 14820 gag 376-405 (26) 14850 14860 14870 14880
* * * * *
RGGGACMGAAAAGGATTRTCAAGTGCTTCAACTGTGGAAGGAAGGCCATMTGCTARGAATTGCAGACCTCCCTCGGAG
YCCTGKCTTTTCTTAAYAGTTACGAAGTTGACACCTTCTCTCCGGTAKAGCGATYCTTAACGTCCTGGAGGGGACCTC
X G X K R I X K C F N C G K E G H X A X N C R P P L E>

14890 14900 14910 rev 76-105 (129) 14940 14950 14960
* * * * *
AGACTGMACCTGGATTGCTCCGAGGATWGCGRACCTCCGGCACACAGCAAAGCCACAGAGACAGGAGTGGGACT
TCTGACTGGACCTAACGAGGCTCCTAWCGCYGTGGAGGCGGTGTGTCGTTTCGGTTCGGTGTCTCTGTCTCACCCTGA
R L X L D C S E D X X T S G T Q Q S Q G T E T G V G L>

14970 14980 14990 15000 pol 781-810 (86) 15030 15040
* * * * *
CGTGGCTGTGCATGTGGCCAGCGGATATATCGAAGCCGAAGTGATCCCTGCGAACTGGACAGGAACCGCTTACTTTM
GCACCGACACGTACACCGGTCGCTATATAGCTTCGGCTTCACTAGGGACGGCTTTGACCTGTCTTTGGCGAATGAAAK
V A V H V A S G Y I E A E V I P A E T G Q E T A Y F>

15050 15060 15070 15080 15090 env 200-229 (150) 15120
* * * * *
TCCTCAAGATTARGCCTGTGGTCAGCACACAGCTCCTGCTCAACGGTAGCCTCGCTGAAGAGGAARTCRRTATCAGAAGC
AGGAGTTCTAATYCGGACACCAGTCGTGTGTCGAGGACGAGTTGCCATCGGAGCGACTTCTCCTTYAGYAATAGTCTTCG
X L K I X P V V S T Q L L L N G S L A E E E X X I R S>

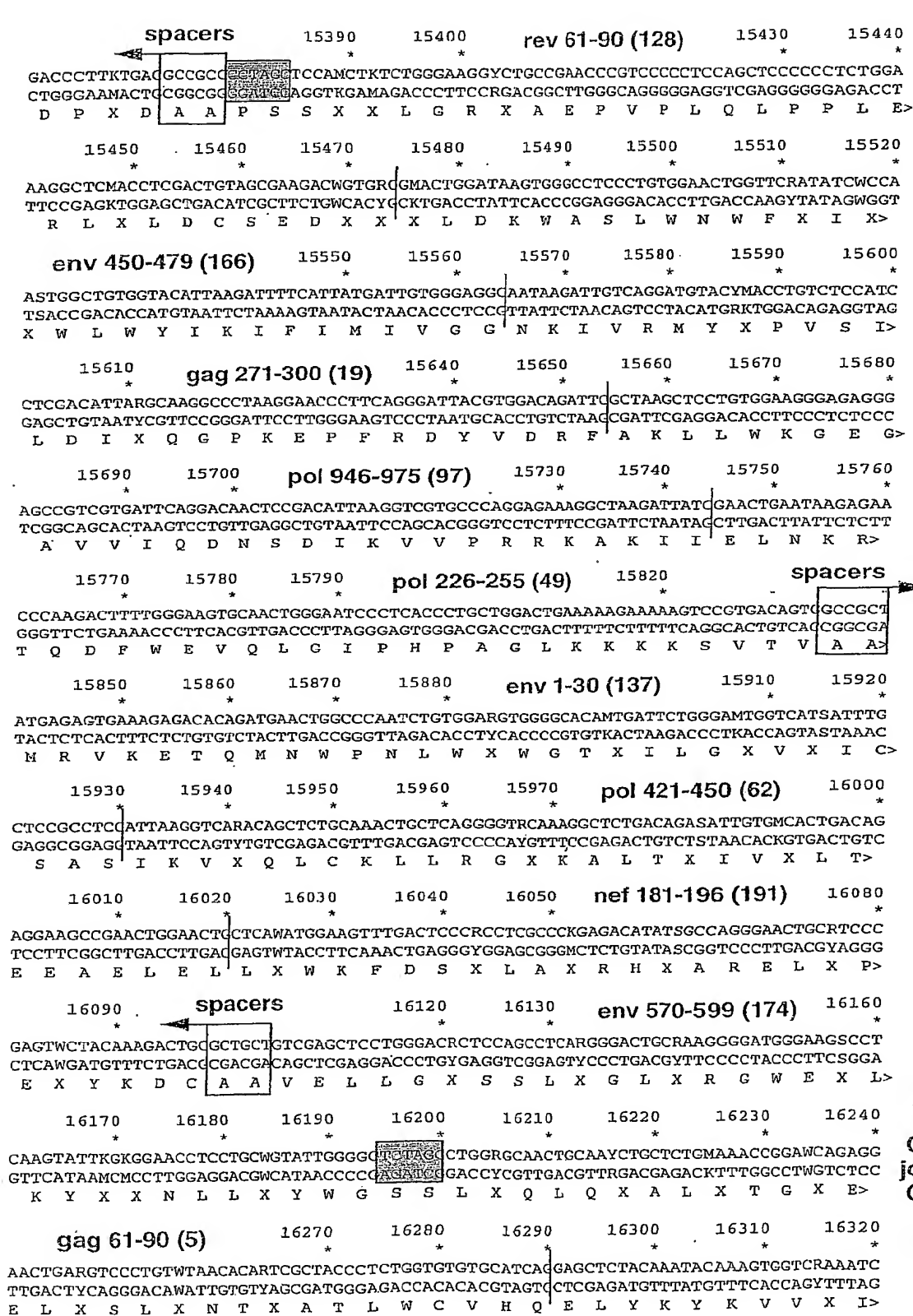
15130 15140 15150 15160 15170 pol 406-435 (61) 15200
* * * * *
GAAAACYTTACCRATAACAACTGGTCGGCAAAGTGAATTTGGGCTTCCCAAATCTACSTGGCATCAAAGTGARGCAACT
CTTTTGAATGGYTATTGTTGACCAGCCGTTTGACTTAACCCGAAGGTTTAGATGSGACCGTAGTTTCACTYCGTTGA
E N X T X N K L V G K L N W A S Q I Y X G I K V X Q L>

15210 15220 15230 15240 15250 env 121-139 (145) 15280
* * * * *
GTGTAAGCTCCTGAGAGGCRCCAAGCCCTCACCCCTCTGTGTGTGACACTGAATTGCACAAACGCTAACCTCATCAATG
CACATTCGAGGACTCTCCGYGGTTTCGGGAGTGGGAGACACACTGTGACTTAACGTGTTTGCATTTGGAGTAGTTAC
C K L L R G X K A L T P L C V T L N C T N A N L I N>

spacers 15310 15320 15330 tat 76-102 (123) 15360
* * * * *
TGAATGCTGCTCAAMCCAGAGGCGATAACCCCTACCGRTCCRAAGAGTCCAAGAAARAGGTCCMGTTCAAGRCAGAGACA
ACTTACGACGTTTGGTCTCCGCTATTGGGATGGCYAGGGYTTCTCAGGTCTCTTTCAGCKCAGGTTCTYGTCTCTGT
V N A A Q X R G D N P T X P X E S K K X V X S K X E T>

C4
join
C5FIGURE 15 (Cont)
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C5
join
C6C6
join
C7FIGURE 15 (Cont)
SUBSTITUTE SHEET (RULE 26)

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16330 env 270-299 (154) 16360 16370 16380 16390 16400
* * * * * *
RAACCCCTCGGCRRTGCCCTACCARAGCCAAAAGGAGAGTGGTCSAGAGAGAGAAAAGCTCACCGAWATCGTCMCACT
YTTGGGGAGCCGYAACGGGGATGTYTCGGTTTCTCTCACCAGSTCTCTCTTTTCGAGTGGCTWTAGCAGKGTGA
X P L G X A P T X A K R R V V X R E K R L T X I V X L>

16410 16420 pol 436-465 (63) 16450 16460 16470 16480
* * * * * *
CACCGAAGAGGCTGAGCTGGAGCTGGMGGAAAACAGAGAGATTCTGARGGAACCCGTCACGGAGTGTATAGAGTGCTCG
GTGGCTTCTCCGACTCGACCTCGACCKCCTTTGTCTCTCTAAGACTYCCFTGGGCAGGTGCCTCACATATCTCACGAGC
T E E A E L E L X E N R E I L X E P V H G V Y R V L>

16490 16500 16510 gag 361-390 (25) 16540 16550 16560
* * * * * *
CCGAAGCCATGAGCCAAGYCAMCMATGCCAACATCATGATGCAGAGAGGCAATTTTCARAGGCCMAAGAGAATCRTCAAA
GGCTTCGGTACTCGGTTTCRGTGKTACGGTTGTAGTACTACGCTCTCCGTTAAAGTYTCGGKTTTCTCTTAGYAGTTT
A E A M S Q X X X A N I M M Q R G N F X G X K R I X K>

16570 16580 16590 16600 nef 61-90 (183) 16630 16640
* * * * * *
CAAGAGGAAGAGGRGGTCGGCTTCCCGTCAGGCCCTCAGGTCCCACTGAGACCTATGACCTACAAAGSAGCCRTCGATCT
GTCTCTCTTCTCCYCCAGCCGAAGGGGCAGTCCGGAGTCCAGGGTGACTCTGGATACTGGATGTTTCTCSTGGYAGCTAGA
Q E E E X V G F P V R P Q V P L R P M T Y K X A X D L>

16650 16660 16670 16680 16690 gag 286-315 (20) 16720
* * * * * *
GTCCYTCTTCARACAGGGACCCAAAGAGCCTTTCAGAGACTATGTGGATAGGTTTTCWAAAACCCCTCAGGGCTGAGCAAG
CAGGRAGAAGTYTGTCCTGGGTTTCTCGGAAAGTCTCTGATACACCTATCCAAAAGTTTGGGAGTCCCGACTCGTTC
S X F X Q G P K E P F R D Y V D R F X K T L R A E Q>

16730 16740 16750 16760 16770 gag 16-45 (2) 16800
* * * * * *
CCWCACAGGAWGTGAAAAATGGGAGAAAATCAGACTGAGACCTGGTGGCAAAAAGAAATACARAMTGAAACACMTTGTG
GGWGTGTCCTWCACCTTTTACCCCTCTTTAGTCTGACTCTGGACACCGTTTCTTTATGTYTKACTTTGTGKAACAC
A X Q X V K N W E K I R L R P G G K K K Y X X K H X V>

16810 16820 16830 16840 16850 pol 646-675 (77) 16880
* * * * * *
TGGGCTCCAGGGAAGTGGAAAGGTTTGCCCTCCAGTATGCCCTCGGCATCATCCWAGCCCAACCCGATARGTCCGAGTC
ACCCGGAGGTCCCTTGACCTTTCCAAACCGAGGGTCATACGGGAGCCGTAGTAGGWTGCGGTTGGGCTATYACGGCTCAG
W A S R E L E R F A S Q Y A L G I I X A Q P D X S E S>

16890 16900 16910 16920 16930 16940 16950 16960
* * * * * * *
CGAGSTCGTGARTCAGATTATCGAAVAGCTCATCAAGAAATTGCGCGTCCGCGRAKGGACAGACAGARTCATTTAGGTCG
GCTCSAGCACTYAGTCTAATAGCTTBTCTGAGTAGTCTCTTCTAACGGCAGCGGCYTMCTGTCTGTCTYAGTAACTCCAGC
E X V X Q I I E X L I K K I A V A X X T D R X I E V>

env 615-644 (177) 16990 17000 17010 17020 17030 17040
* * * * * *
YCCAAAGGGCTKGGAGAGCCATTCTGMAATATCCCCASGAGAATCAGACACCTCGCCGGAAGGTGGCCCGTCARG
RGGTTTCCCGAMCCTCTCGGTAAGACKTATAGGGGTSCTCTTAGTCTGTCTGAGCGGCCCTCCACCGGGCAGTYC
X Q R A X R A I L X I P X R I R Q T R L A G R W P V X>

17050 pol 811-840 (88) 17080 17090 17100 17110 17120
* * * * * *
RYAATCCATACCGATAACCGAAGCAATTTACAAAGCRTRCCGTCAAGGCTGCCTGCTGGTGGGCTGATGTGARACAGCT
YRTTAGGTATGGCTATTGCCCTTCGTAAAGTGTTTCGYGAYGGCAGTTCGACGGACGACCACCCGCTACACTYTGTCGA
X I H T D N G S N F T S X X V K A A C W W A D V X Q L>

17130 17140 pol 511-540 (68) 17170 17180 17190 spacers
* * * * * *
CACCGMAGYCGTCCAGAAARTCGCTACCGAAAGCATTGTGATATGGGGAAAGACACCCAAAGTTTCARACTGCCTATCGCTG
GTGGCKTCRGCAGGTCTTTTACGGATGGCTTTCTGTAACACTATAACCCCTTTCTGTGGGTTCAAGTYTGACGGATAACGAC
T X X V Q K X A T E S I V I W G K T P K F X L P I A>

spacers BglII EcoRI
CGGCCAGCAACGAGAACATGGASRCCATGGCTGCTTGAAGATCTGAATTCGCC
GGCGGTGCTGTGCTCTGTACCTSYGGTACCGACGACTCTAGACTTAACCGG
A A S N E N M X X M A A R S E F A>

Flu NP epi (Mouse) Stop

C7
join
C8

FIGURE 15 (Cont)

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10 20 30 40 50 60 70 80

GCGGGATTCACCATGAGCCCTTTCGAAATACCTTCAGCWCCTSCAATGCACACACGGAATCAATACCGGTGCTGCTCCAT
CCGCCTAGGTGGTACTGTCCGGGAACGTTKTTTTSCAGTCGWGGCACGTTACGTGTGTGCTTGTAGTYTGCGGCAGCACAGGTG
G . G S T M T G P C X N V S X V Q C T H G I X P V V S T>

90 100 110 120 130 140 150 160

TCCCTGARAAGCCTCTWCAATACCRTCGCCACACTGTGGTGCGTCCACCACAAAGGATTGASG
Q L L L N G S L X S L X N T X A T L W C V H Q R I X>

170 180 190 200 210 220 230 240

TCARGGACACAAAGGAAGCCCTCGACAAAATCGAACTCGGCGATGGCGGAGGCGCTGAWAGGCAAGGCACCTCCAGCTCC
V X D T K E A L D K I E L G D G G G A X R Q G T S S S>

250 260 270 280 290 300 310 320

YTCARCTTTCCACAAATCACACTGTGGCAAAGGCCTCTGGTCACCGAACCCCTTCAGAAMAMAGAATCCCCGAWATGGTGAT
X X F P Q I T L W Q R P L V T E P F R X X N P X M V I>

330 340 350 360 370 380 390 400

TTACCACTACATGGACGATCTGTATGTGGGAAGCGATCTGGAAATCGGACAGCATTTTACCAACCCCGATAAGAAACACC
Y Q Y M D D L Y V G S D L E I G Q H F T T P D K K H>

410 420 430 440 450 460 470 480

AAAAGGANAGGACATCTTTCGCTTCATAGCAAGATGTCACGCGGCTGCGAGGCTCCAGCTTTCATATTCCTTCAT
Q K E P P P L W M G Y E L H P D R W T V Q P X X F P Q>

490 500 510 520 530 540 550 560

TAATGGGAGACCGTCCGAGGGGAGCACTGTAGTTTTAGCCGCTGTCTGAGTWTCTCCGAGACGAGCTGTGTCCGAGGR
I T L W Q R P L V T X K I G G Q L X E A L L D T G S X>

570 580 590 600 610 620 630 640

ACCGTCCTTTCTTTGCATCCGTTGCATCTSCGCGAGGAGTCTCGTKYTCTAGTGGTTATGGGATAGRAGCTCGTTGGGG
G R K K R R Q R R X A P Q S X X D H Q Y P I X E Q P>

650 660 670 680 690 700 710 720

AGRGGAAGAAATCCCTTTTGGACCGAAAGGCKGTTCCAYTTGGGTCTCTCAAARGGTGCTTGTCTGTGYCTCGGTATCG
L X F F R E N L A F X Q G X A R E F X S E Q T X A N S>

730 740 750 760 770 780 790 800

X X S R K S P Q I S G E S S X X L G X G T K N A A T S>

810

TGAATTCGCC

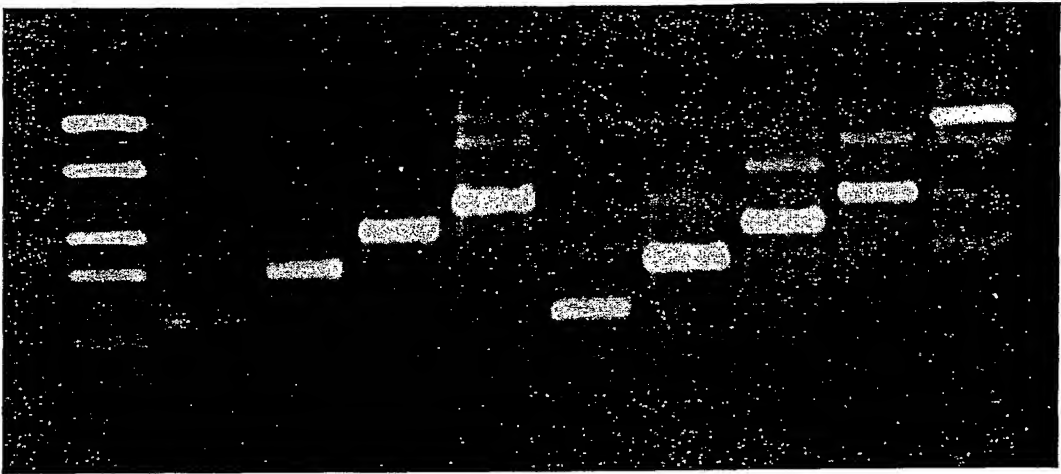
E F A>

FIGURE 16

FIGURE 16

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A 1 2 3 4 5 6 7 8 9 10



B — A —||— B —||— C —|

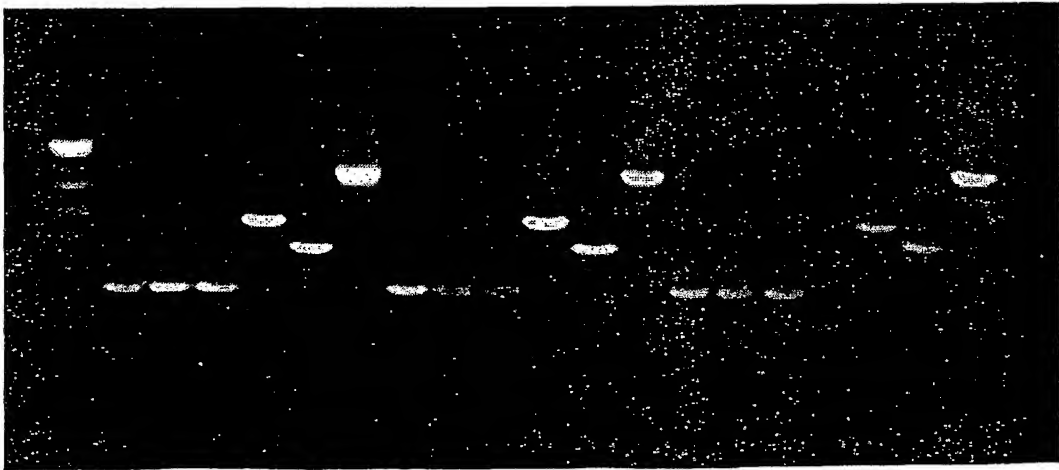


FIGURE 17

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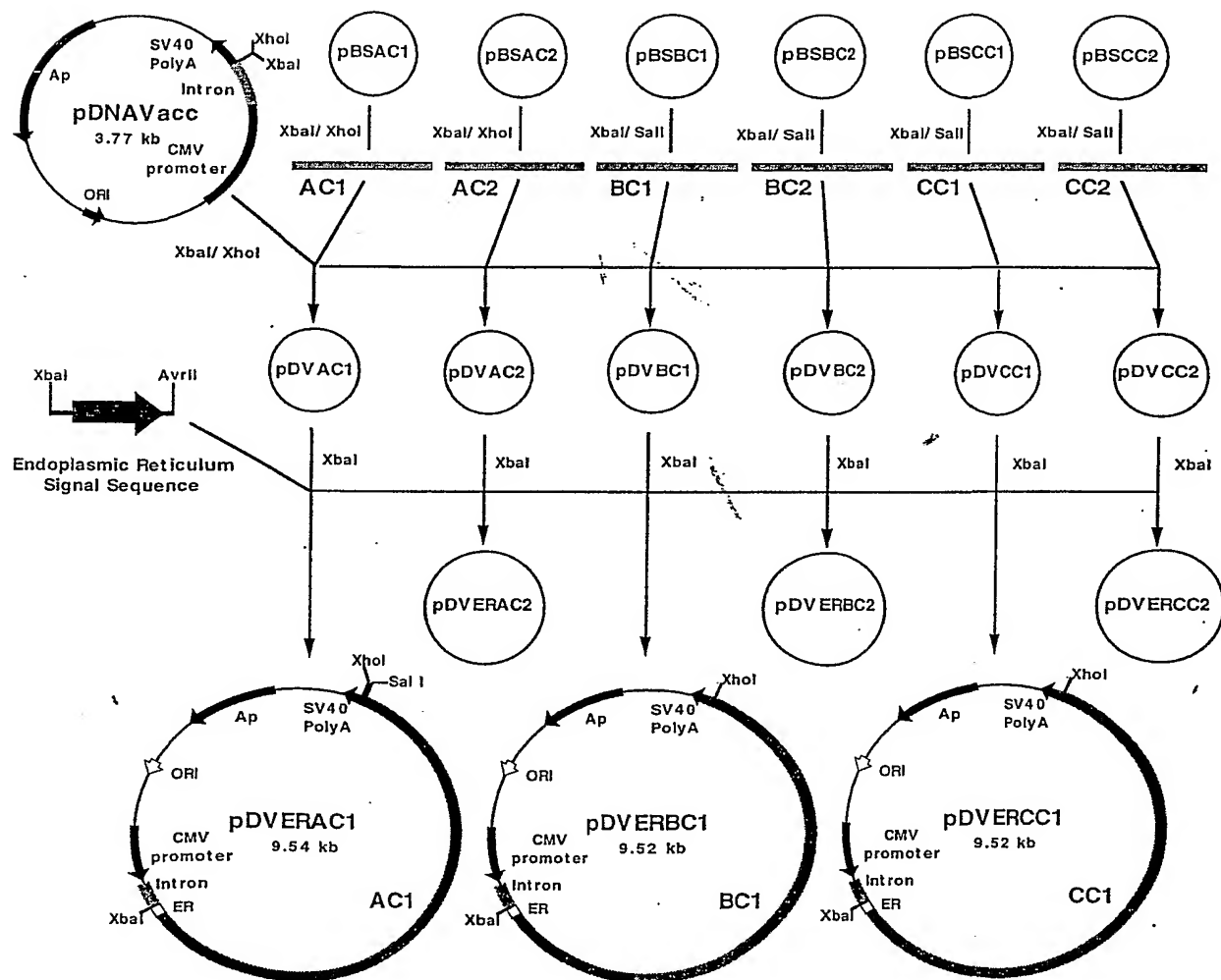


FIGURE 18A

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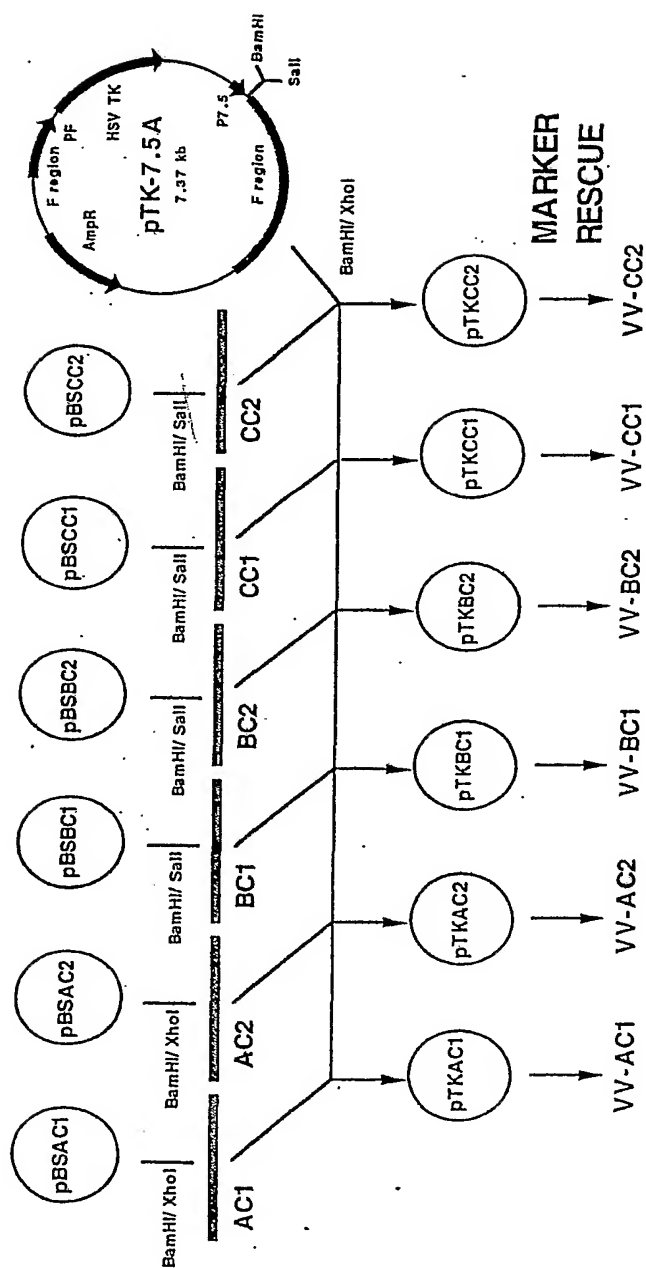


FIGURE 18B

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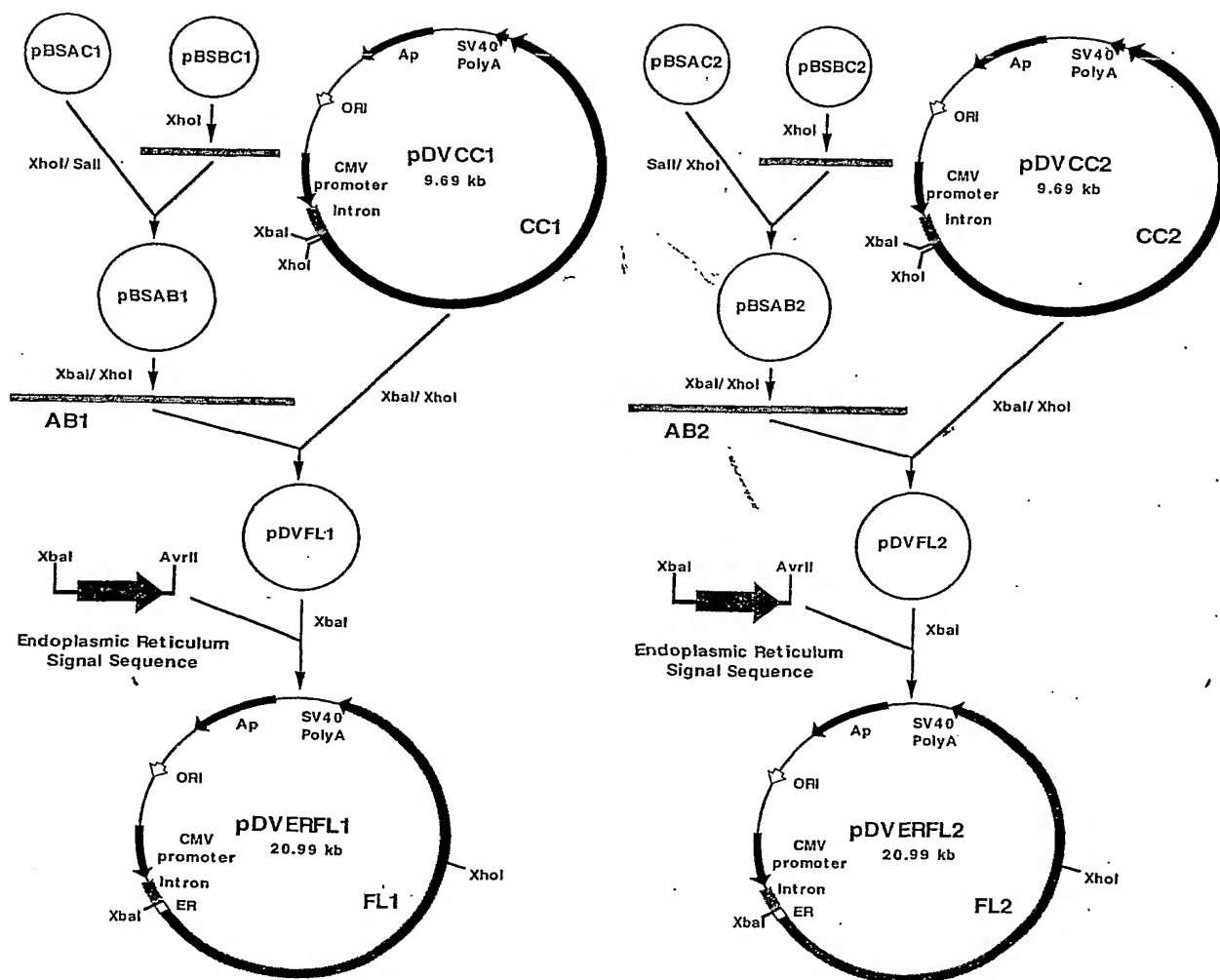
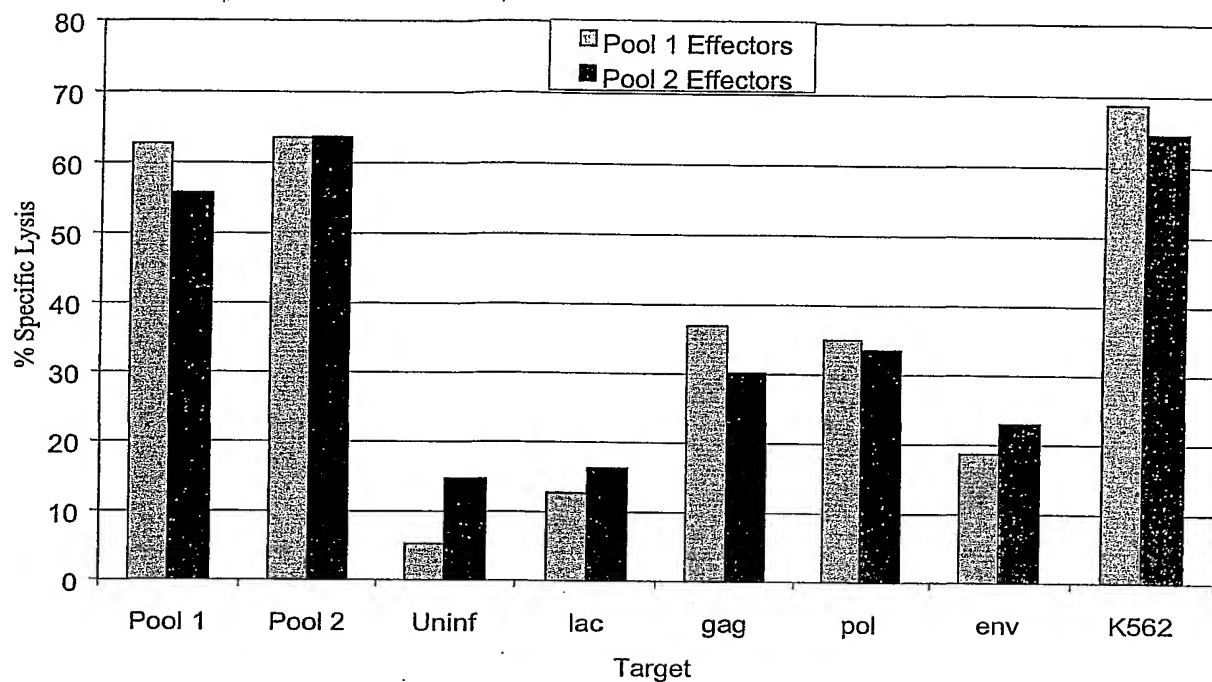


FIGURE 18C

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Subject1



Subject2

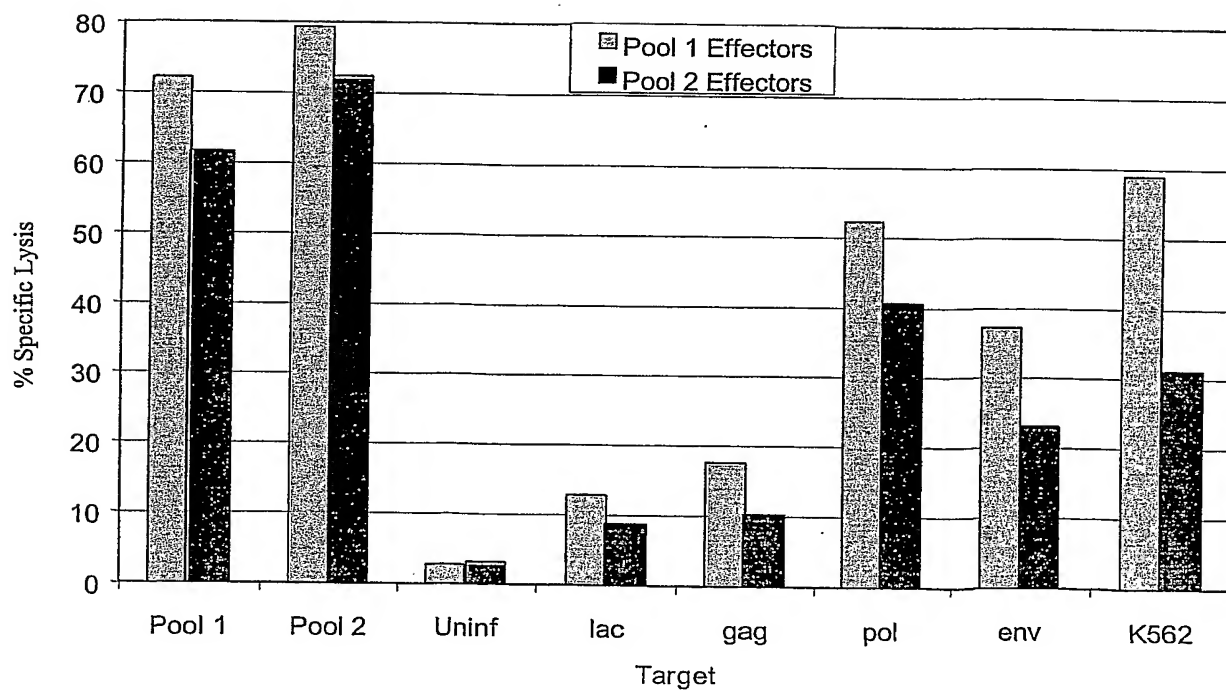


FIGURE 19

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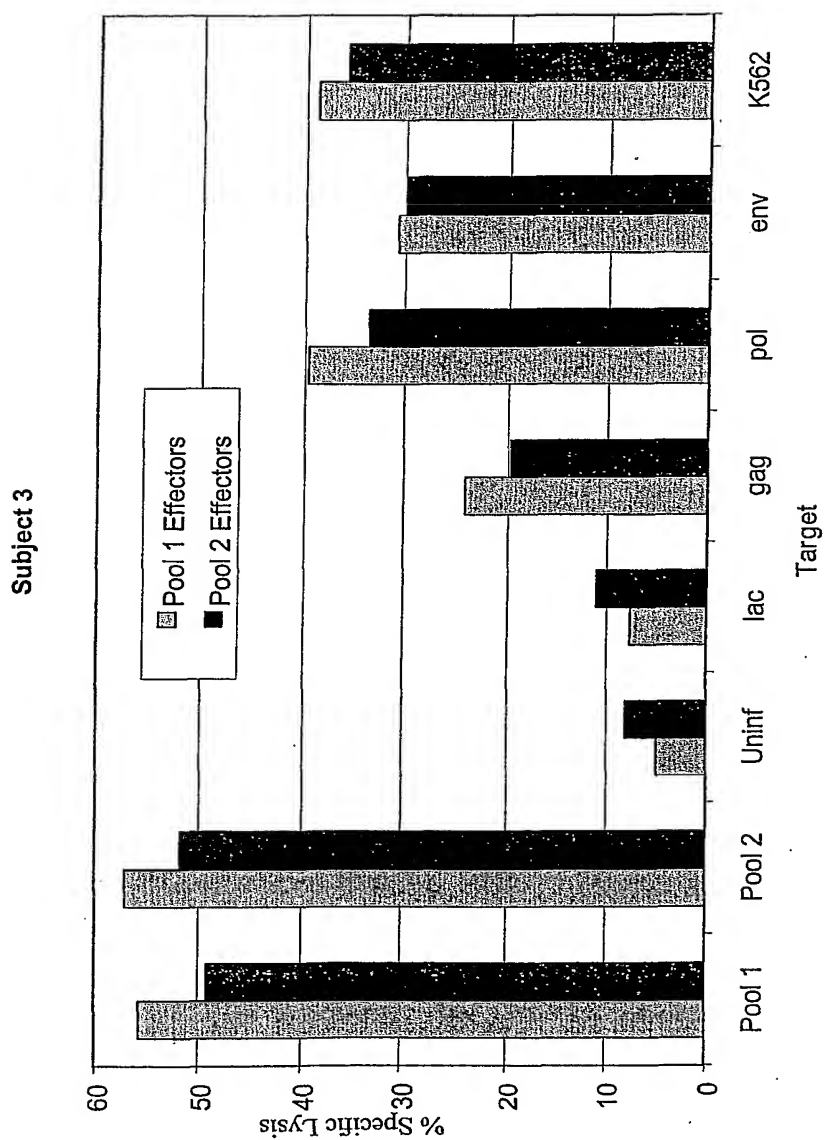


FIGURE 19 (Cont)

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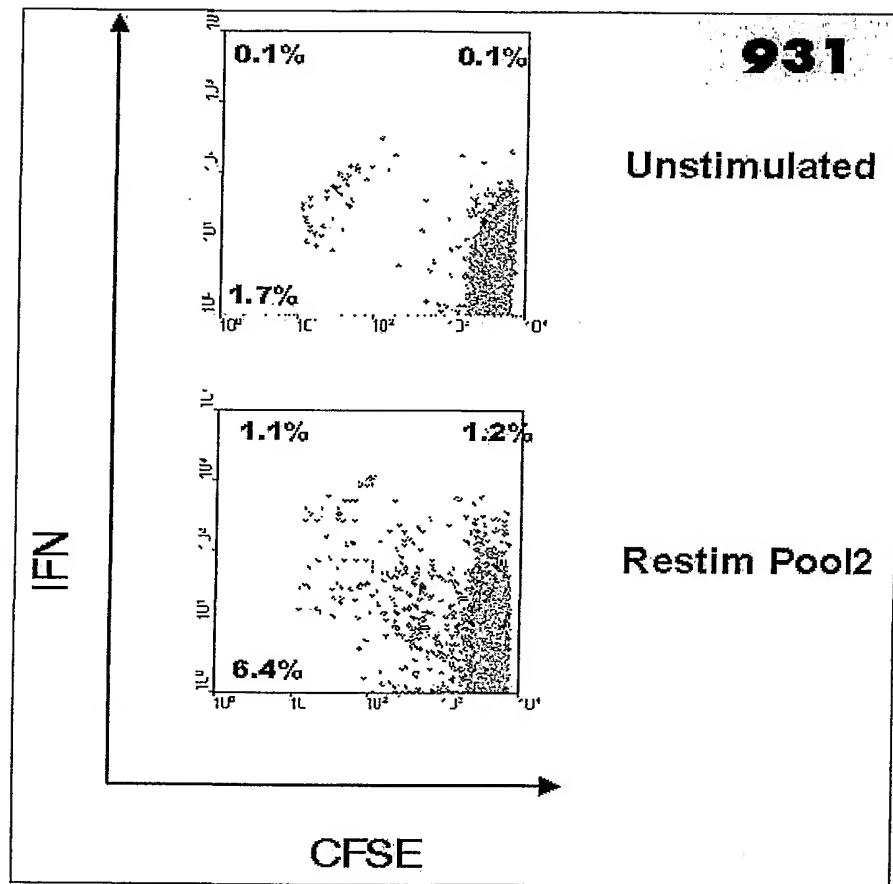


Figure 20

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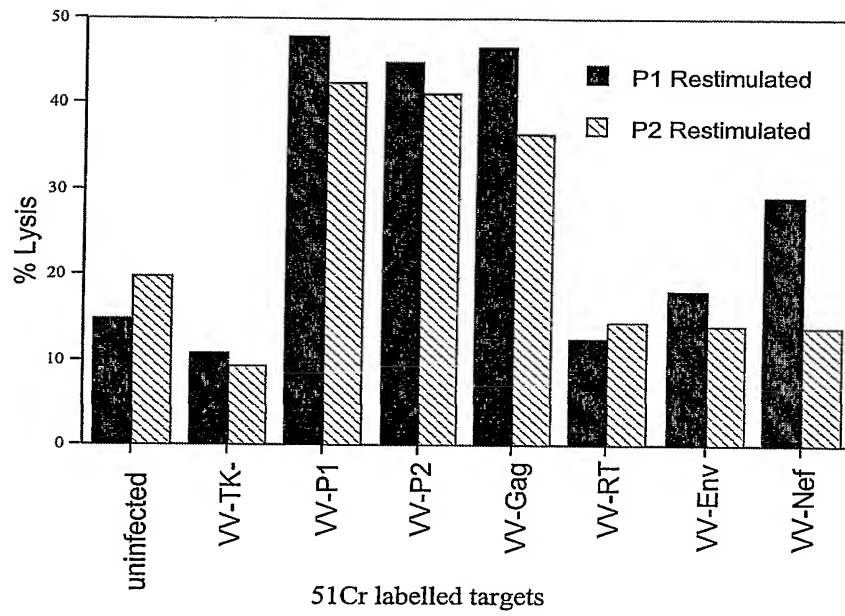


Figure 21

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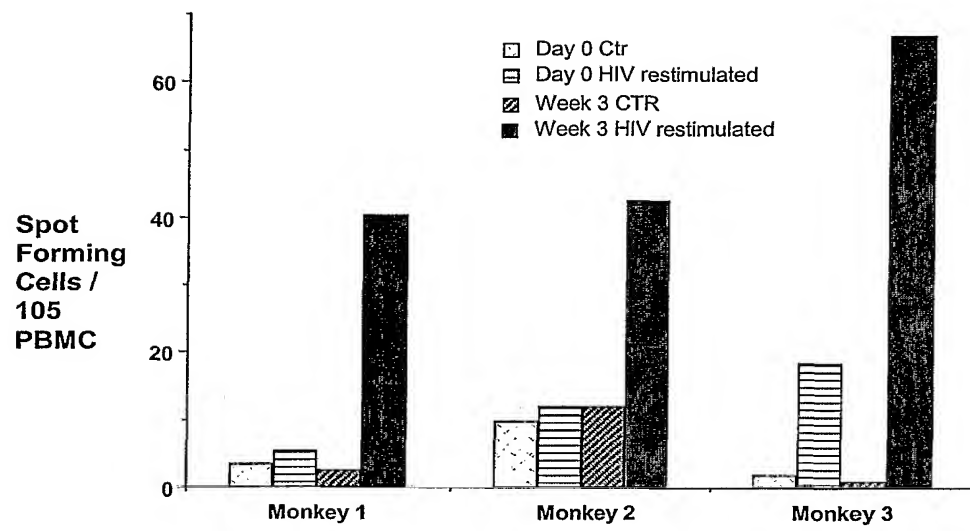


Figure 22A

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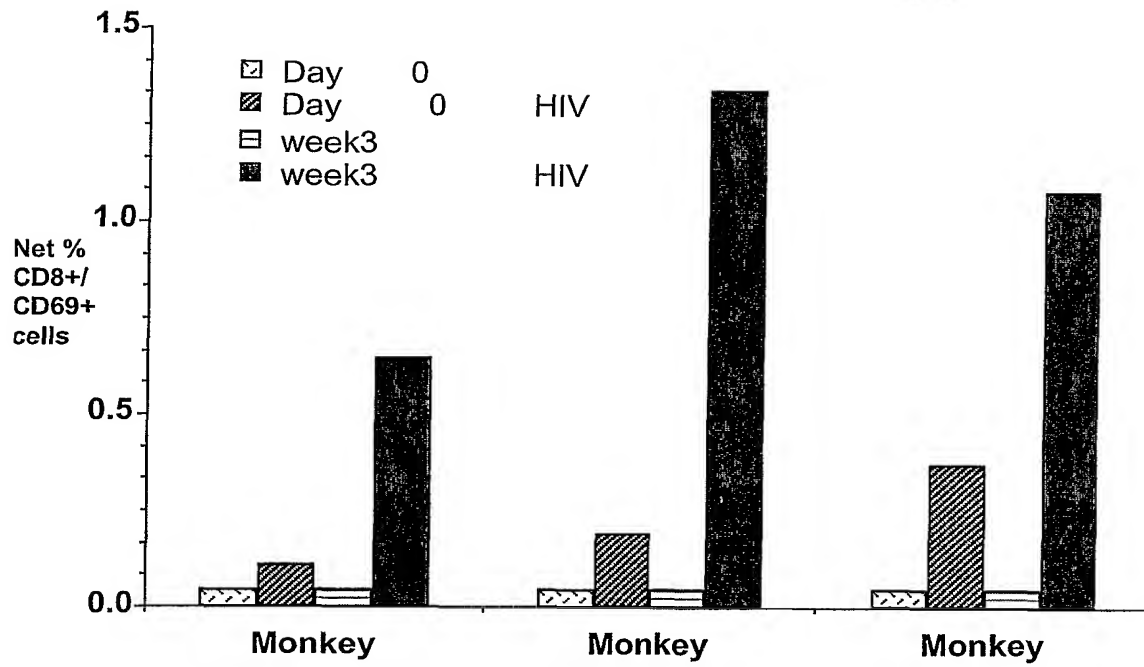


Figure 22B

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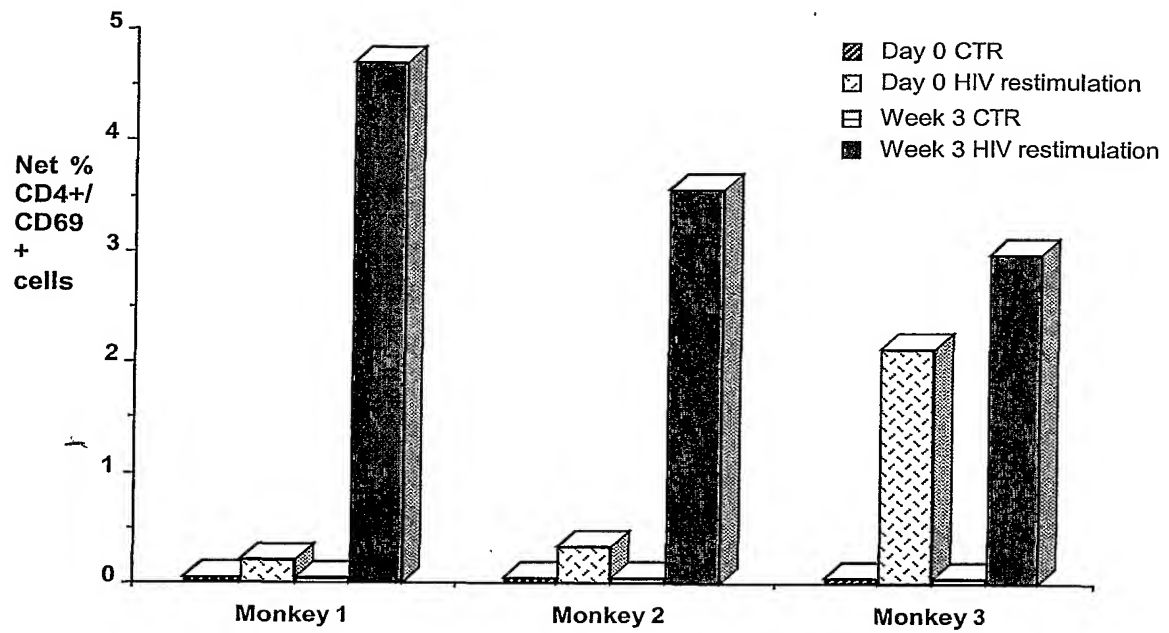


Figure 22C

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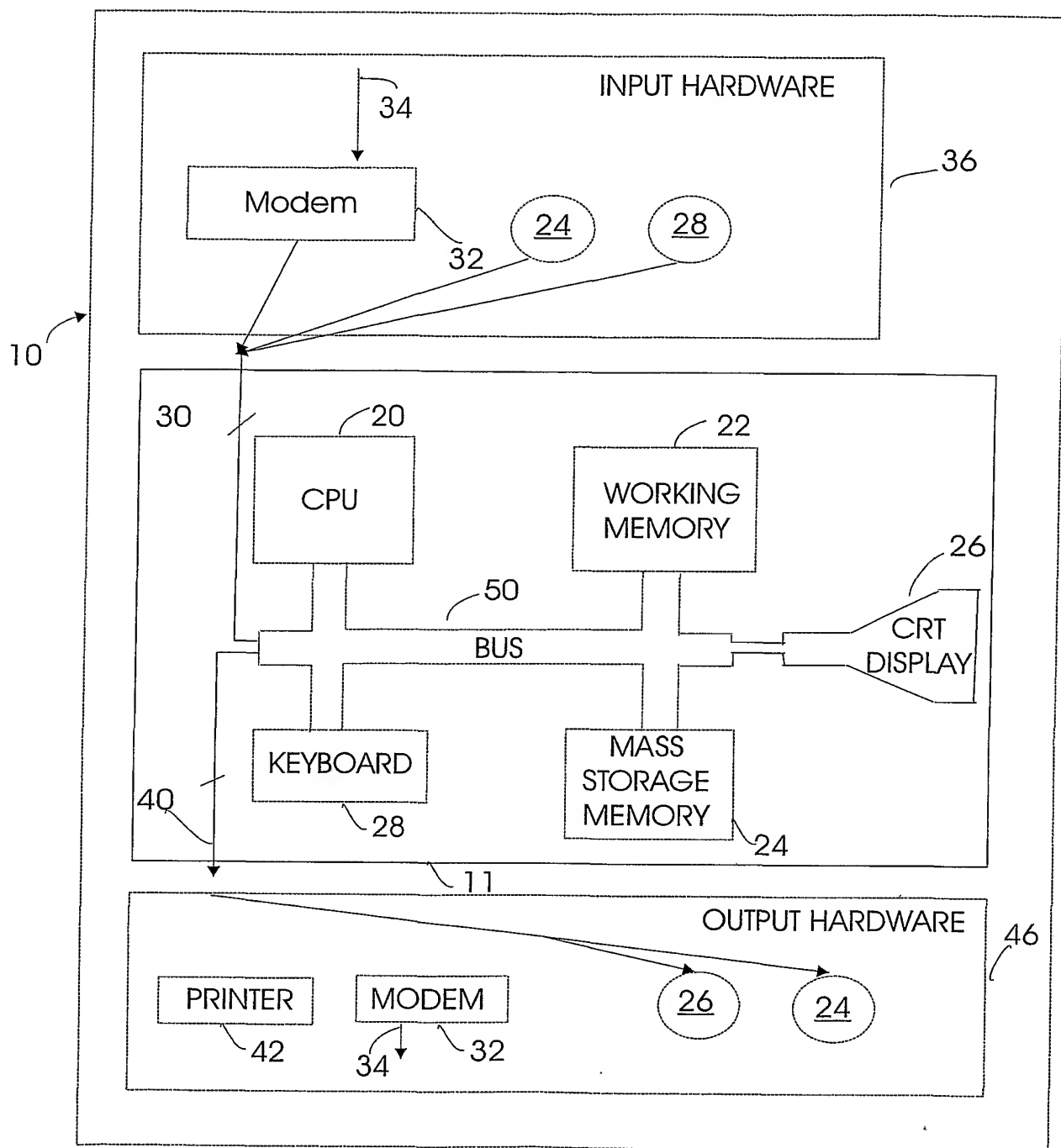


FIGURE 23

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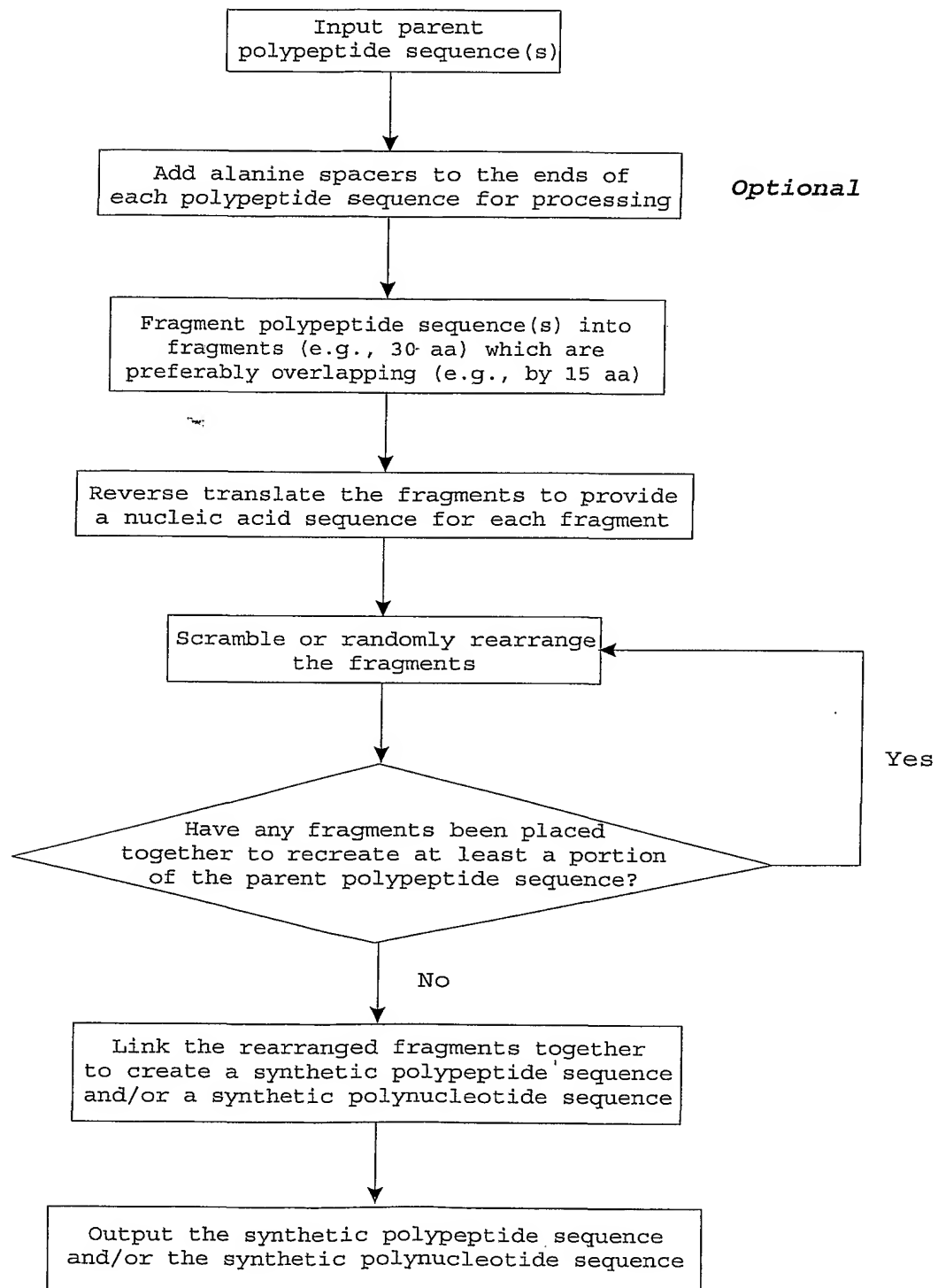


Figure 24

```

/* Scramble */
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/* Includes */

#include <stdio.h>
#include <stdlib.h>
#include <string.h>
#include <time.h>

/* Constant definitions */

/* Version Information */
#define VERSION_NO "0.2"
#define VERSION_DATE "04/03/1999"

/* Misc */
#define KEYBOARD_BUFFER_SIZE 256 /*size of keyboard read buffer */
#define LEN_CODON 4 /*length of codon (including
null) */
#define BUFFER_SIZE 10000 /*size of file read buffer */
#define TRUE 1 /*boolean true */
#define FALSE 0 /*boolean false */

/* Error codes */
#define E_NOERROR 0 /*no error */
#define E_NOINFILE 1 /*genes file not found */
#define E_MALLOC 2 /*memory allocation error */
#define E_FILEREAD 3 /*file read error */
#define E_CREATE_OUTPUT_FILE 4 /*error creating output file */
#define E_OVERLAP 5 /*segment overlap >= length

/* Structure definitions */

typedef struct gene GENE;
typedef GENE * P_GENE;
typedef struct gene_segment GENE_SEGMENT;
typedef GENE_SEGMENT * P_GENE_SEGMENT;
struct gene {
    char * name;
    char * data;
    P_GENE next_gene;
};

struct gene_segment {
    P_GENE p_gene;
    int number;
    int offset;
    int first_codon_choice;
    char * amino_data;
    char * dna_data;
    P_GENE_SEGMENT next_seg;
};

```

Figure 25

/* Function prototypes */

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```

int prolog();
int get_parameters();
int read_int(char * prompt);
int load_genes();
int add_gene(char * gene_name,char * gene_data);
void insert_gene(P_GENE * head,P_GENE new_gene);
int add_aa();
int split_genes();
int split_gene(P_GENE g);
int insert_segment(P_GENE_SEGMENT * head_seg,P_GENE_SEGMENT new_seg);
int convert_segments_aa_to_dna();
int convert_aa_to_dna(char * aa_ptr,char * dna_ptr,int first_choice);
char * codon(char acid_char,int preferred);
int perform_scramble();
int scramble_segments();
int adjacent_segments();
int display_genes();
int write_output_file();
void strip_newline(char * strip_str);
void pad_amino_string(char * amino_ptr, char * padded_ptr);
int even(int test_num);
void read_str(char * prompt,char * string);
char * read_nonblank_line(char * buf,int buf_size,FILE * in_file);
int user_confirmation();
void test();

```

/* Global variables */

```

char * codon_table[26][2] = {
/* A 00 */ {"GCC","GCT"},
/* - 01 */ {"???","???"},
/* C 02 */ {"TGC","TGT"},
/* D 03 */ {"GAC","GAT"},
/* E 04 */ {"GAG","GAA"},
/* F 05 */ {"TTC","TTT"},
/* G 06 */ {"GGC","GGA"},
/* H 07 */ {"CAC","CAT"},
/* I 08 */ {"ATC","ATT"},
/* - 09 */ {"???","???"},
/* K 10 */ {"AAG","AAA"},
/* L 11 */ {"CTG","CTC"},
/* M 12 */ {"ATG","ATG"},
/* N 13 */ {"AAC","AAT"},
/* - 14 */ {"???","???"},
/* P 15 */ {"CCC","CCT"},
/* Q 16 */ {"CAG","CAA"},
/* R 17 */ {"AGG","AGA"},
/* S 18 */ {"AGC","TCC"},
/* T 19 */ {"ACC","ACA"},
/* - 20 */ {"???","???"},
/* V 21 */ {"GTG","GTC"},
/* W 22 */ {"TGG","TGG"},

```

Figure 25 (Cont)

```

/* - 23 */ {"???", "???"},
/* Y 24 */ {"TAC", "TAT"},
/* - 25 */ {"???", "???"},
};

```

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```

char * error_text[] = {
/* 00 */ ""
/* 01 */ "ERROR: Input file not found!"
/* 02 */ "ERROR: Memory allocation error"
/* 03 */ "ERROR: File read error"
/* 04 */ "ERROR: Could not create output file"
/* 05 */ "ERROR: Segment overlap must be less than segment length"
};

```

```

char disease_name[KEYBOARD_BUFFER_SIZE];
char input_file_name[KEYBOARD_BUFFER_SIZE];
char output_file_name[KEYBOARD_BUFFER_SIZE];
int num_genes = 0;
int num_segments = 0;
int len_segment;
int segment_overlap;
P_GENE first_gene = NULL;
P_GENE_SEGMENT first_segment = NULL;
P_GENE_SEGMENT * scrambled_segments = NULL;

```

```

/* Mainline */

```

```

void main() {
    int error = E_NOERROR;

    printf("Scramble - Version %s, %s\n\n", VERSION_NO, VERSION_DATE);

    /* Initial processing */
    if (!error)
        error = prolog();

    /* Get various program parameters from user */
    if (!error)
        error = get_parameters();

    /* Load genes from genes file */
    if (!error)
        error = load_genes();

    /* Add 'AA' to start and end of all genes */
    if (!error)
        error = add_aa();

    /* Split genes into overlapping chunks */
    if (!error)
        error = split_genes();

    /* Convert segment amino acid to dna */
    if (!error)
        error = convert_segments_aa_to_dna();
}

```

Figure 25 (Cont)

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```

/* Scramble the segments */
if (!error)
    error = perform_scramble();

/* Write output file */
if (!error)
    error = write_output_file();

/* Show error if there was one */
if (error)
    printf("%s\n",error_text[error]);
}

/* prolog() */
/* Perform any initial processing required */

int prolog() {
    /* Seed the random number generator, using the system clock */
    /* Don't run the program more than once in the same second! */
    /* Or we'll get the same randomisation!!!!!!!!!!!!!!!!!!!! */
    srand(time(NULL));

    return E_NOERROR;
}

/* get_parameters() */
/* Ask for various parameters from the user (stdin) */
/* Disease name */
/* Input file name */
/* Output file name */
/* Segment length */

int get_parameters() {
    int valid;

    read_str("Enter disease name : ",disease_name);
    read_str("Enter input file name : ",input_file_name);
    read_str("Enter output file name : ",output_file_name);

    valid = FALSE;
    while (!valid) {
        len_segment = read_int("Enter segment length : ");
        if (len_segment % 2)
            printf("Segment length must be even!\n");
        else
            valid = TRUE;
    }
    segment_overlap = len_segment / 2;

    return E_NOERROR;
}

/* load_genes() */

```

Figure 25 (Cont)

```

/* Load the genes from the input file */
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int load_genes() {
    FILE * input_file;
    char name_buf[BUFFER_SIZE];
    char data_buf[BUFFER_SIZE];
    int rc;

    /* Open genes file for reading */
    if (NULL == (input_file = fopen(input_file_name,"r")))
        return E_NOINFILE;

    printf("Loading genes from: %s\n",input_file_name);
    num_genes = 0;
    /* Read gene name */
    while (NULL != read_nonblank_line(name_buf,BUFFER_SIZE,input_file)) {
        /* Read the gene data */
        if (NULL != read_nonblank_line(data_buf,BUFFER_SIZE,input_file)) {
            /* Allocate memory for new gene and add to list */
            if (rc = add_gene(name_buf,data_buf))
                break;
        }
    }
    /* Close genes file */
    fclose(input_file);

    return rc;
}

/* add_gene() */
/* Allocate memory for new gene, then insert in list */

int add_gene(char * gene_name,char * gene_data) {
    P_GENE new_gene;

    /* Allocate storage for new gene */
    if (NULL == (new_gene = malloc(sizeof(GENE))))
        return E_MALLOCC;
    /* Initialise new gene */
    new_gene->next_gene = NULL;
    /* Allocate storage for gene name (+1 for null) */
    if (NULL == (new_gene->name = malloc(strlen(gene_name)+1)))
        return E_MALLOCC;
    /* Store gene name */
    strcpy(new_gene->name,gene_name);
    /* Allocate storage for gene data (+1 for null) */
    if (NULL == (new_gene->data = malloc(strlen(gene_data)+1)))
        return E_MALLOCC;
    /* Store gene data */
    strcpy(new_gene->data,gene_data);
    /* Insert the new gene into linked list */
    insert_gene(&first_gene,new_gene);
    /* Increment num_genes */
    num_genes++;
}

```

Figure 25 (Cont)

```

        return E_NOERROR;
    }

    /* insert_gene() */
    /* Insert gene into linked list */

    void insert_gene(P_GENE * head_gene, P_GENE new_gene) {
        P_GENE * cur_ptr = head_gene;

        while (NULL != (*cur_ptr))
            cur_ptr = &((*cur_ptr)->next_gene);

        *cur_ptr = new_gene;
    }

    /* add_aa() */
    /* Add 'AA' to the start and end of every gene */

    int add_aa() {
        P_GENE cur_gene = first_gene;
        char * new_data;

        while (NULL != cur_gene) {
            /* Allocate storage to fit the gene plus four characters */
            new_data = malloc(strlen(cur_gene->data)+5);
            /* Shift gene data to new storage, add "AA" */
            strcpy(new_data, "AA");
            strcat(new_data, cur_gene->data);
            strcat(new_data, "AA");
            /* Free previous gene data storage */
            free(cur_gene->data);
            /* Set gene data pointer to new storage */
            cur_gene->data = new_data;
            /* Advance to next gene */
            cur_gene = cur_gene->next_gene;
        }

        return E_NOERROR;
    }

    /* split_genes() */
    /* Split the genes into overlapping segments */

    int split_genes() {
        P_GENE cur_gene = first_gene;
        P_GENE_SEGMENT cur_seg = first_segment;

        printf("Splitting genes into segments...\n");

        /* Split the genes into segments */
        while (NULL != cur_gene) {
            /* Split the gene */
            split_gene(cur_gene);
            /* Advance to next gene */
        }
    }

```

Figure 25 (Cont)

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```

        cur_gene = cur_gene->next_gene;
    }

    /* Count the number of segments */
    num_segments = 0;
    cur_seg = first_segment;
    while (NULL != cur_seg) {
        num_segments++;
        cur_seg = cur_seg->next_seg;
    }

    return E_NOERROR;
}

/* split_gene() */
/* Split a gene into overlapping segments */

int split_gene(P_GENE g) {
    char * seg_ptr;
    char * seg_buf;
    P_GENE_SEGMENT new_segment = NULL;
    int done;
    int seg_ctr = 0;

    /* Allocate memory for segment buffer */
    if (NULL == (seg_buf = malloc(len_segment+1)))
        return E_MALLOCC;

    /* Insert a null at the end of the segment buffer, */
    /* so we can use it as a string */
    seg_buf[len_segment] = '\0';

    /* Set segment pointer to start of gene data */
    seg_ptr = g->data;

    done = FALSE;
    while (!(done)) {
        /* So we know if we copied data */
        seg_buf[0] = '\0';

        /* Copy a segment of gene data to the segment buffer */
        memcpy(seg_buf, seg_ptr, len_segment);

        /* If there was some gene data copied to the buffer */
        if (NULL != seg_buf[0]) {
            /* Allocate storage for a new segment */
            if (NULL == (new_segment = malloc(sizeof(GENE_SEGMENT))))
                return E_MALLOCC;

            /* Increment segment counter */
            seg_ctr++;

            /* Setup the new segment */
            new_segment->p_gene = g;
            new_segment->number = seg_ctr;
            new_segment->offset = seg_ptr - g->data + 1;
            new_segment->next_seg = NULL;
        }
    }
}

```

Figure 25 (Cont)

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```

        if (NULL == (new_segment->amino_data = malloc(len_segment+1)))
            return E_MALLOC;
        if (NULL == (new_segment->dna_data = malloc(len_segment*3+1)))
            return E_MALLOC;
        new_segment->amino_data[0] = '\0';
        new_segment->dna_data[0] = '\0';
        /* Copy segment data from buffer to new segment */
        strcpy(new_segment->amino_data, seg_buf);
        /* Insert new segment into chain from gene */
        insert_segment(&first_segment, new_segment);
    }

    /* If we didn't read a full segment, we are finished! */
    if (strlen(seg_buf) < len_segment)
        done = TRUE;
    /* Otherwise, advance segment pointer to next segment in buffer */
    else
        seg_ptr = seg_ptr + len_segment - segment_overlap;
}

/* insert_segment() */
/* Insert a segment node at the end of the list */

int insert_segment(P_GENE_SEGMENT * head_seg, P_GENE_SEGMENT new_seg) {
    P_GENE_SEGMENT * cur_ptr = head_seg;

    while (NULL != (*cur_ptr))
        cur_ptr = &((*cur_ptr)->next_seg);

    *cur_ptr = new_seg;
}

/* convert_segments_aa_to_dna */
/* Go thru segments, and for each, convert amino acids to dna */

int convert_segments_aa_to_dna() {
    P_GENE_SEGMENT cur_seg = first_segment;
    int first_choice = 1;
    int alternate;

    printf("Converting to DNA...\n");

    /* Work out if we need to alternate the first codon choice or not */
    /* Don't need to do this anymore, since the segment length is */
    /* forced to be even, and the overlap is half the length (odd). */
    /* alternate = ((even(len_segment) && even(segment_overlap))
        || (!even(len_segment) && !even(segment_overlap))); */
    alternate = FALSE;

    while (NULL != cur_seg) {
        cur_seg->first_codon_choice = first_choice;
        convert_aa_to_dna(cur_seg->amino_data, cur_seg->dna_data,
            cur_seg->first_codon_choice);
    }
}

```

Figure 25 (Cont)

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```

        /* Address next segment */
        cur_seg = cur_seg->next_seg;

        /* If we are alternating, alternate the first codon choice */
        /*if (alternate)
            if (1 == first_choice)
                first_choice = 2;
            else
                first_choice = 1;*/
    }

    return E_NOERROR;
}

/* convert_aa_to_dna */
/* Converts a string of amino acid to dna */
/* NOTE: assumes that buffer at dna_ptr is large enough to hold dna!!! */

int convert_aa_to_dna(char * aa_ptr, char * dna_ptr, int first_choice) {
    char * p_codon;
    int cur_preferred = first_choice;

    while ('\0' != *aa_ptr) {
        p_codon = codon(*aa_ptr, cur_preferred);
        strcat(dna_ptr, p_codon);
        /* If we didn't find a codon, log a warning */
        if (0 == strcmp(p_codon, "???0"))
            printf("WARNING: no codon found for amino acid!\n");

        /* Alternate current preferred codon */
        if (1 == cur_preferred)
            cur_preferred = 2;
        else
            cur_preferred = 1;

        aa_ptr++;
    }

    return E_NOERROR;
}

/* codon */
/* Returns a pointer to a codon corresponding to the amino acid passed */
/* The codon pointer is to 3 characters, plus a terminating null */

char * codon(char acid_char, int preferred) {
    int codon_table_index;
    char * codon_ptr;

    /* Determine index into codon_table (table starts at 'A') */
    codon_table_index = acid_char - 'A';

    /* Set pointer to appropriate codon */
    codon_ptr = codon_table[codon_table_index][preferred-1];

```

Figure 25 (Cont)

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```

        return codon_ptr;
    }

/* display_genes() */
/* Display the name and data for all genes */

int display_genes() {
    P_GENE cur_gene = first_gene;

    while (NULL != cur_gene) {
        printf("%s\n", cur_gene->name);
        printf("%s\n", cur_gene->data);
        cur_gene = cur_gene->next_gene;
    }

    return E_NOERROR;
}

/* perform_scramble() */
/* Scramble the segments */
/* Check for adjacent segments. If there are, rescramble */

int perform_scramble() {
    int done = FALSE;
    int rc = E_NOERROR;

    while (TRUE) {
        rc = scramble_segments();
        if (E_NOERROR == rc)
            if (adjacent_segments()) {
                printf("Adjacent segments detected! Rescramble? (y/n) ");
                if (!user_confirmation()) {
                    printf("WARNING: Adjacent segments in output\n");
                    break;
                }
            }
        else
            break;
    }

    return rc;
}

/* scramble_segments() */
/* Randomly scramble the segments, putting pointers in scrambled_segments[] */

int scramble_segments() {
    P_GENE_SEGMENT cur_seg = first_segment;
    int i, j;
    P_GENE_SEGMENT temp;

    printf("Scrambling segments...\n");

```

Figure 25 (Cont)

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```

/* Allocate storage for array of segment pointers */
if (NULL == (scrambled_segments = malloc(sizeof(P_GENE_SEGMENT)*num_segments)))
    return E_MALLOCC;

/* First, initialise scrambled_segments in same order as linked list */
i = 0;
while (cur_seg != NULL) {
    scrambled_segments[i] = cur_seg;
    cur_seg = cur_seg->next_seg;
    i++;
}

/* Now, randomly scramble the segments */
for (i=0;i<num_segments;i++) {
    j = rand() % num_segments;
    temp = scrambled_segments[i];
    scrambled_segments[i] = scrambled_segments[j];
    scrambled_segments[j] = temp;
}

return E_NOERROR;
}

/* adjacent_segments() */
/* Determine if the scrambled segment order has resulted in */
/* two segments which were adjacent originally (ie every */
/* second one) have ended up adjacent. */

int adjacent_segments() {
    int i;
    int rc = 0;
    P_GENE_SEGMENT cur_seg;
    P_GENE_SEGMENT next_seg;

    for (i=0;i<num_segments-1;i++) {
        /* Address current and next segments */
        cur_seg = scrambled_segments[i];
        next_seg = scrambled_segments[i+1];
        /* Do segments come from same gene, and are two apart? */
        if (((cur_seg->p_gene == next_seg->p_gene)
            && ((cur_seg->number == (next_seg->number)+2)
            || (cur_seg->number == (next_seg->number)-2))))
            return 1;
    }
    return 0;
}

/* write_output_file() */
/* Write out segments (in initial non-scrambled order) */
/* Write out synthetic protein (in scrambled order) */
/* Write out synthetic dna (in scrambled order) */

int write_output_file() {
    FILE * output_file;

```

Figure 25 (Cont)

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```

char * amino_buffer;
P_GENE_SEGMENT cur_seg;
int i;

/* Open output file for writing (erase any contents) */
if (NULL == (output_file = fopen(output_file_name,"w")))
    return E_CREATE_OUTPUT_FILE;

/* Allocate memory for padded amino string buffer */
if (NULL == (amino_buffer = malloc(len_segment*3+1)))
    return E_MALLOC;

printf("Writing output file: %s\n",output_file_name);

/* Write output file header information */
fprintf(output_file,"Scramble %s - Output File\n",VERSION_NO);
fprintf(output_file,"\n");
fprintf(output_file,"Disease name   : %s\n",disease_name);
fprintf(output_file,"Input filename  : %s\n",input_file_name);
fprintf(output_file,"Output filename : %s\n",output_file_name);
fprintf(output_file,"Number genes   : %d\n",num_genes);
fprintf(output_file,"Number segments : %d\n",num_segments);
fprintf(output_file,"Segment length  : %d\n",len_segment);
fprintf(output_file,"Segment overlap : %d\n",segment_overlap);

/* Write out segments in initial non-scrambled order */
fprintf(output_file,"\n");
fprintf(output_file,"Segments in original order:\n");
fprintf(output_file,"-----\n");
cur_seg = first_segment;
while (NULL != cur_seg) {
    /* Format amino data to line up with codons */
    pad_amino_string(cur_seg->amino_data,amino_buffer);
    fprintf(output_file,"Gene      : %s\n",cur_seg->p_gene->name);
    fprintf(output_file,"Segment#  : %d\n",cur_seg->number);
    fprintf(output_file,"Offset    : %d\n",cur_seg->offset);
    fprintf(output_file,"1st Codon : %d\n",cur_seg->first_codon_choice);
    fprintf(output_file,"%s\n",amino_buffer);
    fprintf(output_file,"%s\n",cur_seg->dna_data);
    fprintf(output_file,"\n");
    cur_seg = cur_seg->next_seg;
}

/* Write out segment names in scrambled order */
fprintf(output_file,"Segments in scrambled order:\n");
fprintf(output_file,"-----\n");
for (i=0;i<num_segments;i++) {
    /* Format amino data to line up with codons */
    pad_amino_string(scrambled_segments[i]->amino_data,amino_buffer);
    /* Write segment details */
    fprintf(output_file,"%s # %d\n",scrambled_segments[i]->p_gene->name,
        scrambled_segments[i]->number);
    fprintf(output_file,"%s\n",amino_buffer);
    fprintf(output_file,"%s\n",scrambled_segments[i]->dna_data);
    fprintf(output_file,"\n");
}

```

Figure 25 (Cont)

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```

    }

    /* Write synthetic protein in one long string */
    fprintf(output_file,"Synthetic Protein:\n");
    fprintf(output_file,"-----\n");
    for (i=0;i<num_segments;i++)
        fprintf(output_file,"%s",scrambled_segments[i]->amino_data);

    fprintf(output_file,"\n\n");

    /* Write synthetic dna in one long string */
    fprintf(output_file,"Synthetic DNA:\n");
    fprintf(output_file,"-----\n");
    for (i=0;i<num_segments;i++)
        fprintf(output_file,"%s",scrambled_segments[i]->dna_data);

    return E_NOERROR;
}

/* strip_newline() */
/* Replace the first newline character with a null */

void strip_newline(char * strip_str) {
    char * newline_pos;

    /* Find the newline char */
    newline_pos = strchr(strip_str,'\n');

    /* If we found one, replace it with a null */
    if (NULL != newline_pos)
        newline_pos[0] = '\0';
}

/* pad_amino_string */
/* Copy amino chars from amino_ptr to padded_ptr, padding each */
/* side with a space. */

void pad_amino_string(char * amino_ptr, char * padded_ptr) {

    while ('\0' != *amino_ptr) {
        *padded_ptr = ' ';
        padded_ptr++;
        *padded_ptr = *amino_ptr;
        padded_ptr++;
        *padded_ptr = ' ';
        padded_ptr++;
        amino_ptr++;
    }

    /* Stick a null at the end of the padded string */
    *padded_ptr = '\0';
}

/* even() */
/* True if test_num is even, otherwise false */

```

Figure 25 (Cont)

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```

int even(int test_num) {
    return !(test_num % 2);
}

/* read_int() */
/* Read an integer from stdin. Keep trying until valid int > 0 entered. */
/* Return the integer read, or 0 if error reading from stdin. */

int read_int(char * prompt) {
    char buffer[KEYBOARD_BUFFER_SIZE];
    int value_read;
    int valid = FALSE;

    while (!valid) {
        printf("%s",prompt);
        valid = TRUE;
        fgets(buffer,KEYBOARD_BUFFER_SIZE,stdin);
        if (1 != sscanf(buffer,"%d",&value_read))
            valid = FALSE;
        if (valid && (value_read < 1))
            valid = FALSE;
        if (!valid)
            printf("Positive integer value please!\n");
    }

    return value_read;
}

/* read_str() */
/* Read a string from the user (stdin) */
/* Strip the newline from it */

void read_str(char * prompt,char * string) {
    char buffer[KEYBOARD_BUFFER_SIZE];

    printf(prompt);
    fgets(buffer,KEYBOARD_BUFFER_SIZE,stdin);
    sscanf(buffer,"%s",string);
}

/* read_nonblank_line() */
/* Read a line from file until we get a non-blank one */

char * read_nonblank_line(char * buf,int buf_size,FILE * in_file) {
    char * return_ptr;

    /* Read lines until we get a non-black one, or EOF */
    do
        return_ptr = fgets(buf,buf_size,in_file);
    while ((NULL != return_ptr) && ((' ' == buf[0]) || ('\n' == buf[0])));

    /* If we got a line, change the newline char to a null */
    if (NULL != return_ptr)
        strip_newline(buf);
}

```

Figure 25 (Cont)

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```
        return return_ptr;
    }

    /* user_confirmation() */
    /* Read input from user. If user types 'y', return 1, otherwise 0 */
    int user_confirmation() {
        char buffer[KEYBOARD_BUFFER_SIZE];

        fgets(buffer, KEYBOARD_BUFFER_SIZE, stdin);
        if (('y' == buffer[0]) || ('Y' == buffer[0]))
            return 1;
        else
            return 0;
    }

    /* test() */
    /* For debugging/development */
    void test() {
        char str[100];
        printf("Enter something: ");
        fgets(str, 100, stdin);
        printf("line1\n");
        printf("%s", str);
        printf("line2\n");
        fgets(str, 100, stdin);
    }
```

Figure 25 (Cont)

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HepC Savine design

HepC 1a consensus polyprotein sequence used for scramble program

MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARRPEGRTWAQ
 PGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVR
 VLEDGVNYATGNLPGCSFSIFLLALLSCLTVPASAYQVRNSTGLYHVTNDCPNSSIVYEADAILHTPGCVPCVREGN
 ASRCVWAMTPTVATRDGKLPATQLRRHIDLLVGSATLCSALYVGDLCGSVFLVGLFTFSPRRHWTTQGCNCSIYPGH
 ITGHRMAWDMMNWSPTAALVMAQLLRIPQAILDMIAGAHWGVLAGIAYFSMVGNWAKVLVLLLFAGVDAETHVTGG
 NAGRRTTSLVSLTPGAKQNIQLINTNGSWHINSTALNCNESLNTGWLGLFYQHKFNSSGCPERLASCRRLTDFDQG
 WGPISYANGSGPDQRPYCWYPPKPCGIVPAKSVCGPVYCFTPSPVVVGTTDRSGAPTYSWGANDTDVFLNNTTRPPL
 GNWFGCTWMNSTGFTKVCGAPPCVIGGAGNNTLHCPTDCFRKHPEATYSRCGSGPWITPRCLVDYPYRLWHYPCTINY
 TIFKVRMYVGGVEHRLEAACNWTRGERCDLEDORSELSPLLLSTTQWQVLPSCSFTTLPALSTGLIHLHQNIQNDVQYL
 YGVGSSIASWAIKWEYVVLFLLLADARVCSCLWMMLLSQABAALLENLVLNAAASLAGTHGLVSFLVFFCFAYLYKG
 RWVPGAVYALYGMWPLLLLLLLALPQRAYALDTEVAASCGGVVLVGLMALTLSPYYKRYISWCLWWLQYFLTRVEAQLH
 VWVPLNVRGGRDAVILLMCVHPTLVFDITKLLAVFGPLWILQASLLKVPYFVRVQGLLRICALARKMIGGHYVQM
 AIIKLGALTGTYYVNLHTPLRDWAHNGLRDLAVAVEPVVFSQMETKLTWGAADTAACGDIINGLPVSARRGREILLGP
 ADGMVSKGWRLLAPITAYAQOTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAGTRTIAS
 PKGPFVIQMYTNDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPISYKLGSSGGPLL
 CPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMRSPVFTDNSSPPAVPQSFQVAHLHAPTSGSKSTKVPAAYAAQG
 YKVLVLNPSVAATLGFAYMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGLADGGCSGGAYDIIICDECHSTDATS
 LGIGTVLDQAEATAGARLVVLATATPPGSVTVPHNIEEVALSTTGEIPFYGKAIPLEVIKGRHLIFCHSKKKCDELA
 AKLVALGINAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTGDFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAV
 SRTQRRGRTRGRGKPGIYRFVAPGERPSGMFDSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWE
 VFTGLTHIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPRTLHGPTPLLYRLGAVQNEVTLT
 HPVTKYIMTMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRIVLSGKPAIIPDREVLRYREFDEMEECQHL
 YIEQGMMLABEQFKQKALGLLQTASRQAEVIAPAVQTNWQKLEVFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAFT
 AAVTSPITTSQTLLFNILGGWVAAQLAAPGAATAFVGAGLAGAAIGSVGLGKVLVDILAGYGAGVAGALVAFKIMS
 GEVPSTEDLVNLLPALISPGALVVGVCAILRRHVGPGEVAVQWMNRLLIAFASRGNHVSPTHYVPESDAAARVTAI
 LSSLTVTQLRLRLHQWISSECTTPCSGSLRDIWDWICEVLSDFKTWLKAKLMPQLPGIPFVSCQRGYKGVWRGDGIMH
 TRCHCGAETIGHVKNGTMRIVGPRTCRNMWSGTFPINAYTTGCTPLPAPNYTFALWRVSAEEYVEIRRVGDFHYVTG
 MTNDNLKCPQVPSPEFFTELDGVRRLHRFAPPCKPLLREEVSFVRGLHEYPVGSQLPCEPEPDVAVLTSMLTDP
 SHITAE AAGRRRLARGSPPSMASSASQLSAPSLKATCTANHDSFDAELIEANLLWRQEMGNITRVESENKV
 VILDSFDPVLA EDEREISVPAEILRKSRRFAQALPVWARPDYNPPLVETWKKPDYEPVVGHCPLPPPRSP
 PVPVPPRKRRTVVLTESTL STALABELATKSFSSSTSGITGDNTTTSSEAPSGCPCPDSDAESYSMPLEGE
 PGDPDLSGDSWSTVSSEAGTEDVV CCSMSYSWTGALVTPCAAEEQKLPINALSNSLLRHHNLVYSTTSR
 SACQRQKKVTFDRLQVLDSHYQDVLKEVKAAAS KVKANLLSVEEACSLTPPHSAKSKFGYGA
 KDVRCHARKAVAHINSVWKDILLEDVTPIDTTIMAKNEVFCVQPEKGGR KPARLIVFPDLGVRV
 CEKMALYDVVSKLPLAVMGSSYGFQYSPGQVFEFLVQAWKSKKTPMGFSYDTRCFDSTVTESD
 IRTEAIYQCCDLDPQARVAIKSLTERLYVGGPLTNSRGENGCRYRCRASGVLTTSCNTLT
 CYIKARAACRAAGLQD CTMLVCGDDLVLVICESAGVQEDAASLRAFTEAMTRYSA
 PPDPPEYDLELITSCSSNVSVAHDGAGKRVYYLTRDP TTPLARAAWETARHTPVNSWL
 GNIIMFAPTLWARMILMTHFFSVLIARDQLEQALDCEIYGACYSIEPLDLPIIQRL
 HGLSAFSLHSYSPGEINRVAACLRLKLGVPPLRAWRHRARSVRARLLARGGRAAICGKYL
 FNWAVRTKLKLTPIAAAGR LDLSGWFTAGYSGGDIYHSVSHARPRWFWFCLLLAAGVG
 IYLLPNR

Scramble - Output File

Scramble version : 0.1 beta, 08/02/1999
 Num. genes : 1
 Num. segments : 201
 Segment length : 30
 Segment overlap : 15

Segments in original order:

 Gene : HepC1a
 Segment# : 1
 Offset : 1
 1st Codon : 1
 A A M S T N P K P Q R K T K R N T N R R P Q D V K F P G G G
 CCCGCTATGTCCACCAATCCCAACCCCAAGGAAAAACCAAGGAATACCAATAGGAGACCCCAAGACGTCAAGTTTCCCGGAGGCGGA

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Gene : HepC1a
Segment# : 2
Offset : 16
1st Codon : 1
N T N R R P Q D V K F P G G G Q I V G G V Y L L P R R G P R
AACACAAACAGAAGGCCTCAGGATGTGAAATTCCTGGCGGAGGCCAAATCGTCGGCGGAGTGATCTGCTCCCCAGAAGGGGACCCAGA

Gene : HepC1a
Segment# : 3
Offset : 31
1st Codon : 1
Q I V G G V Y L L P R R G P R L G V R A T R K T S E R S Q P
CAGATTGTGGGAGGCGTCTACCTCCTGCCTAGGAGAGGCCCTAGGCTCGGCGTCAGGGCTACCAGAAAGACAAGCGAAAGGTCCCAGCCT

Gene : HepC1a
Segment# : 4
Offset : 46
1st Codon : 1
L G V R A T R K T S E R S Q P R G R R Q P I P K A R R P E G
CTGGGAGTGAGAGCCACAAGGAAAACCTCCGAGAGAAGCCAACCCAGAGGCAGAAGGCAACCCATTCCCAAAGCCAGAAGGCCTGAGGGA

Gene : HepC1a
Segment# : 5
Offset : 61
1st Codon : 1
R G R R Q P I P K A R R P E G R T W A Q P G Y P W P L Y G N
AGGGGAAGGAGACAGCCTATCCCTAAGGCTAGGAGACCCGAAGGCAGAACCTGGGCCCAACCCGATACCCCTTGGCCTCTGTATGGCAAT

Gene : HepC1a
Segment# : 6
Offset : 76
1st Codon : 1
R T W A Q P G Y P W P L Y G N E G C G W A G W L L S P R G S
AGGACATGGGCTCAGCCTGGCTATCCCTGGCCCCTCTACGGAACGAAGGCTGTGGCTGGGCCGATGGCTCCTGTCCCCAGAGGCTCC

Gene : HepC1a
Segment# : 7
Offset : 91
1st Codon : 1
E G C G W A G W L L S P R G S R P S W G P T D P R R R S R N
GAGGGATGCGGATGGGCTGGCTGGCTGCTCAGCCCTAGGGGAAGCAGACCCTCTGGGGACCCACAGACCCTAGGAGAAGGTCCAGGAAT

Gene : HepC1a
Segment# : 8
Offset : 106
1st Codon : 1
R P S W G P T D P R R R S R N L G K V I D T L T C G F A D L
AGGCCTAGCTGGGGCCCTACCGATCCCAGAAGGAGAAGCAGAAACCTCGGCAAAGTGATGACACACTGACATGCGGATTCGCTGACCTC

Gene : HepC1a
Segment# : 9
Offset : 121
1st Codon : 1
L G K V I D T L T C G F A D L M G Y I P L V G A P L G G A A
CTGGGAAAGGTCATCGATACCCTCACCTGTGGCTTTGCGGATCTGATGGGCTATATCCCTCTGGTCGGCGCTCCCTCGGCGGAGCCGCT

Gene : HepC1a
Segment# : 10
Offset : 136
1st Codon : 1
M G Y I P L V G A P L G G A A R A L A H G V R V L E D G V N
ATGGGATACATTCCCTCGTGGGAGCCCTCTGGGAGGCGCTGCCAGAGCCCTCGCCCATGGCGTCAGGGTCCTGGAAGACGGAGTGAAT

Gene : HepC1a
Segment# : 11
Offset : 151
1st Codon : 1
R A L A H G V R V L E D G V N Y A T G N L P G C S F S I F L
AGGGCTCTGGCTCACGGAGTGAGAGTGCTCGAGGATGGCGTCAACTATGCCACAGGCAATCTGCCTGGCTGTAGCTTTAGCATTTTCTCT

Gene : HepC1a
Segment# : 12
Offset : 166

Figure 26 (cont)

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1st Codon : 1
Y A T G N L P G C S F S I F L L A L L S C L T V P A S A Y Q
TACGCTACCGGAAACCTCCCGGATGCTCCTTCTCCATCTTTCTGCTCGCCCTCCTGCTGCCTCACCGTCCCGCTAGCGCTTACCAA

Gene : HepC1a
Segment# : 13
Offset : 181
1st Codon : 1
L A L L S C L T V P A S A Y Q V R N S T G L Y H V T N D C P
CTGGCTCTGCTCAGTGTGTGACAGTGCCTGCCCTCCGCCTATCAGGTGAGGAATAGCACAGGCCTCTACCATGTGACAAACGATTGCCCT

Gene : HepC1a
Segment# : 14
Offset : 196
1st Codon : 1
V R N S T G L Y H V T N D C P N S S I V Y E A A D A I L H T
GTGAGAACTCCACCGACTGTATCACGTACCAATGACTGTCCCAATAGCTCCATCGTCTACGAAGCCGCTGACGCTATCCTCCACACA

Gene : HepC1a
Segment# : 15
Offset : 211
1st Codon : 1
N S S I V Y E A A D A I L H T P G C V P C V R E G N A S R C
AACTCCAGCATTTGTATGAGGCTGCCGATGCCATTCTGCATACCCCTGGCTGTGTGCCCTTGCCTCAGGGAAGGCAATGCCTCCAGGTGT

Gene : HepC1a
Segment# : 16
Offset : 226
1st Codon : 1
P G C V P C V R E G N A S R C W V A M T P T V A T R D G K L
CCCGATGCGTCCCTGTGTGAGAGAGGGAAACGCTAGCAGATGCTGGGTGGCTATGACACCCACAGTGGCTACCAGAGACGGAAGCTC

Gene : HepC1a
Segment# : 17
Offset : 241
1st Codon : 1
W V A M T P T V A T R D G K L P A T Q L R R H I D L L V G S
TGGGTGCGCATGACCCCTACCGTCGCCACAAGGGATGGCAAACCTGCCTGCCACACAGCTCAGGAGACACATTGACCTCCTGGTGGCTCC

Gene : HepC1a
Segment# : 18
Offset : 256
1st Codon : 1
P A T Q L R R H I D L L V G S A T L C S A L Y V G D L C G S
CCCGTACCCAACCTGAGAAGGCATATCGATCTGCTCGTGGGAAGCGCTACCCCTCTGCTCCGCCCTCTACGTGCGCGATCTGTGTGGCTCC

Gene : HepC1a
Segment# : 19
Offset : 271
1st Codon : 1
A T L C S A L Y V G D L C G S V F L V G Q L F T F S P R R H
GCCACACTGTGTAGCGCTCTGTATGTGGGAGACCTCTGCCGAAGCGTCTTCTCGTGGGACAGCTCTTCACATTCTCCCCAGAAGGCAT

Gene : HepC1a
Segment# : 20
Offset : 286
1st Codon : 1
V F L V G Q L F T F S P R R H W T T Q G C N C S I Y P G H I
GTGTTTCTGGTCCGCAACTGTTTACCTTTAGCCCTAGGAGACTGGACCACACAGGGATGCAATTGCTCCATCTATCCCGGACACATT

Gene : HepC1a
Segment# : 21
Offset : 301
1st Codon : 1
W T T Q G C N C S I Y P G H I T G H R M A W D M M M N W S P
TGGACAACCAAGGCTGTAACGTAGCATTTACCCTGGCCATATCACAGGCCATAGGATGGCCTGGGACATGATGATGAACCTGGAGCCCT

Gene : HepC1a
Segment# : 22
Offset : 316
1st Codon : 1
T G H R M A W D M M M N W S P T A A L V M A Q L L R I P Q A
ACCGGACACAGAATGGCTTGGGATATGATGATGAATTGGTCCCCCACAGCCGCTCTGGTCATGGCTCAGCTCCTGAGAATCCCTCAGGCT

Figure 26 (Cont)

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Gene : HepC1a
Segment# : 23
Offset : 331
1st Codon : 1
T A A L V M A Q L L R I P Q A I L D M I A G A H W G V L A G
ACCGCTGCCCTCGTGTATGGCCCAACTGCTCAGGATCCCCAAGCCATTCTGGATATGATTGCCGGAGCCCATTTGGGGAGTGCTCGCCGGA

Gene : HepC1a
Segment# : 24
Offset : 346
1st Codon : 1
I L D M I A G A H W G V L A G I A Y F S M V G N W A K V L V
ATCCTCGACATGATCGCTGGCGCTCACTGGGGCGTCTGGCTGGCATTGCCTATTTCTCCATGGTCGGCAATTGGGCTAAGGTCCTGGTC

Gene : HepC1a
Segment# : 25
Offset : 361
1st Codon : 1
I A Y F S M V G N W A K V L V V L L L F A G V D A E T H V T
ATCGCTTACTTTAGCATGGTGGGAAACTGGGCAAGTGCTCGTGGTCCTGCTCCTGTTTGCCGGAGTGATGCCGAAACCCATGTGACA

Gene : HepC1a
Segment# : 26
Offset : 376
1st Codon : 1
V L L L F A G V D A E T H V T G G N A G R T T S G L V S L L
GTGCTCCTGCTCTTCGCTGGCGTCGACGCTGAGACACACGTACCCGGAGGCAATGCCGAAGGACAACCTCCGGCCTCGTGTCCCTGCTC

Gene : HepC1a
Segment# : 27
Offset : 391
1st Codon : 1
G G N A G R T T S G L V S L L T P G A K Q N I Q L I N T N G
GGCGGAAACGCTGGCAGAACCAAGCGGACTGGTCAGCCTCCTGACACCCGGAGCCAAACAGAATATCCAACCTGATTAACACAAACGGA

Gene : HepC1a
Segment# : 28
Offset : 406
1st Codon : 1
T P G A K Q N I Q L I N T N G S W H I N S T A L N C N E S L
ACCCCTGGCGCTAAGCAAAACATTAGCTCATCAATACCAATGGCTCCTGGCATATCAATAGCACAGCCCTCAACTGTAACGAAAGCCTC

Gene : HepC1a
Segment# : 29
Offset : 421
1st Codon : 1
S W H I N S T A L N C N E S L N T G W L A G L F Y Q H K F N
AGCTGGCACATTAACCTCACCGCTCTGAATTGCAATGAGTCCCTGAATACCGGATGGCTCGCCGGACTGTTTTACCAACACAAATTCAAT

Gene : HepC1a
Segment# : 30
Offset : 436
1st Codon : 1
N T G W L A G L F Y Q H K F N S S G C P E R L A S C R R L T
AACACAGGCTGGCTGGCTGGCCTCTTCTATCAGCATAAGTTTAACTCCAGCGGATGCCCTGAGAGACTGGCTAGCTGTAGGAGACTGACA

Gene : HepC1a
Segment# : 31
Offset : 451
1st Codon : 1
S S G C P E R L A S C R R L T D F D Q G W G P I S Y A N G S
AGCTCCGGCTGTCCCGAAAGGCTCGCCTCCTGCAGAAGGCTCACCGATTTTCGATCAGGGATGGGGACCCATTAGCTATGCCAATGGCTCC

Gene : HepC1a
Segment# : 32
Offset : 466
1st Codon : 1
D F D Q G W G P I S Y A N G S G P D Q R P Y C W H Y P P K P
GACTTTGACCAAGGCTGGGGCCCTATCTCCTACGCTAACGGAAGCGGACCCGATCAGAGACCCTATTGCTGGCACTATCCCCCTAAGCCT

Gene : HepC1a
Segment# : 33

Figure 26 (Cont)

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Offset : 481
 1st Codon : 1
 G P D Q R P Y C W H Y P P K P C G I V P A K S V C G P V Y C
 GGCCCTGACCAAAGGCCTTACTGTTGGCATTACCTCCCAAACCTGTGGCATTGTGCTGCCAAAAGCGTCTGCGGACCCGTCTACTGT

Gene : HepC1a
 Segment# : 34
 Offset : 496
 1st Codon : 1
 C G I V P A K S V C G P V Y C F T P S P V V V G T T D R S G
 TGC GGAATCGTCCCCGCTAAGTCCGTGTGTGGCCCTGTGTATTGCTTTACCCTAGCCCTGTGGTCTGTGGGAACCAAGACAGACAGAAGCGGA

Gene : HepC1a
 Segment# : 35
 Offset : 511
 1st Codon : 1
 F T P S P V V V G T T D R S G A P T Y S W G A N D T D V F V
 TTCACACCCTCCCCGTCGTGGTCTGGGCACAACCGATAGGTCCGGCGCTCCACATACTCCTGGGGAGCCAATGACACAGACGTCTTCGTC

Gene : HepC1a
 Segment# : 36
 Offset : 526
 1st Codon : 1
 A P T Y S W G A N D T D V F V L N N T R P P L G N W F G C T
 GCCCTACCTATAGTGGGGCGCTAACGATACCGATGTGTTTGTGCTCAACAATACCAGACCCCTCTGGGAACTGGTTCTGGATGCACA

Gene : HepC1a
 Segment# : 37
 Offset : 541
 1st Codon : 1
 L N N T R P P L G N W F G C T W M N S T G F T K V C G A P P
 CTGAATAACACAAGGCCTCCCTCGGCAATTGGTTTGGCTGTACCTGGATGAATAGCACAGGCTTTACCAAAGTGTGTGGCGCTCCCCCT

Gene : HepC1a
 Segment# : 38
 Offset : 556
 1st Codon : 1
 W M N S T G F T K V C G A P P C V I G G A G N N T L H C P T
 TGGATGAATCCACCGGATTACAAAGGTCTGCGGAGCCCTCCCTGTGTGATTGGCGGAGCCGAAACAATACCCTCCACTGTCCCACA

Gene : HepC1a
 Segment# : 39
 Offset : 571
 1st Codon : 1
 C V I G G A G N N T L H C P T D C F R K H P E A T Y S R C G
 TCGTTCATCGGAGGCGCTGGCAATAACACACTGCATTGCCCTACCGATTGCTTTAGGAAACACCCTGAGGCTACCTATAGCAGATGCGGA

Gene : HepC1a
 Segment# : 40
 Offset : 586
 1st Codon : 1
 D C F R K H P E A T Y S R C G S G P W I T P R C L V D Y P Y
 GACTGTTTCAGAAAGCATCCCGAAGCCACATACTCCAGGTGTGGCTCCGGCCCTTGATTACCCCTAGGTGTCTGGTCGACTATCCCTAT

Gene : HepC1a
 Segment# : 41
 Offset : 601
 1st Codon : 1
 S G P W I T P R C L V D Y P Y R L W H Y P C T I N Y T I F K
 AGCGGACCCCTGGATCACACCCAGATGCCTCGTGGATTACCCCTACAGACTGTGGCACTATCCCTGTACCATTAACTATACCATTTTCAAA

Gene : HepC1a
 Segment# : 42
 Offset : 616
 1st Codon : 1
 R L W H Y P C T I N Y T I F K V R M Y V G G V E H R L E A A
 AGGCTCTGGCATTACCCCTTGCAATCAATTACACAATCTTTAAGGTGAGGATGTACGTCGGCGGAGTGGAAACAGACTGGAAGCCGCT

Gene : HepC1a
 Segment# : 43
 Offset : 631
 1st Codon : 1
 V R M Y V G G V E H R L E A A C N W T R G E R C D L E D R D

Figure 26 (Cont)

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GTGAGAATGTATGTGGGAGGCGTCGAGCATAGGCTCGAGGCTGCCTGTAAGTGGACCAGAGGCGAAAGGTGTGACCTCGAGGATAGGGAT

Gene : HepC1a
Segment# : 44
Offset : 646
1st Codon : 1
C N W T R G E R C D L E D R D R S E L S P L L L S T T Q W Q
TGCAATTGGACAAGGGGAGAGATGCGATCTGGAAGACAGAGACAGAAGCGAACTGTCCCCCTCCTGCTCAGCACAAACCAATGGCAA

Gene : HepC1a
Segment# : 45
Offset : 661
1st Codon : 1
R S E L S P L L L S T T Q W Q V L P C S F T T L P A L S T G
AGGTCCGAGCTCAGCCCTCTGCTCCTGCCACACAGTGGCAGGTCTGCTTCTCCTTCACAACCCTCCCCGCTCTGTCCACCGGA

Gene : HepC1a
Segment# : 46
Offset : 676
1st Codon : 1
V L P C S F T T L P A L S T G L I H L H Q N I V D V Q Y L Y
GTGCTCCCTGTAGCTTTACCACTGCTGCCCTCAGCACAGGCTCATCCATCTGCATCAGAATATCGTCGACGTCCAGTATCTGTAT

Gene : HepC1a
Segment# : 47
Offset : 691
1st Codon : 1
L I H L H Q N I V D V Q Y L Y G V G S S I A S W A I K W E Y
CTGATTCACCTCCACAAAACATTGTGGATGTGCAATACCTCTACGGAGTGGGAAGCTCCATCGCTAGCTGGGCCATTAAAGTGGGAGTAT

Gene : HepC1a
Segment# : 48
Offset : 706
1st Codon : 1
G V G S S I A S W A I K W E Y V V L L F L L L A D A R V C S
GGCGTCGGCTCCAGCATTGCCCTCCTGGGCTATCAAATGGGAATACGTCGTGCTCCTGTTTCTGCTCCTGGCTGACGCTAGGGTCTGCTCC

Gene : HepC1a
Segment# : 49
Offset : 721
1st Codon : 1
V V L L F L L L A D A R V C S C L W M M L L I S Q A E A A L
TGGGTCTGCTCTTCTCTGCTCGCCGATGCCAGAGTGTGTAGCTGTCTGTGGATGATGCTGCTCATCTCCAGGCTGAGGCTGCCCTC

Gene : HepC1a
Segment# : 50
Offset : 736
1st Codon : 1
C L W M M L L I S Q A E A A L E N L V I L N A A S L A G T H
TGCCTCTGGATGATGCTCCTGATTAGCCAGCCGAGCCGCTCTGGAACCTCGTGATTCTGAATGCCGCTAGCCTCGCCGGAACCCAT

Gene : HepC1a
Segment# : 51
Offset : 751
1st Codon : 1
E N L V I L N A A S L A G T H G L V S F L V F F C F A W Y L
GAGAATCTGGTCATCCTCAACGCTGCCTCCCTGGCTGGCACACACGGACTGGTCAGCTTCTGGTCTTCTTTTGCTTTGCTTGGTACCTC

Gene : HepC1a
Segment# : 52
Offset : 766
1st Codon : 1
G L V S F L V F F C F A W Y L K G R W V P G A V Y A L Y G M
GGCCTCGTGTCTTCTCGTGTCTTTCTGTTTCGCTTGGTATCTGAAAGGCAGATGGGTCCCCGGAGCCGCTACGCTCTGTATGGCATG

Gene : HepC1a
Segment# : 53
Offset : 781
1st Codon : 1
K G R W V P G A V Y A L Y G M W P L L L L L A L P Q R A Y
AAGGGAAGGTGGGTGCCTGGCGCTGTGTATGCCCTCTACGGAATGTGGCCCTCCTGCTCCTGCTCCTGGCTCTGCCTCAGAGAGCCTAT

Gene : HepC1a

Figure 26 (Cont)

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Segment# : 54
Offset : 796
1st Codon : 1
W P L L L L L A L P Q R A Y A L D T E V A A S C G G V V L
TGGCCTCTGCTCCTGCTCCTGCTCGCCCTCCCCCAAAGGGCTTACGCTCTGGATACCGAAGTGGCTGCTCCTGCGGAGGCGTCGTGCTC

Gene : HepC1a
Segment# : 55
Offset : 811
1st Codon : 1
A L D T E V A A S C G G V V L V G L M A L T L S P Y Y K R Y
GCCCTCGACACAGAGTTCGCCCTAGCTGTGGCGGAGTGGTCTGGTTCGGCCTCATGGCTCTGACACTGTCCCCCTATTACAAAAGGTAT

Gene : HepC1a
Segment# : 56
Offset : 826
1st Codon : 1
V G L M A L T L S P Y Y K R Y I S W C L W W L Q Y F L T R V
GTGGGACTGATGGCCCTCACCTCAGCCCTTACTATAAGAGATACATTAGCTGGTGGCTCTGGTGGCTGCAATACTTTCTGACAAGGGTC

Gene : HepC1a
Segment# : 57
Offset : 841
1st Codon : 1
I S W C L W W L Q Y F L T R V E A Q L H V W V P P L N V R G
ATCTCCTGGTGTCTGTGGTGGCTCCAGTATTTCTCACCAGAGTGAAGCCCACTGCATGTGTGGGTGCCTCCCTCAACGTCAGGGGA

Gene : HepC1a
Segment# : 58
Offset : 856
1st Codon : 1
E A Q L H V W V P P L N V R G G R D A V I L L M C V V H P T
GAGGCTCAGTCCACGTCTGGGTCCCCCTCTGAATGTGAGAGGCGGAAGGGATGCCGTCTCCTCTGATGTGCGTCTGTCATCCACACA

Gene : HepC1a
Segment# : 59
Offset : 871
1st Codon : 1
G R D A V I L L M C V V H P T L V F D I T K L L L A V F G P
GGCAGAGACGCTGTGATTCTGCTCATGTGTGGTCCACCCTACCCTCGTGTGTTGACATTACCAAAGTCTCCTGGCTGTGTTTGGCCCT

Gene : HepC1a
Segment# : 60
Offset : 886
1st Codon : 1
L V F D I T K L L L A V F G P L W I L Q A S L L K V P Y F V
CTGGTCTTCGATATCACAAAGCTCCTGCTCGCCGTCTTCGGACCCCTCTGGATTCTGCAAGCCTCCCTGCTCAAGGTCCCCTATTTTCGTC

Gene : HepC1a
Segment# : 61
Offset : 901
1st Codon : 1
L W I L Q A S L L K V P Y F V R V Q G L L R I C A L A R K M
CTGTGGATCCTCCAGGCTAGCCTCCTGAAAGTGCCTTACTTTGTGAGAGTGAAGGCCTCCTGAGAATCTGTGCCCTCGCCAGAAAGATG

Gene : HepC1a
Segment# : 62
Offset : 916
1st Codon : 1
R V Q G L L R I C A L A R K M I G G H Y V Q M A I I K L G A
AGGGTCCAGGGACTGCTCAGGATTTGCGCTCTGGCTAGGAAAATGATTGGCGGACACTATGTGCAAATGGCTATCATTAAAGCTCGGCGCT

Gene : HepC1a
Segment# : 63
Offset : 931
1st Codon : 1
I G G H Y V Q M A I I K L G A L T G T Y V Y N H L T P L R D
ATCGGAGGCCATTACGTCCAGATGGCCATTATCAAAGTGGGAGCCCTCACCGGAACCTATGTGTATAACCATCTGACACCCCTCAGGGAT

Gene : HepC1a
Segment# : 64
Offset : 946
1st Codon : 1

Figure 26 (Cont)

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L T G T Y V Y N H L T P L R D W A H N G L R D L A V A V E P
CTGACAGGCACATACGTCTACAATCACCTCACCCCTCTGAGAGACTGGGCCCATAACGGACTGAGAGACCTCGCCGTCGCCGTCGAGCCT

Gene : HepC1a
Segment# : 65
Offset : 961
1st Codon : 1

W A H N G L R D L A V A V E P V V F S Q M E T K L I T W G A
TGGGCTCACAATGGCCTCAGGGATCTGGCTGTGGCTGTGGAACCCGTCGTGTTTAGCCAAATGGAAACCAAAGTATTACCTGGGGCGCT

Gene : HepC1a
Segment# : 66
Offset : 976
1st Codon : 1

V V F S Q M E T K L I T W G A D T A A C G D I I N G L P V S
GTGGTCTTCTCCAGATGGAGACAAAGCTCATCATGGGGAGCCGATACCGCTGCCTGTGGCGATATCATTAAACGGACTGCCTGTGTCC

Gene : HepC1a
Segment# : 67
Offset : 991
1st Codon : 1

D T A A C G D I I N G L P V S A R R G R E I L L G P A D G M
GACACAGCCGCTTGGCGAGACATTATCAATGGCCTCCCCGTGAGCGCTAGGAGAGGCAGAGAGATTCTGCTCGGCCCTGCCGATGGCATG

Gene : HepC1a
Segment# : 68
Offset : 1006
1st Codon : 1

A R R G R E I L L G P A D G M V S K G W R L L A P I T A Y A
GCCAGAAGGGGAAGGAAATCCTCCTGGGACCCGCTGACGGAATGGTCAGCAAAGGCTGGAGGCTCCTGGCTCCCATTACCGCTTACGCT

Gene : HepC1a
Segment# : 69
Offset : 1021
1st Codon : 1

V S K G W R L L A P I T A Y A Q Q T R G L L G C I I T S L T
GTGTCCAAGGGATGGAGACTGCTCGCCCTATCACAGCCTATGCCAACAGACAAGGGGACTGCTCGGCTGTATCATTTACCTCCCTGACA

Gene : HepC1a
Segment# : 70
Offset : 1036
1st Codon : 1

Q Q T R G L L G C I I T S L T G R D K N Q V E G E V Q I V S
CAGCAAACAGAGGCCTCCTGGGATGCATTATCACAAGCCTCACCGGAAGGGATAAGAATCAGGTCGAGGGAGAGGTCCAGATTGTGTCC

Gene : HepC1a
Segment# : 71
Offset : 1051
1st Codon : 1

G R D K N Q V E G E V Q I V S T A A Q T F L A T C I N G V C
GGCAGAGACAAAACCAAGTGGGAAGCGAAGTGCAAATCGTCAGCACAGCCGCTCAGACATTCTCGCCACATGCATTAAACGGAGTGTGT

Gene : HepC1a
Segment# : 72
Offset : 1066
1st Codon : 1

T A A Q T F L A T C I N G V C W T V Y H G A G T R T I A S P
ACCGCTGCCCCAAACCTTTCTGGCTACCTGTATCAATGGCGTCTGTGGACCGTCTACCATGGCGCTGGCACAAGGACAATCGCTAGCCCT

Gene : HepC1a
Segment# : 73
Offset : 1081
1st Codon : 1

W T V Y H G A G T R T I A S P K G P V I Q M Y T N V D Q D L
TGGACAGTGTATACGGGACCGGAACAGAACCATTCGCCTCCCCAAAGGCCCTGTGATTTCAGATGTACACAAACGTCGACCAAGACCTC

Gene : HepC1a
Segment# : 74
Offset : 1096
1st Codon : 1

K G P V I Q M Y T N V D Q D L V G W P A P Q G S R S L T P C
AAGGGACCCGTCATCCAAATGTATACCAATGTGGATCAGGATCTGGTGGCTGGCCCGCTCCCCAAGGCTCCAGGTCCCTGACACCTGT

Figure 26 (Cont)

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Gene : HepCla
Segment# : 75
Offset : 1111
1st Codon : 1
V G W P A P Q G S R S L T P C T C G S S D L Y L V T R H A D
GTGGGATGGCCTGCCCTCAGGGAAGCAGAAGCCTCACCCCTTGACATGCCGAAGCTCCGACCTCTACCTCGTGACAAGGCATGCCGAT

Gene : HepCla
Segment# : 76
Offset : 1126
1st Codon : 1
T C G S S D L Y L V T R H A D V I P V R R R G D S R G S L L
ACCTGTGGCTCCAGCGATCTGTATCTGGTCACCAGACACGCTGACGTATCCCTGTGAGAAGGAGAGGCGATAGCAGAGGCTCCCTGCTC

Gene : HepCla
Segment# : 77
Offset : 1141
1st Codon : 1
V I P V R R R G D S R G S L L S P R P I S Y L K G S S G G P
GTGATTCCCGTCAGGAGAAGGGGAGACTCCAGGGGAAGCCTCCTGTCCCCAGACCCATTAGCTATCTGAAAGGCTCCAGCGGAGGCCCT

Gene : HepCla
Segment# : 78
Offset : 1156
1st Codon : 1
S P R P I S Y L K G S S G G P L L C P A G H A V G I F R A A
AGCCCTAGGCCTATCTCCTACCTCAAGGGAAGCTCCGGCGGACCCCTCCTGTGTCCCGCTGGCCATGCCGTCCGCATTTTCAGAGCCGCT

Gene : HepCla
Segment# : 79
Offset : 1171
1st Codon : 1
L L C P A G H A V G I F R A A V C T R G V A K A V D F I P V
CTGCTCTGCCCTGCCGACACGCTGTGGGAATCTTTAGGGCTGCCGTCTGCACAAGGGGAGTGGCTAAGGCTGTGGATTTTCATTCCTCGTC

Gene : HepCla
Segment# : 80
Offset : 1186
1st Codon : 1
V C T R G V A K A V D F I P V E N L E T T M R S P V F T D N
GTGTGTACCAGAGGCGTCGCCAAAGCCGTCGACTTTATCCCTGTGGAAAACCTCGAGACAACCATGAGGTCCCCGCTCTTCACAGACAAT

Gene : HepCla
Segment# : 81
Offset : 1201
1st Codon : 1
E N L E T T M R S P V F T D N S S P P A V P Q S F Q V A H L
GAGAATCTGGAAACCACAATGAGAAGCCCTGTGTTTACCGATAACTCCAGCCCTCCCGCTGTGCCTCAGTCCTTCCAAGTGGCTCACCTC

Gene : HepCla
Segment# : 82
Offset : 1216
1st Codon : 1
S S P P A V P Q S F Q V A H L H A P T G S G K S T K V P A A
AGCTCCCCCTGCCGTCCCCCAAAGCTTTCAGGTCGCCCATCTGCATGCCCTACCGGAAGCGGAAAGTCCACCAAAGTGCCTGCCGCT

Gene : HepCla
Segment# : 83
Offset : 1231
1st Codon : 1
H A P T G S G K S T K V P A A Y A A Q G Y K V L V L N P S V
CACGCTCCACAGGCTCCGGCAAAAGCACAAGGTCCCCGCTGCCTATGCCGCTCAGGGATACAAAGTCTCGTGCTCAACCTAGCGTC

Gene : HepCla
Segment# : 84
Offset : 1246
1st Codon : 1
Y A A Q G Y K V L V L N P S V A A T L G F G A Y M S K A H G
TACGCTGCCAAGGCTATAAGGTCCTGGTCCTGAATCCCTCCGTGGCTGCCACACTGGGATTCCGGAGCCTATATGTCCAAGGCTCACGGA

Gene : HepCla
Segment# : 85
Offset : 1261

Figure 26 (Cont)

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1st Codon : 1
A A T L G F G A Y M S K A H G I D P N I R T G V R T I T T G
GCCGCTACCTCGGCTTTGGCGCTTACATGAGCAAAGCCCATGGCATTGACCTAACATTAGGACAGGCGTCAGGACAATCACAACCGGA

Gene : HepC1a
Segment# : 86
Offset : 1276
1st Codon : 1
I D P N I R T G V R T I T T G S P I T Y S T Y G K F L A D G
ATCGATCCCAATATCAGAACCGGAGTGAGAACCATTACCACAGGCTCCCCATTACCTATAGCACATACGGAAGTTTCTGGCTGACGGA

Gene : HepC1a
Segment# : 87
Offset : 1291
1st Codon : 1
S P I T Y S T Y G K F L A D G G C S G G A Y D I I I C D E C
AGCCCTATACATACTCCACCTATGGCAAATTCCTCGCCGATGGCGGATGCTCCGGCGGAGCCTATGACATTATCATTGCGATGAGTGT

Gene : HepC1a
Segment# : 88
Offset : 1306
1st Codon : 1
G C S G G A Y D I I I C D E C H S T D A T S I L G I G T V L
GGCTGTAGCGGAGGCGCTTACGATATCATTATCTGTGACGAATGCCATAGCACAGACGCTACCTCCATCCTCGGCATTGGCACAGTGCTC

Gene : HepC1a
Segment# : 89
Offset : 1321
1st Codon : 1
H S T D A T S I L G I G T V L D Q A E T A G A R L V V L A T
CACTCCACCGATGCCACAAGCATTCTGGGAATCGGAACCGTCTGGATCAGGCTGAGACAGCCGAGCCAGACTGGTCGTGCTCGCCACA

Gene : HepC1a
Segment# : 90
Offset : 1336
1st Codon : 1
D Q A E T A G A R L V V L A T A T P P G S V T V P H P N I E
GACCAAGCCGAAACCGCTGGCGCTAGGCTCGTGGTCTGGCTACCGCTACCCCTCCCGGAAGCGTCACCGTCCCCCATCCAATATCGAA

Gene : HepC1a
Segment# : 91
Offset : 1351
1st Codon : 1
A T P P G S V T V P H P N I E E V A L S T T G E I P F Y G K
GCCACACCCCTGGCTCCGTGACAGTGCCCTCACCTAACATTGAGGAAGTGGCTCTGTCCACCACAGGCGAAATCCCTTTCTATGGCAAA

Gene : HepC1a
Segment# : 92
Offset : 1366
1st Codon : 1
E V A L S T T G E I P F Y G K A I P L E V I K G G R H L I F
GAGGTCGCCCTCAGCACAAACCGGAGAGATTCCCTTTTACGGAAAGCTATCCCTCTGGAAGTGATTAAGGGAGGCAGACACCTCATCTTT

Gene : HepC1a
Segment# : 93
Offset : 1381
1st Codon : 1
A I P L E V I K G G R H L I F C H S K K K C D E L A A K L V
GCCATTCCTTCGAGGTCATCAAAGGCGGAAGGCATCTGATTTTCTGTCACTCCAAGAAAAAGTGTGACGAACTGGCTGCCAAACTGGTC

Gene : HepC1a
Segment# : 94
Offset : 1396
1st Codon : 1
C H S K K K C D E L A A K L V A L G I N A V A Y Y R G L D V
TGCCATAGCAAAAAGAAATGCGATGAGCTCGCCGCTAAGCTCGTGGCTCTGGGAATCAATGCCGTCGCTATTACAGAGGCCTCGACGTC

Gene : HepC1a
Segment# : 95
Offset : 1411
1st Codon : 1
A L G I N A V A Y Y R G L D V S V I P T S G D V V V V A T D
GCCCTCGGCATTAACGCTGTGGCTTACTATAGGGGACTGGATGTGTCCGTGATTCCCAAGCGGAGACGTCGTGGTCTGGCTACCGAT

Figure 26 (Cont)

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Gene : HepC1a
Segment# : 96
Offset : 1426
1st Codon : 1
S V I P T S G D V V V V A T D A L M T G Y T G D F D S V I D
AGCGTCATCCCTACCTCCGGCGATGTGGTCGTGGTCGCCACAGACGCTCTGATGACCGGATACACAGGCGATTTCGATAGCGTCATCGAT

Gene : HepC1a
Segment# : 97
Offset : 1441
1st Codon : 1
A L M T G Y T G D F D S V I D C N T C V T Q T V D F S L D P
GCCCTCATGACAGGCTATACCGGAGACTTTGACTCCGTGATTGACTGTAACACATGCGTCACCCAAACCGTCGACTTTAGCCTCGACCCT

Gene : HepC1a
Segment# : 98
Offset : 1456
1st Codon : 1
C N T C V T Q T V D F S L D P T F T I E T T T L P Q D A V S
TGCAATACCTGTGTGACACAGACAGTGGATTCTCCCTGGATCCCACATTCACAATCGAAACCACAACCCCTCCCCAAGACGCTGTGTCC

Gene : HepC1a
Segment# : 99
Offset : 1471
1st Codon : 1
T F T I E T T T L P Q D A V S R T Q R R G R T G R G K P G I
ACCTTTACCATGAGACAACCACACTGCCTCAGGATGCCGTGAGCAGAACCCAAAGGAGAGGCAGAACCGAAGGGGAAAGCCTGGCATT

Gene : HepC1a
Segment# : 100
Offset : 1486
1st Codon : 1
R T Q R R G R T G R G K P G I Y R F V A P G E R P S G M F D
AGGACACAGAGAAGGGGAAGGACAGGCAGAGGCAACCCGGAATCTATAGGTTGTGGCTCCCGGAGAGAGACCCCTCCGGCATGTTTCGAT

Gene : HepC1a
Segment# : 101
Offset : 1501
1st Codon : 1
Y R F V A P G E R P S G M F D S S V L C E C Y D A G C A W Y
TACAGATTCTGCGCCCTGGCGAAAGGCCCTAGCGGAATGTTTACTCCAGCGTCTGTGTGAGTGTTACGATGCCGGATGCGCTTGGTAT

Gene : HepC1a
Segment# : 102
Offset : 1516
1st Codon : 1
S S V L C E C Y D A G C A W Y E L T P A E T T V R L R A Y M
AGCTCCGTGCTCTGCGAATGCTATGACGCTGGCTGTGCTGGTACGAACCTGACACCCGCTGAGACAACCGTCAGGCTCAGGGCTTACATG

Gene : HepC1a
Segment# : 103
Offset : 1531
1st Codon : 1
E L T P A E T T V R L R A Y M N T P G L P V C Q D H L E F W
GAGCTACCCCTGCCGAAACCACAGTGAGACTGAGAGCTATATGAATACCCCTGGCCTCCCGTCTGCCAAGACCATCTGGAATCTCTGG

Gene : HepC1a
Segment# : 104
Offset : 1546
1st Codon : 1
N T P G L P V C Q D H L E F W E G V F T G L T H I D A H F L
AACACACCCGACTGCCTGTGTGTCAGGATCAGCTCGAGTTTTTGGGAAGGCGTCTTCACAGGCTCACCATATCGATGCCCATTTCTCT

Gene : HepC1a
Segment# : 105
Offset : 1561
1st Codon : 1
E G V F T G L T H I D A H F L S Q T K Q S G E N F P Y L V A
GAGGGAGTGTTTACCGGACTGACACACATTGACGCTCACTTTCTGTCCAGACAAAGCAAAGCGGAGAGAATTTCCCTTACCTCGTGGCT

Gene : HepC1a
Segment# : 106

Figure 26 (Cont)

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Offset : 1576
1st Codon : 1
S Q T K Q S G E N F P Y L V A Y Q A T V C A R A Q A P P P S
AGCCAAACCAACAGTCCGGCGAAAACCTTCCCTATCTGGTTCGCTATCAGGCTACCGTCTGCGCTAGGGCTCAGGCTCCCCCTCCCTCC

Gene : HepC1a
Segment# : 107
Offset : 1591
1st Codon : 1
Y Q A T V C A R A Q A P P P S W D Q M W K C L I R L K P T L
TACCAAGCCACAGTGTGTGCCAGAGCCCAAGCCCCTCCCCCTAGCTGGGACCAATGTGGAAGTGTCTGATTAGGCTCAAGCCTACCCTC

Gene : HepC1a
Segment# : 108
Offset : 1606
1st Codon : 1
W D Q M W K C L I R L K P T L H G P T P L L Y R L G A V Q N
TGGGATCAGATGTGGAATGCCTCATCAGACTGAAACCCACACTGCATGGCCCTACCCCTCTGCTCTACAGACTGGGAGCCGTCCAGAAT

Gene : HepC1a
Segment# : 109
Offset : 1621
1st Codon : 1
H G P T P L L Y R L G A V Q N E V T L T H P V T K Y I M T C
CACGGACCCACACCCCTCCTGTATAGGCTCGGCGCTGTGCAAAACGAAGTGACACTGACACACCCTGTGACAAAGTATATCATGACCTGT

Gene : HepC1a
Segment# : 110
Offset : 1636
1st Codon : 1
E V T L T H P V T K Y I M T C M S A D L E V V T S T W V L V
GAGGTCACCCCTACCCATCCCGTCACCAATACATTATGACATGCATGAGCGCTGACCTCGAGGTCGTGACAAGCACATGGGTCTGGTC

Gene : HepC1a
Segment# : 111
Offset : 1651
1st Codon : 1
M S A D L E V V T S T W V L V G G V L A A L A A Y C L S T G
ATGTCGCCGATCTGGAAGTGGTCACCTCCACCTGGGTGCTCGTGGGAGGCGTCCTGGCTGCCCTCGCCGCTTACTGTCTGTCCACCGGA

Gene : HepC1a
Segment# : 112
Offset : 1666
1st Codon : 1
G G V L A A L A A Y C L S T G C V V I V G R I V L S G K P A
GGCGAGTGCTCGCCGCTCTGGCTGCCTATTCCTCAGCACAGGCTGTGTGGTCATCGTCGGCAGAAATCGTCTGTCCGGCAAACCCGCT

Gene : HepC1a
Segment# : 113
Offset : 1681
1st Codon : 1
C V V I V G R I V L S G K P A I I P D R E V L Y R E F D E M
TGCGTCGTGATTGTGGGAAGGATTGTGCTCAGCGGAAAGCCTGCCATTATCCCTGACAGAGAGGTCCTGTATAGGGAATTGGATGAGATG

Gene : HepC1a
Segment# : 114
Offset : 1696
1st Codon : 1
I I P D R E V L Y R E F D E M E E C S Q H L P Y I E Q G M M
ATCATTCCCGATAGGGAAGTGTCTACAGAGAGTTTGACGAAATGGAAGAGTGTAGCCAACACCTCCCCTATATCGAACAGGGAATGATG

Gene : HepC1a
Segment# : 115
Offset : 1711
1st Codon : 1
E E C S Q H L P Y I E Q G M M L A E Q F K Q K A L G L L Q T
GAGGAATGCTCCAGCATCTGCCTTACATTGAGCAAGGCATGATGCTCGCCGAACAGTTTAAGCAAAGGCTCTGGGACTGCTCCAGACA

Gene : HepC1a
Segment# : 116
Offset : 1726
1st Codon : 1
L A E Q F K Q K A L G L L Q T A S R Q A E V I A P A V Q T N

Figure 26 (Cont)

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CTGGCTGAGCAATTCAAACAGAAAGCCCTCGGCCTCCTGCAAACCGCTAGCAGACAGGCTGAGGTCATCGCTCCCGCTGTGCAAACCAAT

Gene : HepC1a
Segment# : 117
Offset : 1741
1st Codon : 1

A S R Q A E V I A P A V Q T N W Q K L E V F W A K H M W N F
GCCTCCAGGCAAGCCGAAGTGATTGCCCTGCCGTCCAGACAAACTGGCAGAACTGGAAGTGTTTGGGCTAAGCATATGTGGAACCTT

Gene : HepC1a
Segment# : 118
Offset : 1756
1st Codon : 1

W Q K L E V F W A K H M W N F I S G I Q Y L A G L S T L P G
TGGCAAAAGCTCGAGGTCTTCTGGGCCAAACACATGTGGAATTTCATTAGCGGAATCCAATACCTCGCCGGACTGTCCACCCTCCCCGGA

Gene : HepC1a
Segment# : 119
Offset : 1771
1st Codon : 1

I S G I Q Y L A G L S T L P G N P A I A S L M A F T A A V T
ATCTCCGGCATTCAATATCTGGCTGGCCTCAGCACACTGCCCTGGCAATCCCGCTATCGCTAGCCTCATGGCTTTACAGCCGCTGTGACA

Gene : HepC1a
Segment# : 120
Offset : 1786
1st Codon : 1

N P A I A S L M A F T A A V T S P L T T S Q T L L F N I L G
AACCCTGCCATTGCCTCCCTGATGGCCTTTACCGCTGCCGTACCTCCCCCTCACCACAAGCCAAACCTCCTGTTTAACATTCTGGGA

Gene : HepC1a
Segment# : 121
Offset : 1801
1st Codon : 1

S P L T T S Q T L L F N I L G G W V A A Q L A A P G A A T A
AGCCCTCTGACAACCTCCCAGACACTGCTCTTCAATATCCTCGGCGGATGGGTGCGCGCTCAGCTCGCCGCTCCCGGAGCCGCTACCGCT

Gene : HepC1a
Segment# : 122
Offset : 1816
1st Codon : 1

G W V A A Q L A A P G A A T A F V G A G L A G A A I G S V G
GGCTGGGTGGCTGCCCAACTGGCTGCCCTGGCGCTGCCACAGCCTTTGTGGGAGCCGGAAGTGGCTGGCGCTGCCATTGGCTCCGTGGGA

Gene : HepC1a
Segment# : 123
Offset : 1831
1st Codon : 1

F V G A G L A G A A I G S V G L G K V L V D I L A G Y G A G
TTCTGCGGCGCTGGCCTCGCCGAGCCGCTATCGGAAGCGTCGGCCTCGGCAAAGTGCTCGTGGATATCCTCGCCGGATACGGAGCCGGA

Gene : HepC1a
Segment# : 124
Offset : 1846
1st Codon : 1

L G K V L V D I L A G Y G A G V A G A L V A F K I M S G E V
CTGGGAAAGTCTGTGGTCGACATTCTGGCTGGCTATGGCGCTGGCGTCGCCGAGCCCTCGTGGCTTTCAAATCATGAGCGGAGAGGTC

Gene : HepC1a
Segment# : 125
Offset : 1861
1st Codon : 1

V A G A L V A F K I M S G E V P S T E D L V N L L P A I L S
GTGGCTGGCGCTCTGGTCGCCTTTAAGATTATGTCCGGCGAAGTGCTTAGCACAGAGGATCTGGTCAACCTCCTGCCTGCCATTCTGTCC

Gene : HepC1a
Segment# : 126
Offset : 1876
1st Codon : 1

P S T E D L V N L L P A I L S P G A L V V G V V C A A I L R
CCCTCCACCGAAGACCTCGTGAATCTGCTCCCCGCTATCCTCAGCCCTGGCGCTCTGGTCTGGGAGTGGTCTGCGCTGCCATTCTGAGA

Gene : HepC1a

Figure 26 (Cont)

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Segment# : 127
Offset : 1891
1st Codon : 1
P G A L V V G V V C A A I L R R H V G P G E G A V Q W M N R
CCCGGAGCCCTCGTGGTCCGGCGTCGTGTGTGCCGTATCCTCAGGAGACACGTCGGCCCTGGCGAAGGCGCTGTGCAATGGATGAACAGA

Gene : HepC1a
Segment# : 128
Offset : 1906
1st Codon : 1
R H V G P G E G A V Q W M N R L I A F A S R G N H V S P T H
AGGCATGTGGGACCCGGAGAGGGAGCCGTCCAGTGGATGAATAGGCTCATCGCTTTCGCTAGCAGAGGCAATCACGTCAGCCCTACCCAT

Gene : HepC1a
Segment# : 129
Offset : 1921
1st Codon : 1
L I A F A S R G N H V S P T H Y V P E S D A A A R V T A I L
CTGATTGCCTTTTGCTCCAGGGGAAACCATGTGTCCCCACACACTATGTGCCTGAGTCCGACGCTGCCGTAGGGTCACCGCTATCCTC

Gene : HepC1a
Segment# : 130
Offset : 1936
1st Codon : 1
Y V P E S D A A A R V T A I L S S L T V T Q L L R R L H Q W
TACGTCCCGAAAGCGATGCCGCTGCCAGAGTGACAGCCATTCTGTCCAGCCTCACCGTCACCCAACTGCTCAGGAGACTGCATCAGTGG

Gene : HepC1a
Segment# : 131
Offset : 1951
1st Codon : 1
S S L T V T Q L L R R L H Q W I S S E C T T P C S G S W L R
AGCTCCCTGACAGTGACACAGCTCCTGAGAAGGCTCCACCAATGGATTAGCTCCGAGTGTACCACACCCGTAGCGGAAGCTGGCTGAGA

Gene : HepC1a
Segment# : 132
Offset : 1966
1st Codon : 1
I S S E C T T P C S G S W L R D I W D W I C E V L S D F K T
ATCTCCAGCGAATGCACAAACCCCTTGCTCCGGCTCCTGGCTCAGGGATATCTGGGACTGGATCTGTGAGGTCCCTGTCCGACTTTAAGACA

Gene : HepC1a
Segment# : 133
Offset : 1981
1st Codon : 1
D I W D W I C E V L S D F K T W L K A K L M P Q L P G I P F
GACATTTGGGATTGGATTTCGGAAGTGCTCAGCGATTTCAAACCTGGCTGAAAGCCAACTGATGCCCAACTGCCTGGCATTCCCTTT

Gene : HepC1a
Segment# : 134
Offset : 1996
1st Codon : 1
W L K A K L M P Q L P G I P F V S C Q R G Y K G V W R G D G
TGGCTCAAGGCTAAGCTCATGCCTCAGCTCCCCGAATCCCTTTCGTGAGCTGTGAGAGAGGCTATAAGGGAGTGTGGAGGGGAGACGGA

Gene : HepC1a
Segment# : 135
Offset : 2011
1st Codon : 1
V S C Q R G Y K G V W R G D G I M H T R C H C G A E I T G H
GTGTCTGCCAAAGGGGATACAAAGGCGTCTGGAGAGGCGATGGCATTATGCATACCAGATGCCATTGCGGAGCCGAAATCACAGGCCAT

Gene : HepC1a
Segment# : 136
Offset : 2026
1st Codon : 1
I M H T R C H C G A E I T G H V K N G T M R I V G P R T C R
ATCATGCACACAAGGTGTCACTGTGGCGCTGAGATTACCGGACACGTCAAGAATGGCACAATGAGAATCGTCGGCCCTAGGACATGCAGA

Gene : HepC1a
Segment# : 137
Offset : 2041
1st Codon : 1

Figure 26 (Cont)

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V K N G T M R I V G P R T C R N M W S G T F P I N A Y T T G
GTGAAAAACGGAACCATGAGGATTGTGGGACCCAGAACCTGTAGGAATATGTGGAGCGGAACCTTTCCCATTAACGCTTACACAACCGGA

Gene : HepC1a
Segment# : 138
Offset : 2056
1st Codon : 1

N M W S G T F P I N A Y T T G P C T P L P A P N Y T F A L W
AACATGTGGTCCGGCACATTCCCTATCAATGCCTATACCACAGGCCCTTGACACCCCTCCCCGCTCCCAATTACACATTCGCTCTGTGG

Gene : HepC1a
Segment# : 139
Offset : 2071
1st Codon : 1

P C T P L P A P N Y T F A L W R V S A E E Y V E I R R V G D
CCTGTACCCCTCTGCCTGCCCTAACTATACCTTTGCCCTCTGGAGAGTGTCCGCCGAAGAGTATGTGGAAATCAGAAGGGTCGGCGAT

Gene : HepC1a
Segment# : 140
Offset : 2086
1st Codon : 1

R V S A E E Y V E I R R V G D F H Y V T G M T T D N L K C P
AGGGTCAGCGCTGAGGAATACGTCGAGATTAGGAGAGTGGGAGACTTTCACTATGTGACAGGCATGACCACAGACAATCTGAAATGCCCT

Gene : HepC1a
Segment# : 141
Offset : 2101
1st Codon : 1

F H Y V T G M T T D N L K C P C Q V P S P E F F T E L D G V
TTCCATTACGTCACCGGAATGACAACCGATAACCTCAAGTGTCCCTGTCAGGTCCCCTCCCCGAATTCTTTACCGAACTGGATGGCGTC

Gene : HepC1a
Segment# : 142
Offset : 2116
1st Codon : 1

C Q V P S P E F F T E L D G V R L H R F A P P C K P L L R E
TGCCAAGTGCCTAGCCCTGAGTTTTTCACAGAGCTCGACGGAGTGAGACTGCATAGGTTTGCCCTCCCTGTAAGCCTCTGCTCAGGGAA

Gene : HepC1a
Segment# : 143
Offset : 2131
1st Codon : 1

R L H R F A P P C K P L L R E E V S F R V G L H E Y P V G S
AGGCTCCACAGATTGCTCCCCCTTGCAAACCCCTCCTGAGAGAGGAAGTGTCTTCAGAGTGGGACTGCATGAGTATCCCGTCGGCTCC

Gene : HepC1a
Segment# : 144
Offset : 2146
1st Codon : 1

E V S F R V G L H E Y P V G S Q L P C E P E P D V A V L T S
GAGGTCAGCTTTAGGGTCGGCTCCACGAATACCTGTGGGAAGCCAAGTGCCTTGCGAACCCGAACCCGATGTGGCTGTGCTCACCTCC

Gene : HepC1a
Segment# : 145
Offset : 2161
1st Codon : 1

Q L P C E P E P D V A V L T S M L T D P S H I T A E A A G R
CAGCTCCCCGTGTAGCCTGAGCTGACGTGCGCGTCTGACAAGCATGCTGACAGACCCTAGCCATATCACAGCCGAAGCCGCTGGCAGA

Gene : HepC1a
Segment# : 146
Offset : 2176
1st Codon : 1

M L T D P S H I T A E A A G R R L A R G S P P S M A S S S A
ATGCTCACCGATCCCTCCACATTACCGCTGAGGCTGCCGGAAGGAGACTGGCTAGGGGAAGCCCTCCCTCCATGGCTAGCTCCAGCGCT

Gene : HepC1a
Segment# : 147
Offset : 2191
1st Codon : 1

R L A R G S P P S M A S S S A S Q L S A P S L K A T C T A N
AGGCTCGCCAGAGGCTCCCCCTAGCATGGCTCCAGCTCCGCTCCAGCTCAGCGCTCCCTCCCTGAAAGCCACATGCACAGCCAAT

Figure 26 (Cont)

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Gene : HepC1a
Segment# : 148
Offset : 2206
1st Codon : 1
S Q L S A P S L K A T C T A N H D S P D A E L I E A N L L W
AGCCAACTGTCCGCCCTAGCCTCAAGGCTACCTGTAECGCTAACCATGACTCCCCCGATGCCGAAC TGATTGAGGCTAACCTCCTGTGG

Gene : HepC1a
Segment# : 149
Offset : 2221
1st Codon : 1
H D S P D A E L I E A N L L W R Q E M G G N I T R V E S E N
CACGATAGCCCTGACGCTGAGCTCATCGAAGCCAATCTGCTCTGGAGACAGGAAATGGGAGGCAATATCACAAGGGTCGAGTCCGAGAAT

Gene : HepC1a
Segment# : 150
Offset : 2236
1st Codon : 1
R Q E M G G N I T R V E S E N K V V I L D S F D P L V A E E
AGGCAAGAGATGGGCGGAACATTACCAGAGTGGAAGCGAAAACAAAGTGGTCATCCTCGACTCCTTCGATCCCTCGTGGCTGAGGAA

Gene : HepC1a
Segment# : 151
Offset : 2251
1st Codon : 1
K V V I L D S F D P L V A E E D E R E I S V P A E I L R K S
AAGGTCGTGATTCTGGATAGCTTTGACCTCTGGTCGCCGAAGAGGATGAGAGAGAGATTAGCGTCCCGCTGAGATTCTGAGAAAGTCC

Gene : HepC1a
Segment# : 152
Offset : 2266
1st Codon : 1
D E R E I S V P A E I L R K S R R F A Q A L P V W A R P D Y
GACGAAAGGGAATCTCCGTGCCTGCCGAATCCTCAGGAAAAGCAGAAGGTTTGCCCAAGCCCTCCCCGTCTGGGCTAGGCCTGACTAT

Gene : HepC1a
Segment# : 153
Offset : 2281
1st Codon : 1
R R F A Q A L P V W A R P D Y N P P L V E T W K K P D Y E P
AGGAGATTGCTCAGGCTCTGCCTGTGTGGGCCAGACCCGATTACAATCCCCCTCTGGTCGAGACATGGAAAAGCCTGACTATGAGCCT

Gene : HepC1a
Segment# : 154
Offset : 2296
1st Codon : 1
N P P L V E T W K K P D Y E P P V V H G C P L P P P R S P P
AACCTTCCCCCTCGTGAAACCTGGAAGAAACCCGATTACGAACCCCTGTGGTCCACGATGCCCTCTGCCTCCCCCTAGGTCCCCCCT

Gene : HepC1a
Segment# : 155
Offset : 2311
1st Codon : 1
P V V H G C P L P P P R S P P V P P P R K K R T V V L T E S
CCCGTCGTGCATGGCTGTCCCTTCCCCCTCCCAGAAGCCCTCCCGTCCCCCCTCCCAGAAAGAAAAGGACAGTGGTCTTGACAGAGTCC

Gene : HepC1a
Segment# : 156
Offset : 2326
1st Codon : 1
V P P P R K K R T V V L T E S T L S T A L A E L A T K S F G
GTGCTTCCCCCTAGGAAAAGAGAACCCTCGTGCTCACCAGAAAGCACACTGTCCACCGCTCTGGCTGAGCTCGCCACAAAGTCTTTCGGA

Gene : HepC1a
Segment# : 157
Offset : 2341
1st Codon : 1
T L S T A L A E L A T K S F G S S S T S G I T G D N T T T S
ACCTCAGCAGCCCTCGCCGAACCTGGCTACCAAAAGCTTTGGCTCCAGCTCCACCTCCGGCATTACCGGAGACAATACCACAACCTCC

Gene : HepC1a
Segment# : 158
Offset : 2356

Figure 26 (Cont)

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1st Codon : 1
S S S T S G I T G D N T T T S S E P A P S G C P P D S D A E
AGCTCCAGCACAAAGCGAATCACAGGCGATAACACAACCACAAGCTCCGAGCCTGCCCTAGCGGATGCCCTCCCGATAGCGATGCCGAA

Gene : HepC1a
Segment# : 159
Offset : 2371
1st Codon : 1
S E P A P S G C P P D S D A E S Y S S M P P L E G E P G D P
AGCGAACCCGCTCCCTCCGGCTGTCCCCCTGACTCCGACGCTGAGTCTACTCCAGCATGCCCCCTCTGGAAGGCGAACCCGGAGACCCT

Gene : HepC1a
Segment# : 160
Offset : 2386
1st Codon : 1
S Y S S M P P L E G E P G D P D L S D G S W S T V S S E A G
AGCTATAGCTCCATGCCCTCCCTCGAGGGAGAGCCTGGCGATCCCGATCTGTCCGACGGAAGCTGGAGCACAGTGTCCAGCGAAGCCGGA

Gene : HepC1a
Segment# : 161
Offset : 2401
1st Codon : 1
D L S D G S W S T V S S E A G T E D V V C C S M S Y S W T G
GACCTCAGCGATGGCTCCTGGTCCACCGTCAGCTCCGAGGCTGGCACAGAGGATGTGGTCTGCTGTAGCATGAGCTATAGCTGGACCCGGA

Gene : HepC1a
Segment# : 162
Offset : 2416
1st Codon : 1
T E D V V C C S M S Y S W T G A L V T P C A A E E Q K L P I
ACCGAAGACGTCGTGTGTGCTCCATGTCTACTCCTGGACAGGCGCTCTGGTCACCCCTTGCGCTGCCGAAGAGCAAAGCTCCCCATT

Gene : HepC1a
Segment# : 163
Offset : 2431
1st Codon : 1
A L V T P C A A E E Q K L P I N A L S N S L L R H H N L V Y
GCCCTCGTGACACCCTGTGCGGCTGAGGAACAGAAACTGCCTATCAATGCCCTCAGCAATAGCCTCCTGAGACACCATAACCTCGTGTAT

Gene : HepC1a
Segment# : 164
Offset : 2446
1st Codon : 1
N A L S N S L L R H H N L V Y S T T S R S A C Q R Q K K V T
AACGTCCTGTCCAACCTCCCTGCTCAGGCATCACAACTCTGGTCTACTCCACCACAAGCAGAAGCGCTTGCCAAAGGCAAAGAAAGTGACA

Gene : HepC1a
Segment# : 165
Offset : 2461
1st Codon : 1
S T T S R S A C Q R Q K K V T F D R L Q V L D S H Y Q D V L
AGCACAACCTCCAGGTCCGCTGTGAGAGACAGAAAAAGTCCACCTTTGACAGACTGCAAGTGCTCGACTCCCCTATCAGGATGTGCTC

Gene : HepC1a
Segment# : 166
Offset : 2476
1st Codon : 1
F D R L Q V L D S H Y Q D V L K E V K A A A S K V K A N L L
TTCGATAGGCTCCAGGTCCTGGATAGCCATTACCAAGACGTCCTGAAAGAGGTCAAGGCTGCGCTAGCAAAGTGAAAGCCAATCTGCTC

Gene : HepC1a
Segment# : 167
Offset : 2491
1st Codon : 1
K E V K A A A S K V K A N L L S V E E A C S L T P P H S A K
AAGGAAGTGAAAGCCGCTGCCTCCAAGGTCAAGGCTAACCTCCTGTCCGTGGAAGAGGCTTGCTCCCTGACACCCCTCACTCCGCCAAA

Gene : HepC1a
Segment# : 168
Offset : 2506
1st Codon : 1
S V E E A C S L T P P H S A K S K F G Y G A K D V R C H A R
AGCGTCGAGGAAGCCTGTAGCCTCACCCCTCCCATAGCGCTAAGTCCAAGTTTGCTGATGGCGCTAAGGATGTGAGATGCCATGCCAGA

Figure 26 (Cont)

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Gene : HepC1a
Segment# : 169
Offset : 2521
1st Codon : 1
S K F G Y G A K D V R C H A R K A V A H I N S V W K D L L E
AGCAAATTCGGATACGGAGCCAAAGACGTCAGGTGTCACGCTAGGAAAGCCGTCGCCATATCAATAGCGTCTGGAAAGACCTCCTGGAA

Gene : HepC1a
Segment# : 170
Offset : 2536
1st Codon : 1
K A V A H I N S V W K D L L E D S V T P I D T T I M A K N E
AAGGCTGTGGCTCACATTAACCTCCGTGTGGAAGGATCTGCTCGAGGATAGCGTCACCCCTATCGATACCACAATCATGGCCAAAACGAA

Gene : HepC1a
Segment# : 171
Offset : 2551
1st Codon : 1
D S V T P I D T T I M A K N E V F C V Q P E K G G R K P A R
GACTCCGTGACACCCATTGACACAACCATTATGGCTAAGAATGAGGTCTTCTGTGTGCAACCCGAAAAGGGAGGCAGAAAGCCTGCCAGA

Gene : HepC1a
Segment# : 172
Offset : 2566
1st Codon : 1
V F C V Q P E K G G R K P A R L I V F P D L G V R V C E K M
GTGTTTTGCGTCCAGCCTGAGAAAGGCGGAAGGAAACCCGCTAGGCTCATCGTCTTCCCTGACCTCGGCGTCAGGGTCTGCGAAAAGATG

Gene : HepC1a
Segment# : 173
Offset : 2581
1st Codon : 1
L I V F P D L G V R V C E K M A L Y D V V S K L P L A V M G
CTGATTGTGTTTCCCGATCTGGGAGTGAGAGTGTGTGAGAAAATGGCTCTGTATGACGTCGTGTCCAAGCTCCCCCTCGCCGTCTATGGGA

Gene : HepC1a
Segment# : 174
Offset : 2596
1st Codon : 1
A L Y D V V S K L P L A V M G S S Y G F Q Y S P G Q R V E F
GCCCTCTACGATGTGGTCAGCAAACCTGCCTCTGGCTGTGATGGGCTCCAGCTATGGCTTTCAGTATAGCCCTGGCCAAAGGGTCGAGTTT

Gene : HepC1a
Segment# : 175
Offset : 2611
1st Codon : 1
S S Y G F Q Y S P G Q R V E F L V Q A W K S K K T P M G F S
AGCTCCTACGATTCCAATACTCCCCGACAGAGAGTGGAAATTCCTCGTGCAAGCCTGGAAGTCCAAGAAAACCCCTATGGGATTCTCC

Gene : HepC1a
Segment# : 176
Offset : 2626
1st Codon : 1
L V Q A W K S K K T P M G F S Y D T R C F D S T V T E S D I
CTGGTCCAGGCTTGGAAAAGCAAAAGACACCCATGGGCTTTAGCTATGACACAAGGTGTTTCGATAGCACAGTGACAGAGTCCGACATT

Gene : HepC1a
Segment# : 177
Offset : 2641
1st Codon : 1
Y D T R C F D S T V T E S D I R T E E A I Y Q C C D L D P Q
TACGATACCAGATGCTTTGACTCCACCGTCACCGAAAGCGATATCAGAACCGAAGAGGCTATCTATCAGTGTTCGATCTGGATCCCCAA

Gene : HepC1a
Segment# : 178
Offset : 2656
1st Codon : 1
R T E E A I Y Q C C D L D P Q A R V A I K S L T E R L Y V G
AGGACAGAGGAAGCCATTTACCAATGCTGTGACCTCGACCCTCAGGCTAGGGTCGCCATTAAGTCCCTGACAGAGAGACTGTATGTGGGA

Gene : HepC1a
Segment# : 179

Figure 26 (Cont)

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Offset : 2671
1st Codon : 1
A R V A I K S L T E R L Y V G G P L T N S R G E N C G Y R R
GCCAGAGTGGCTATCAAAGCCTCACCAGAAAGGCTCTACGTCGGCGGACCCCTCACCAATAGCAGAGGCGAAAACCTGTGGCTATAGGAGA

Gene : HepC1a
Segment# : 180
Offset : 2686
1st Codon : 1
G P L T N S R G E N C G Y R R C R A S G V L T T S C G N T L
GGCCCTCTGACAACTCCAGGGGAGAGAATTGCGGATACAGAAGGTGTAGGGCTAGCGGAGTGCTCACCACAAGCTGTGGCAATACCCTC

Gene : HepC1a
Segment# : 181
Offset : 2701
1st Codon : 1
C R A S G V L T T S C G N T L T C Y I K A R A A C R A A G L
TGCAGAGCCTCCGGCGTCTGACAACCTCCTGCGGAAACACACTGACATGCTATATCAAAGCCAGAGCCGCTTGCAGAGCCGCTGGCCTC

Gene : HepC1a
Segment# : 182
Offset : 2716
1st Codon : 1
T C Y I K A R A A C R A A G L Q D C T M L V C G D D L V V I
ACCTGTACATTAAGGCTAGGGCTGCCTGTAGGGCTGCCGACTGCAAGACTGTACCATGCTGGTCTGCGGAGACGATCTGGTCGTGATT

Gene : HepC1a
Segment# : 183
Offset : 2731
1st Codon : 1
Q D C T M L V C G D D L V V I C E S A G V Q E D A A S L R A
CAGGATTGCACAATGCTCGTGTGTGGCGATGACCTCGTGGTCATCTGTAGTCCGCCGAGTGCAAGAGGATGCCGCTAGCCTCAGGGCT

Gene : HepC1a
Segment# : 184
Offset : 2746
1st Codon : 1
C E S A G V Q E D A A S L R A F T E A M T R Y S A P P G D P
TGCGAAAGCGTGGCGTCCAGGAAGACGCTGCCTCCCTGAGAGCCTTTACCGAAGCCATGACCAGATACTCCGCCCCCTCCCGGAGACCTC

Gene : HepC1a
Segment# : 185
Offset : 2761
1st Codon : 1
F T E A M T R Y S A P P G D P P Q P E Y D L E L I T S C S S
TTCAGAGGCTATGACAAGGTATAGCGCTCCCCCTGGCGATCCCCCTCAGCCTGAGTATGACCTCGAGCTCATCACAAGCTGTAGCTCC

Gene : HepC1a
Segment# : 186
Offset : 2776
1st Codon : 1
P Q P E Y D L E L I T S C S S N V S V A H D G A G K R V Y Y
CCCCAACCCGAATACGATCTGGAACTGATTACCTCCTGCTCCAGCAATGTGTCCGTGGCTCAGGATGGCGCTGGCAAAAGGGTCTACTAT

Gene : HepC1a
Segment# : 187
Offset : 2791
1st Codon : 1
N V S V A H D G A G K R V Y Y L T R D P T T P L A R A A W E
AACGTCAGCGTCGCCCATGACGGAGCCGGAAGAGAGTGTATTACCTCACCAGAGACCCCTACCACACCCCTCGCCAGAGCCGCTTGGGAA

Gene : HepC1a
Segment# : 188
Offset : 2806
1st Codon : 1
L T R D P T T P L A R A A W E T A R H T P V N S W L G N I I
CTGACAAGGGATCCCAACCCCTCTGGCTAGGGCTGCCTGGGAGACAGCCAGACACACCCGTCACCTCTGGCTCGGCAATATCAT

Gene : HepC1a
Segment# : 189
Offset : 2821
1st Codon : 1
T A R H T P V N S W L G N I I M F A P T L W A R M I L M T H

Figure 26 (Cont)

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ACCGCTAGGCATACCCCTGTGAATAGCTGGCTGGGAAACATTATCATGTTCCGCTCCCACACTGTGGGCCAGAATGATTCTGATGACCCAT

Gene : HepC1a
Segment# : 190
Offset : 2836
1st Codon : 1

M F A P T L W A R M I L M T H F F S V L I A R D Q L E Q A L
ATGTTTGCCCTACCCCTCTGGGCTAGGATGATCCTCATGACACACTTTTCTCCGTGCTCATCGCTAGGGATCAGCTCGAGCAAGCCCTC

Gene : HepC1a
Segment# : 191
Offset : 2851
1st Codon : 1

F F S V L I A R D Q L E Q A L D C E I Y G A C Y S I E P L D
TTCTTTAGCGTCTGATTGCCAGAGACCAACTGGAACAGGCTCTGGATTGCGAAATCTATGGCGCTTGCTATAGCATTGAGCCTCTGGAT

Gene : HepC1a
Segment# : 192
Offset : 2866
1st Codon : 1

D C E I Y G A C Y S I E P L D L P P I I Q R L H G L S A F S
GACTGTGAGATTTACGGAGCTGTACTCCATCGAACCCCTCGACCTCCCCCTATCATTCAGAGACTGCATGGCCTCAGCGCTTTCTCC

Gene : HepC1a
Segment# : 193
Offset : 2881
1st Codon : 1

L P P I I Q R L H G L S A F S L H S Y S P G E I N R V A A C
CTGCCTCCATTATCCAAAGGCTCCACGGACTGTCCGCCTTTAGCCTCCACTCCTACTCCCCGGAGAGATTAACAGAGTGGCTGCCTGT

Gene : HepC1a
Segment# : 194
Offset : 2896
1st Codon : 1

L H S Y S P G E I N R V A A C L R K L G V P P L R A W R H R
CTGCATAGCTATAGCCCTGGCGAAATCAATAGGGTCGCCGCTTGCTCAGGAAACTGGGAGTGCCTCCCCCTCAGGGCTGGAGACACAGA

Gene : HepC1a
Segment# : 195
Offset : 2911
1st Codon : 1

L R K L G V P P L R A W R H R A R S V R A R L L A R G G R A
CTGAGAAAGCTCGGCGTCCCCCTCTGAGAGCCTGGAGGCATAGGGCTAGGTCCGTGAGAGCCAGACTGCTCGCCAGAGGCGGAAGGGCT

Gene : HepC1a
Segment# : 196
Offset : 2926
1st Codon : 1

A R S V R A R L L A R G G R A A I C G K Y L F N W A V R T K
GCCAGAAGCTCAGGGCTAGGCTCCTGGCTAGGGGAGGCAGAGCCGCTATCTGTGGCAAATACCTCTTCAATTGGGCTGTGAGAACCAAA

Gene : HepC1a
Segment# : 197
Offset : 2941
1st Codon : 1

A I C G K Y L F N W A V R T K L K L T P I A A A G R L D L S
GCCATTGCGGAAAGTATCTGTTTAACTGGGCCGTCAGGACAAAGCTCAAGCTCACCCCTATCGCTGCCGCTGGCAGACTGGATCTGTCC

Gene : HepC1a
Segment# : 198
Offset : 2956
1st Codon : 1

L K L T P I A A A G R L D L S G W F T A G Y S G G D I Y H S
CTGAACTGACACCCATTGCGGCTGCCGGAAGGCTCGACCTCAGCGGATGGTTTACCGCTGGCTATAGCGGAGGCGATATCTATCACTCC

Gene : HepC1a
Segment# : 199
Offset : 2971
1st Codon : 1

G W F T A G Y S G G D I Y H S V S H A R P R W F W F C L L L
GGCTGGTTACAGCCGGATACTCCGGCGGAGACATTTACCATAGCGTCAGCCATGCCAGACCCAGATGGTTTTGGTTTTGCCTCCTGCTC

Gene : HepC1a

Figure 26 (Cont)

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Segment# : 200
Offset : 2986
1st Codon : 1
V S H A R P R W F W F C L L L L A A G V G I Y L L P N R A A
GTGTCCACGCTAGGCTAGGTGTTCTGGTTCTGTCTGCTCCTGCTCGCCGCTGGCGTCCGCATTACCTCCTGCCTAACAGAGCCGCT

Gene : HepC1a
Segment# : 201
Offset : 3001
1st Codon : 1
L A A G V G I Y L L P N R A A
CTGGCTGCCGGAGTGGGAATCTATCTGCTCCCAATAGGGCTGCC

Segments in scrambled order:

HepC1a #77
V I P V R R R G D S R G S L L S P R P I S Y L K G S S G G P
GTGATTCCTCGTACGAGAAAGGGGAGACTCCAGGGGAAGCCTCCTGTCCCCCAGACCCATTAGCTATCTGAAAGGCTCCAGCGGAGGCCCT

HepC1a #68
A R R G R E I L L G P A D G M V S K G W R L L A P I T A Y A
GCCAGAAGGGGAAGGGAAATCCTCCTGGGACCCGCTGACGGAATGGTCAGCAAAGGCTGGAGGCTCCTGGCTCCCATTACCGCTTACGCT

HepC1a #143
R L H R F A P P C K P L L R E E V S F R V G L H E Y P V G S
AGGCTCCACAGATTGCTCCCCCTTGCAAACCCCTCCTGAGAGAGGAAGTGTCTTCAGAGTGGGACTGCATGAGTATCCCGTCGGCTCC

HepC1a #66
V V F S Q M E T K L I T W G A D T A A C G D I I N G L P V S
GTGGTCTTCTCCAGATGGAGACAAAGCTCATCACATGGGGAGCCGATACCGCTGCCTGTGGCGATATCATTAACGGACTGCCTGTGTCC

HepC1a #79
L L C P A G H A V G I F R A A V C T R G V A K A V D F I P V
CTGCTCTGCCCTGCCGGACACGCTGTGGGAATCTTTAGGGCTGCCGTCTGCACAAGGGGAGTGGCTAAGGCTGTGGATTTCATTCCCGTC

HepC1a #113
C V V I V G G R I V L S G K P A I I P D R E V L Y R E F D E M
TGCCTCGTGATTGTGGGAAGGATTGTGCTCAGCGGAAAGCCTGCCATTATCCCTGACAGAGAGGTCTGTATAGGAATTCGATGAGATG

HepC1a #139
P C T P L P A P N Y T F A L W R V S A E E Y V E I R R V G D
CCCTGTACCCCTCTGCCTGCCCTAACTATACCTTTGCCCTCTGGAGAGTGTCCGCCGAAGAGTATGTGGAAATCAGAAGGGTCCGGCGAT

HepC1a #174
A L Y D V V S K L P L A V M G S S Y G F Q Y S P G Q R V E F
GCCCTCTACGATGTGGTCAGCAAAGCTGCTCTGGCTGTGATGGGCTCCAGCTATGGCTTTTCACTATAGCCCTGGCCAAAGGGTCCAGATTT

HepC1a #57
I S W C L W W L Q Y F L T R V E A Q L H V W V P P L N V R G
ATCTCCTGGTGTCTGTGGTGGCTCCAGTATTTCTCACCAGAGTGAAGCCCAACTGCATGTGTGGGTGCCCTCCCTCAACGTACAGGGGA

HepC1a #51
E N L V I L N A A S L A G T H G L V S F L V F F C F A W Y L
GAGAATCTGGTCATCCTCAACGCTGCCTCCCTGGCTGGCACACACGGACTGGTCAGCTTTCTGGTCTTCTTTTGCTTTGCCTGGTACCTC

HepC1a #193
L P P I I Q R L H G L S A F S L H S Y S P G E I N R V A A C
CTGCCTCCATTATCCAAAGGCTCCACGGACTGTCCGCCTTTAGCCTCCACTCCTACTCCCCGGAGAGATTACAGAGTGGCTGCCTGT

HepC1a #154
N P P L V E T W K K P D Y E P P V V H G C P L P P P R S P P
AACCCTCCCTCGTGGAAACCTGGAAGAAACCCGATTACGAACCCCTGTGGTCCACGGATGCCCTCTGCCTCCCCCTAGGTCCCCCCT

HepC1a #48
G V G S S I A S W A I K W E Y V V L L F L L L A D A R V C S
GGCGTCGGCTCCAGCATTCCTCCTGGGCTATCAAATGGGAATACGTCGTGCTCCTGTTTCTGCTCCTGGCTGACGCTAGGGTCTGCTCC

HepC1a #37
L N N T R P P L G N W F G C T W M N S T G F T K V C G A P P
CTGAATAACACAAGGCCTCCCTCGGCAATTGGTTTGGCTGTACCTGGATGAATAGCACAGGCTTTACCAAAGTGTGTGGCGCTCCCCCT

HepC1a #185
F T E A M T R Y S A P P G D P P Q P E Y D L E L I T S C S S

Figure 26 (Cont)

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TTCACAGAGGCTATGACAAGGTATAGCGCTCCCCCTGGCGATCCCCCTCAGCCTGAGTATGACCTCGAGCTCATCACAAGCTGTAGCTCC

HepC1a #54

W P L L L L L A L P Q R A Y A L D T E V A A S C G G V V L
TGGCCTCTGCTCCTGCTCGCCCTCCCCAAAGGGCTTACGCTCTGGATACCGAAGTGGCTGCCTCCTGCGGAGGCGCTGCTC

HepC1a #70

Q Q T R G L L G C I I T S L T G R D K N Q V E G E V Q I V S
CAGCAAACCAGAGGCTCCTGGGATGCATTATCACAAGCCTCACCGAAGGGATAAGAATCAGGTGAGGGAGAGGTCCAGATTGTGTCC

HepC1a #82

S S P P A V P Q S F Q V A H L H A P T G S G K S T K V P A A
AGCTCCCCCCTGCCGTCCCCCAAAGCTTTTCAGGTGCGCCATCTGCATGCCCCCTACCGGAAGCGGAAAGTCCACCAAAGTGCCCTGCCGCT

HepC1a #104

N T P G L P V C Q D H L E F W E G V F T G L T H I D A H F L
AACACACCCGACTGCCTGTGTGTCAGGATCACCTCGAGTTTGGGAAGGCGCTCTTCACAGGCCTCACCCATATCGATGCCCATTTTCCTC

HepC1a #26

V L L L F A G V D A E T H V T G G N A G R T T S G L V S L L
GTGCTCCTGCTCTTCGCTGGCGTCGACGCTGAGACACACGTACCCGGAGGCAATGCCGAAGGACAACCTCCGGCCTCGTGTCCCTGCTC

HepC1a #110

E V T L T H P V T K Y I M T C M S A D L E V V T S T W V L V
GAGGTACCCCTACCCATCCCGTCACCAAAATACATTATGACATGCATGAGCGCTGACCTCGAGGTGCTGACAAGCACATGGGTCTCTGGT

HepC1a #56

V G L M A L T L S P Y Y K R Y I S W C L W W L Q Y F L T R V
GTGGGACTGATGGCCCTCACCTCAGCCCTTACTATAAGAGATACATTAGCTGGTGCCTCTGGTGGCTGCAATACTTTCTGACAAGGGTC

HepC1a #197

A I C G K Y L F N W A V R T K L K L T P I A A A G R L D L S
GCCATTGCGGAAAGTATCTGTTTAACTGGGCGTCAGGACAAAGCTCAAGCTCACCCCTATCGCTGCCGCTGGCAGACTGGATCTGTCC

HepC1a #25

I A Y F S M V G N W A K V L V V L L L F A G V D A E T H V T
ATCGTTACTTTAGCATGGTGGGAACTGGGCCAAAGTGCTCGTGGTCTCTGCTCCTGTTTGGCCGAGTGGATGCCGAAACCCATGTGACA

HepC1a #147

R L A R G S P P S M A S S S A S Q L S A P S L K A T C T A N
AGGCTCGCCAGAGGCTCCCCCCTAGCATGGCCTCCAGCTCCGCCCTCCAGCTCAGCGCTCCCTCCCTGAAAGCCACATGCACAGCCAAT

HepC1a #52

G L V S F L V F F C F A W Y L K G R W V P G A V Y A L Y G M
GGCTCGTGTCTCTTCCTCGTGTCTTTCTGTTTCGCTTGGTATCTGAAAGGCAGATGGGTCCCCGGAGCCGCTACGCTCTGTATGGCATG

HepC1a #145

Q L P C E P E P D V A V L T S M L T D P S H I T A E A A G R
CAGTCCCCCTGTGAGCCTGAGCCTGACGTCGCCGCTCCTGACAAGCATGCTGACAGACCCTAGCCATATCACAGCCGAAGCCGCTGGCAGA

HepC1a #171

D S V T P I D T T I M A K N E V F C V Q P E K G G R K P A R
GACTCCGTGACACCCATTGACACAACCATTTATGGCTAAGAATGAGGTCTTCTGTGTGCAACCCGAAAGGGAGGCAGAAAGCCTGCCAGA

HepC1a #84

Y A A Q G Y K V L V L N P S V A A T L G F G A Y M S K A H G
TACGCTGCCAAAGGCTATAAGGTCTGGTCTGAATCCCTCCGTGGCTGCCACACTGGGATTGCGAGCCTATATGTCCAAGGCTCACGGA

HepC1a #14

V R N S T G L Y H V T N D C P N S S I V Y E A A D A I L H T
GTGAGAACTCCACCGGACTGTATCACGTACCAATGACTGTCCCAATAGCTCCATCGTCTACGAAGCCGCTGACGCTATCCTCCACACA

HepC1a #175

S S Y G F Q Y S P G Q R V E F L V Q A W K S K K T P M G F S
AGTCCTACGGATTCCAATACTCCCCCGACAGAGAGTGGAATTCCTCGTGCAAGCCTGGAAGTCCAAGAAAACCCCTATGGGATTCTCC

HepC1a #67

D T A A C G D I I N G L P V S A R R G R E I L L G P A D G M
GACACAGCCGCTTGCGGAGACATTATCAATGGCCTCCCCGTGAGCGCTAGGAGAGGCAGAGAGATTCTGCTCGGCCCTGCCGATGGCATG

HepC1a #148

S Q L S A P S L K A T C T A N H D S P D A E L I E A N L L W
AGCCAACGTGTCGCCCTAGCCTCAAGGCTACCTGTACCGCTAACCATGACTCCCCGATGCCGAAGTATTGAGGCTAACCTCCTGTGG

Figure 26 (Cont)

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HepC1a #120

N P A I A S L M A F T A A V T S P L T T S Q T L L F N I L G.
AACCTGCCATTGCCCTCCCTGATGGCCTTTACCGCTGCCGTACCTCCCCCTCACCACAAGCCAAACCCTCCTGTTTAAACATTCTGGGA

HepC1a #176

L V Q A W K S K K T P M G F S Y D T R C F D S T V T E S D I
CTGGTCCAGGCTTGGAAAAGCAAAAGACACCCATGGGCTTTAGCTATGACACAAGGTGTTTCGATAGCACAGTGACAGAGTCCGACATT

HepC1a #152

D E R E I S V P A E I L R K S R R F A Q A L P V W A R P D Y
GACGAAAGGAAATCTCCGTGCCTGCCGAAATCCTCAGGAAAAGCAGAAGGTTTGCCCAAGCCCTCCCCGTCTGGGCTAGGCTGACTAT

HepC1a #190

M F A P T L W A R M I L M T H F F S V L I A R D Q L E Q A L
ATGTTTGCCCTACCTCTGGGCTAGGATGATCCTCATGACACACTTTTCTCCGTGCTCATCGCTAGGGATCAGCTCGAGCAAGCCCTC

HepC1a #96

S V I P T S G D V V V V A T D A L M T G Y T G D F D S V I D
AGCGTCATCCCTACCTCCGGCGATGTGGTCTGGTTCGCCACAGACGCTCTGATGACCGGATACACAGGCGATTTCGATAGCGTCATCGAT

HepC1a #94

C H S K K K C D E L A A K L V A L G I N A V A Y Y R G L D V
TGCCATAGCAAAAAGAAATGCGATGAGCTCGCCGCTAAGCTCGTGGCTCTGGGAATCAATGCCGTGCGCTATTACAGAGGCCCTCGACGTC

HepC1a #46

V L P C S F T T L P A L S T G L I H L H Q N I V D V Q Y L Y
GTGCTCCCTGTAGCTTTACCACACTGCCTGCCCTCAGCACAGGCCCTCATCCATCTGCATCAGAATATCGTCGACGTCCAGTATCTGTAT

HepC1a #53

K G R W V P G A V Y A L Y G M W P L L L L L A L P Q R A Y
AAGGGAAGGTGGGTGCCTGGCGCTGTGTATGCCCTCTACGGAATGTGGCCCCCTCTGCTCCTGCTCCTGGCTCTGCCTCAGAGAGCCTAT

HepC1a #87

S P I T Y S T Y G K F L A D G G C S G G A Y D I I I C D E C
AGCCCTATCACATACTCCACCTATGGCAAATTCCTCGCCGATGGCGGATGCTCCGGCGAGCCTATGACATTATCATTTGCGATGAGTGT

HepC1a #196

A R S V R A R L L A R G G R A A I C G K Y L F N W A V R T K
GCCAGAAGCGTCAGGGCTAGGCTCCTGGCTAGGGGAGGCAGAGCCGCTATCTGTGGCAAATACCTCTTCAATTGGGCTGTGAGAACCAAA

HepC1a #170

K A V A H I N S V W K D L L E D S V T P I D T T I M A K N E
AAGGCTGTGGCTCACATTAACTCCGTGTGGAAGGATCTGCTCGAGGATAGCGTCACCCCTATCGATACCACAATCATGGCCAAAAACGAA

HepC1a #35

F T P S P V V V G T T D R S G A P T Y S W G A N D T D V F V
TTCACACCCTCCCCGTGCTGGTCGGCACAACCGATAGGTCCGGCGCTCCACATACTCCTGGGGAGCCAATGACACAGACGTCTTCGTC

HepC1a #16

P G C V P C V R E G N A S R C W V A M T P T V A T R D G K L
CCCGGATGCGTCCCTGTGTGAGAGAGGGAACGCTAGCAGATGCTGGGTGGCTATGACACCCACAGTGGCTACCAGAGACGGAAAGCTC

HepC1a #183

Q D C T M L V C G D D L V V I C E S A G V Q E D A A S L R A
CAGGATTGCACAATGCTCGTGTGTGGCGATGACCTCGTGGTCACTGTGAGTCCGCCGAGTGCAAGAGGATGCCGCTAGCCTCAGGGCT

HepC1a #125

V A G A L V A F K I M S G E V P S T E D L V N L L P A I L S
GTGGCTGGCGCTCTGGTCGCCCTTTAAGATTATGTCCGGCGAAGTGCCTAGCACAGAGGATCTGGTCAACCTCCTGCCTGCCATTCTGTCC

HepC1a #177

Y D T R C F D S T V T E S D I R T E E A I Y Q C C D L D P Q
TACGATACCGATGCTTTGACTCCACCGTCACCGAAAGCGATATCAGAACCGAAGAGGCTATCTATCAGTGTTCGATCTGGATCCCCAA

HepC1a #103

E L T P A E T T V R L R A Y M N T P G L P V C Q D H L E F W
GAGCTCACCCCTGCCGAAACCACAGTGAGACTGAGAGCCTATATGAATACCCCTGGCCTCCCGTCTGCCAAGACCATCTGGAATTCTGG

HepC1a #186

P Q P E Y D L E L I T S C S S N V S V A H D G A G K R V Y Y
CCCCAACCCGAATACGATCTGGAAGTATTACCTCCTGCTCCAGCAATGTGTCCGTGGCTCACGATGGCGCTGGCAAAGGGTCTACTAT

Figure 26 (Cont)

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HepC1a #9

L G K V I D T L T C G F A D L M G Y I P L V G A P L G G A A
CTGGGAAAGGTTCATCGATACCCCTCACCTGTGGCTTTGCCGATCTGATGGGCTATATCCCTCTGGTCGGCGCTCCCTCGGCGAGCCGCT

HepC1a #93

A I P L E V I K G G R H L I F C H S K K K C D E L A A K L V
GCCATTCCCTCGAGGTTCATCAAAGCGGAAGGCATCTGATTTTCTGTCTACTCCAAGAAAAGTGTGACGAACTGGCTGCCAAACTGGTC

HepC1a #112

G G V L A A L A A Y C L S T G C V V I V G R I V L S G K P A
GGCGGAGTGCTCGCCGCTCTGGCTGCCTATTGCCTCAGCACAGGCTGTGTGGTCATCGTCGGCAGAATCGTCCTGTCCGGCAAACCCGCT

HepC1a #184

C E S A G V Q E D A A S L R A F T E A M T R Y S A P P G D P
TGCGAAAGCGCTGGCGTCCAGGAAGACGCTGCCTCCCTGAGAGCCTTTACCGAAGCCATGACCAGATACTCCGCCCCCTCCCGGAGACCCT

HepC1a #199

G W F T A G Y S G G D I Y H S V S H A R P R W F W F C L L L
GGCTGGTTTCACAGCCGGATACTCCGGCGGAGACATTTACCATAGCGTCAGCCATGCCAGACCCAGATGGTTTGGTTTGCCTCCTGCTC

HepC1a #158

S S S T S G I T G D N T T T S S E P A P S G C P P D S D A E
AGCTCCAGCACAAAGCGGAATCACAGGCGATAACACAACACAAGCTCCGAGCCTGCCCTAGCGGATGCCCTCCCGATAGCGATGCCGAA

HepC1a #100

R T Q R R G R T G R G K P G I Y R F V A P G E R P S G M F D
AGGACACAGAGAAGGGGAAGGACAGGCAGAGGCAAACCCGGAATCTATAGGTTTGTGGCTCCCGGAGAGAGACCCTCCGGCATGTTTCGAT

HepC1a #43

V R M Y V G G V E H R L E A A C N W T R G E R C D L E D R D
GTGAGAATGTATGTGGGAGGCGTCGAGCATAGGCTCGAGGCTGCCTGTAAGTGGACAGAGGCGAAAGGTGTGACCTCGAGGATAGGGAT

HepC1a #58

E A Q L H V W V P P L N V R G G R D A V I L L M C V V H P T
GAGGCTCAGCTCCACGTCTGGGTCCCCCTCTGAATGTGAGAGGCGGAAGGGATGCCGTCATCCTCCTGATGTGCGTCGTGCATCCCCA

HepC1a #4

L G V R A T R K T S E R S Q P R G R R Q P I P K A R R P E G
CTGGGAGTGAGAGCCACAAGGAAAACCTCCGAGAGAAGCCAACCCAGAGGCAGAAGGCAACCCATTCCCAAAGCCAGAAGGCTGAGGGA

HepC1a #187

N V S V A H D G A G K R V Y Y L T R D P T T P L A R A A W E
AACGTCAGCGTCGCCCATTGACGGAGCCGGAAGAGAGTGTATTACCTCACCAGAGACCCTACCACACCCTCGCCAGAGCCGCTTGGGA

HepC1a #159

S E P A P S G C P P D S D A E S Y S S M P P L E G E P G D P
AGCGAACCCGCTCCCTCCGGCTGTCCCCCTGACTCCGACGCTGAGTCCTACTCCAGCATGCCCCCTCTGGAAGGCGAACCCGGAGACCCT

HepC1a #63

I G G H Y V Q M A I I K L G A L T G T Y V Y N H L T P L R D
ATCGGAGGCCATTACGTCCAGATGGCCATTATCAAAGTGGGAGCCCTCACCAGAACCTATGTGTATAACCATCTGACACCCCTCAGGGAT

HepC1a #126

P S T E D L V N L L P A I L S P G A L V V G V V C A A I L R
CCCTCCACCGAAGACCTCGTGAATCTGCTCCCCGCTATCCTCAGCCCTGGCGCTCTGGTCGTGGGAGTGGTCTGCGCTGCCATTCTGAGA

HepC1a #24

I L D M I A G A H W G V L A G I A Y F S M V G N W A K V L V
ATCCTCGACATGATCGCTGGCGCTCACTGGGGCGTCTGGCTGGCATTGCCTATTTCTCCATGGTCGGCAATTGGGCTAAGGTCCTGGTC

HepC1a #7

E G C G W A G W L L S P R G S R P S W G P T D P R R R S R N
GAGGGATGCGGATGGGCTGGCTGGCTGCTCAGCCCTAGGGGAAGCAGACCCTCCTGGGGACCCACAGACCCTAGGAGAAGGTCCAGGAAT

HepC1a #21

W T T Q G C N C S I Y P G H I T G H R M A W D M M M N W S P
TGGACAACCAAGGCTGTAAGTGTAGCATTTACCCTGGCCATATCACAGGCCATAGGATGGCCTGGGACATGATGATGAAGTGGAGCCCT

HepC1a #17

W V A M T P T V A T R D G K L P A T Q L R R H I D L L V G S
TGGGTCGCCATGACCCCTACCGTCGCCACAAGGGATGGCAAAGTGCCTGCCACACAGCTCAGGAGACACATTGACCTCCTGGTCGGCTCC

HepC1a #42

Figure 26 (Cont)

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R L W H Y P C T I N Y T I F K V R M Y V G G V E H R L E A A
 AGGCTCTGGCATTACCTTGCACAATCAATTACACAATCTTAAAGGTCAGGATGTACGTGCGCGGAGTGGAACACAGACTGGAAGCCGCT

HepC1a #172

V F C V Q P E K G G R K P A R L I V F P D L G V R V C E K M
 GTGTTTTCGCTCCAGCCTGAGAAAGGCGGAAGGAAACCCGCTAGGCTCATCGTCTTCCCTGACCTCGGCGTCAGGGTCTGCGAAAAGATG

HepC1a #10

M G Y I P L V G A P L G G A A R A L A H G V R V L E D G V N
 ATGGGATACATTCCCTCGTGGGAGCCCTCTGGGAGGCGCTGCCAGAGCCCTCGCCCATGGCGTCAGGGTCTGGAAGACGGAGTGAAT

HepC1a #27

G G N A G R T T S G L V S L L T P G A K Q N I Q L I N T N G
 GCGGAAACCTGGCAGAACCACAAGCGGACTGGTCAGCCTCCTGACACCCGGAGCCAAACAGAATATCCAACCTGATTAACACAAACGGA

HepC1a #13

L A L L S C L T V P A S A Y Q V R N S T G L Y H V T N D C P
 CTGGCTCTGCTCAGTGTCTGACAGTGCCTCCGCTATCAGGTACAGGAATAGCACAGGCCTCTACCATGTGACAAACGATTGCCCT

HepC1a #71

G R D K N Q V E G E V Q I V S T A A Q T F L A T C I N G V C
 GGCAGAGACAAAACCAAGTGAAGGCGAAGTGCAAAATCGTCAGCACAGCCGCTCAGACATTCTCGCCACATGCATTAAACGGAGTGTGT

HepC1a #18

P A T Q L R R H I D L L V G S A T L C S A L Y V G D L C G S
 CCCGCTACCCAACCTGAGAAGGCATATCGATCTGCTCGTGGGAAGCGCTACCCTCTGCTCCGCCCCTACGTGCGCGATCTGTGTGGCTCC

HepC1a #83

H A P T G S G K S T K V P A A Y A A Q G Y K V L V L N P S V
 CACGCTCCACAGGCTCCGGCAAAAGCACAAAGGTCCCCGCTGCCTATGCCGCTCAGGGATACAAAGTGCTCGTGTCTCAACCCCTAGCGTC

HepC1a #6

R T W A Q P G Y P W P L Y G N E G C G W A G W L L S P R G S
 AGGACATGGGCTCAGCCTGGCTATCCCTGGCCCCCTACGGAACGAAAGGCTGTGGCTGGGCGGATGGCTCCTGTCCCCCAGAGGCTCC

HepC1a #162

T E D V V C C S M S Y S W T G A L / V T P C A A E E Q K L P I
 ACCGAAGACGTCGTGTGTGCTCCATGTCTACTCTGGACAGGCGCTCTGGTCACCCCTTGCGCTGCCGAAGAGCAAAAGCTCCCCATT

HepC1a #55

A L D T E V A A S C G G V V L V G L M A L T L S P Y Y K R Y
 GCCCTCGACACAGAGGTCGCGCTAGCTGTGGCGGAGTGGTCTGGTCCGCCCTCATGGCTCTGACACTGTCCCCCTATTACAAAAGGTAT

HepC1a #38

W M N S T G F T K V C G A P P C V I G G A G N N T L H C P T
 TGGATGAACCTCACCGGATTACAAAGGTCTGCGGAGCCCTCCCTGTGTGATTGGCGGAGCCGGAACAATACCCTCCACTGTCCCACA

HepC1a #168

S V E E A C S L T P P H S A K S K F G Y G A K D V R C H A R
 AGCGTCGAGGAAGCCTGTAGCCTCACCCCTCCCATAGCGCTAAGTCCAAGTTGGCTATGGCGCTAAGGATGTGAGATGCCATGCCAGA

HepC1a #119

I S G I Q Y L A G L S T L P G N P A I A S L M A F T A A V T
 ATCTCCGGCATTAGTATCTGGCTGGCCTCAGCACACTGCCTGGCAATCCCGCTATCGCTAGCCTCATGGCTTTTACAGCCGCTGTGACA

HepC1a #3

Q I V G G V Y L L P R R G P R L G V R A T R K T S E R S Q P
 CAGATTGTGGGAGGCGTCTACCTCCTGCCTAGGAGAGGCCCTAGGCTCGGCGTCAGGGCTACCAGAAAGACAAGCGAAAGGTCCCAGCCT

HepC1a #194

L H S Y S P G E I N R V A A C L R K L G V P P L R A W R H R
 CTGCATAGCTATAGCCCTGGCGAAATCAATAGGGTCGCGCTTGCTCAGGAACTGGGAGTGCCTCCCTCAGGGCTTGGAGACACAGA

HepC1a #189

T A R H T P V N S W L G N I I M F A P T L W A R M I L M T H
 ACCGCTAGGCATACCCCTGTGAATAGCTGGCTGGGAAACATTATCATGTTTCGCTCCCACTGTGGGCCAGAAATGATTTCTGATGACCCAT

HepC1a #81

E N L E T T M R S P V F T D N S S P P A V P Q S F Q V A H L
 GAGAATCTGGAAACCACAATGAGAAGCCCTGTGTTTACCGATAACTCCAGCCCTCCCGCTGTGCCTCAGTCTTCCAAGTGGCTCACCTC

HepC1a #91

A T P P G S V T V P H P N I E E V A L S T T G E I P F Y G K

Figure 26 (Cont)

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GCCACACCCCCTGGCTCCGTGACAGTGCCTCACCTAACATTGAGGAAGTGGCTCTGTCCACCACAGGCGAAATCCCTTTCTATGGCAA

HepC1a #60

L V F D I T K L L L A V F G P L W I L Q A S L L K V P Y F V
CTGGTCTTCGATATCACAAAGCTCCTGCTCGCCGTCTTCGGACCCCTCTGGATTCTGCAAGCCTCCCTGCTCAAGGTCCCTATTTCGTC

HepC1a #23

T A A L V M A Q L L R I P Q A I L D M I A G A H W G V L A G
ACCGCTGCCCTCGTGATGGCCCACTGCTCAGGATTCCCAAGCCATTCTGGATATGATTGCCGAGCCCATTTGGGGAGTGCTCGCCGGA

HepC1a #98

C N T C V T Q T V D F S L D P T F T I E T T T L P Q D A V S
TGCAATACCTGTGTGACACAGACAGTGGATTCTCCCTGGATCCACATTACAAATCGAAACCACAACCTCCCCAAGACGCTGTGTCC

HepC1a #109

H G P T P L L Y R L G A V Q N E V T L T H P V T K Y I M T C
CAGGACCCACACCCCTCCTGTATAGGCTCGGCGCTGTGCAAAACGAAGTGACACTGACACACCCCTGTGACAAAGTATATCATGACCTGT

HepC1a #179

A R V A I K S L T E R L Y V G G P L T N S R G E N C G Y R R
GCCAGAGTGGCTATCAAAAGCCTCACCGAAAGGCTCTACGTGCGCGGACCCCTCACCAATAGCAGAGGCGAAAAGTGTGGCTATAGGAGA

HepC1a #39

C V I G G A G N N T L H C P T D C F R K H P E A T Y S R C G
TGCGTCATCGGAGGCGCTGGCAATAACACACTGCATTGCCCTACCGATTGCTTTAGGAAACACCCCTGAGGCTACCTATAGCAGATGCGGA

HepC1a #76

T C G S S D L Y L V T R H A D V I P V R R R G D S R G S L L
ACCTGTGGCTCCAGCGATCTGTATCTGGTCACCAGACAGCTGACGTCATCCCTGTGAGAAGGAGAGGCGATAGCAGAGGCTCCCTGCTC

HepC1a #138

N M W S G T F P I N A Y T T G P C T P L P A P N Y T F A L W
AACATGTGGTCCGGCACATTCCTTATCAATGCCTATACCACAGGCCCTTGACACCCCTCCCGCTCCCAATTACACATTGCTCTGTGG

HepC1a #89

H S T D A T S I L G I G T V L D Q A E T A G A R L V V L A T
CACTCCACCGATGCCACAAGCATCTGGGAATCGGAACCGTCTGGATCAGGCTGAGACAGCCGAGCCAGACTGGTCGTGCTCGCCACA

HepC1a #130

Y V P E S D A A A R V T A I L S S L T V T Q L L R R L H Q W
TACGTCCCCGAAAGCGATGCCGCTGCCAGAGTGACAGCCATTCTGTCCAGCCTCACCGTCACCCAAGTCTCAGGAGACTGCATCAGTGG

HepC1a #8

R P S W G P T D P R R R S R N L G K V I D T L T C G F A D L
AGGCCCTAGCTGGGGCCCTACCGATCCCAGAAGGAGAAGCAGAAACCTCGGCAAGTGATTGACACACTGACATGCGGATTGCTGACCTC

HepC1a #33

G P D Q R P Y C W H Y P P K P C G I V P A K S V C G P V Y C
GGCCCTGACCAAAGGCCTTACTGTTGGCATTACCTCCCAAACCTGTGGCATTGTGCCTGCCAAAAGCGTCTGCGGACCCGTCTACTGT

HepC1a #115

E E C S Q H L P Y I E Q G M M L A E Q F K Q K A L G L L Q T
GAGGAATGCTCCAGCATCTGCCTTACATTGAGCAAGGCATGATGCTCGCCGAACAGTTTAAGCAAAAGGCTCTGGGACTGCTCCAGACA

HepC1a #107

Y Q A T V C A R A Q A P P P S W D Q M W K C L I R L K P T L
TACCAAGCCACAGTGTGTGCCAGAGCCCAGCCCTCCCCCTAGCTGGGACCAATGTGGAAGTGTCTGATTAGGCTCAAGCCTACCCCTC

HepC1a #34

C G I V P A K S V C G P V Y C F T P S P V V V G T T D R S G
TGCGGAATCGTCCCCGCTAAGTCCGTGTGTGGCCCTGTGTATTGCTTTACCCCTAGCCCTGTGGTCTGTGGGAACCACAGACAGAAGCGGA

HepC1a #131

S S L T V T Q L L R R L H Q W I S S E C T T P C S G S W L R
AGCTCCCTGACAGTGACACAGCTCCTGAGAAGGCTCCACCAATGGATTAGCTCCGAGTGACCAACCCCTGTAGCGGAAGCTGGCTGAGA

HepC1a #161

D L S D G S W S T V S S E A G T E D V V C C S M S Y S W T G
GACCTCAGCGATGGCTCCTGGTCCACCTCAGCTCCGAGGCTGGCACAGAGGATGTGGTCTGCTGTAGCATGAGCTATAGCTGGACCGGA

HepC1a #108

W D Q M W K C L I R L K P T L H G P T P L L Y R L G A V Q N
TGGGATCAGATGTGGAATGCCTCATCAGACTGAAACCCACACTGCATGGCCCTACCCCTGCTCTACAGACTGGGAGCCGTCCAGAAT

Figure 26 (Cont)

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HepC1a #116

L A E Q F K Q K A L G L L Q T A S R Q A E V I A P A V Q T N
CTGGCTGAGCAATTCAAACAGAAAGCCCTCGGCCTCCTGCAAACCGCTAGCAGACAGGCTGAGGTCATCGCTCCCGCTGTGCAAACCAAT

HepC1a #118

W Q K L E V F W A K H M W N F I S G I Q Y L A G L S T L P G
TGGCAAAAGCTCGAGGTCTTCTGGGCCAAACACATGTGGAATTTTCATTAGCGGAATCCAATACCTCGCCGGACTGTCCACCCTCCCCGGA

HepC1a #129

L I A F A S R G N H V S P T H Y V P E S D A A A R V T A I L
CTGATTGCCTTTGCCTCCAGGGGAAACCATGTGTCCCCACACACTATGTGCCTGAGTCCGACGCTGCCGCTAGGGTCACCGCTATCCTC

HepC1a #19

A T L C S A L Y V G D L C G S V F L V G Q L F T F S P R R H
GCCCACTGTGTAGCGCTCTGTATGTGGGAGACCTCTGCGGAAGCGTCTTCTCGTGGGACAGCTCTTCACATTCTCCCCAGAGGCAT

HepC1a #102

S S V L C E C Y D A G C A W Y E L T P A E T T V R L R A Y M
AGTCCGTGCTCTGCGAATGCTATGACGCTGGCTGTGCCTGGTACGAAGTACACCCGCTGAGACAACCGTCAGGCTCAGGGCTTACATG

HepC1a #122

G W V A A Q L A A P G A A T A F V G A G L A G A A I G S V G
GGCTGGGTGGCTGCCCACTGGCTGCCCTGGCGCTGCCACAGCCTTTGTGGGAGCCGGACTGGCTGGCGCTGCCATTGGCTCCGTGGGA

HepC1a #29

S W H I N S T A L N C N E S L N T G W L A G L F Y Q H K F N
AGCTGGCACATTAACCTCCACCGCTCTGAATTGCAATGAGTCCCTGAATACCGGATGGCTCGCCGGACTGTTTTACCAACACAAATTCAAT

HepC1a #164

N A L S N S L L R H H N L V Y S T T S R S A C Q R Q K K V T
AAGCTCTGTCCAACCTCCCTGCTCAGGCATCACAATCTGGTCTACTCCACCACAAGCAGAAGCGCTTGCCAAAGGCAAAAGAAAGTGACA

HepC1a #1

A A M S T N P K P Q R K T K R N T N R R P Q D V K F P G G G
GCCGCTATGTCCCAATCCCAACCCCAAGGAAAACCAAAAGGAATACCAATAGGAGACCCCAAGACGTCAAGTTTCCCGAGGCGGA

HepC1a #106

S Q T K Q S G E N F P Y L V A Y Q A T V C A R A Q A P P P S
AGCCAAACCAACAGTCCGGCGAAAACCTTTCCCTATCTGGTTCGCCTATCAGGCTACCGTCTGCGCTAGGGCTCAGGCTCCCCCTCCCTCC

HepC1a #36

A P T Y S W G A N D T D V F V L N N T R P P L G N W F G C T
GCCCCACCTATAGCTGGGGCGTAACGATACCGATGTGTTTGTGCTCAACAATACCAGACCCCTCTGGGAAACTGGTTCGGATGCACA

HepC1a #156

V P P P R K K R T V V L T E S T L S T A L A E L A T K S F G
GTGCCTCCCCCTAGGAAAAAGAGAACCGTTCGTGCTCACCGAAAGCACACTGTCCACCGCTCTGGCTGAGCTCGCCACAAAGTCCTTCGGA

HepC1a #165

S T T S R S A C Q R Q K K V T F D R L Q V L D S H Y Q D V L
AGCACAACTCCAGGTCCGCCTGTCTAGAGACAGAAAAAGGTACCTTTGACAGACTGCAAGTGCTCGACTCCCCTATCAGGATGTGCTC

HepC1a #90

D Q A E T A G A R L V V L A T A T P P G S V T V P H P N I E
GACCAAGCCGAAACCGCTGGCGCTAGGCTCGTGGTCTGCTACCGCTACCCCTCCCGGAAGCGTCACCGTCCCCCATCCAATATCGAA

HepC1a #141

F H Y V T G M T T D N L K C P C Q V P S P E F F T E L D G V
TTCCATTACGTCACCGGAATGACAACCGATAACCTCAAGTGTCCCTGTACAGTCCCTCCCCGAATTCTTTACCGAACTGGATGGCGTC

HepC1a #198

L K L T P I A A A G R L D L S G W F T A G Y S G G D I Y H S
CTGAAACTGACACCCATTGCGCTGCCGGAAGGCTCGACCTCAGCGGATGGTTTACCGCTGGCTATAGCGGAGGCGATATCTATCACTCC

HepC1a #117

A S R Q A E V I A P A V Q T N W Q K L E V F W A K H M W N F
GCCTCCAGGCAAGCCGAGTGATTGCCCTGCCGTCCAGACAACTGGCAGAAACTGGAAGTGTTTTGGGCTAAGCATATGTGGAACTTT

HepC1a #181

C R A S G V L T T S C G N T L T C Y I K A R A A C R A A G L
TGCAGAGCCTCCGGCGTCTGTGACAACCTCCTGCGGAAACACACTGACATGTATATCAAAGCCAGAGCCGCTTGACAGAGCCGCTGGCCTC

Figure 26 (Cont)

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HepC1a #166

F D R L Q V L D S H Y Q D V L K E V K A A A S K V K A N L L
TTCGATAGGCTCCAGGTCTGGATAGCCATTACCAAGACGTCTGAAAGAGGTCAAGGCTGCCGCTAGCAAAGTGAAAGCCAATCTGCTC

HepC1a #180

G P L T N S R G E N C G Y R R C R A S G V L T T S C G N T L
GGCCCTCTGACAAACTCCAGGGGAGAGAATTGCGGATACAGAAGGTGTAGGGCTAGCGGAGTGCTCACCACAAGCTGTGGCAATACCCCTC

HepC1a #136

I M H T R C H C G A E I T G H V K N G T M R I V G P R T C R
ATCATGCACACAAGGTGTCACTGTGGCGCTGAGATTACCGGACACGTCAAGAATGGCACAATGAGAATCGTCGGCCCTAGGACATGCAGA

HepC1a #144

E V S F R V G L H E Y P V G S Q L P C E P E P D V A V L T S
GAGGTCAGCTTTAGGGTCGGCCTCCACGAATACCCTGTGGGAAGCCAACCTGCCTTGCGAACCCGAACCCGATGTGGCTGTGCTCACCTCC

HepC1a #167

K E V K A A A S K V K A N L L S V E E A C S L T P P H S A K
AAGGAAGTGAAAGCCGCTGCCTCCAAGGTCAAGGCTAACCTCCTGTCCGTGGAAGAGGCTTGCTCCCTGACACCCCTCACTCCGCCAAA

HepC1a #59

G R D A V I L L M C V V H P T L V F D I T K L L L A V F G P
GGCAGAGACGCTGTGATTCTGCTCATGTGTGTGGTCCACCCTACCCTCGTGTGTTGACATTACCAAACCTGCTCCTGGCTGTGTTGGCCCT

HepC1a #146

M L T D P S H I T A E A A G R R L A R G S P P S M A S S S A
ATGCTCACGATCCCTCCCACATTACCGCTGAGGCTGCCGGAAGGAGACTGGCTAGGGGAAGCCCTCCCTCCATGGCTAGCTCCAGCGCT

HepC1a #78

S P R P I S Y L K G S S G G P L L C P A G H A V G I F R A A
AGCCCTAGGCCTATCTCCTACCTCAAGGGAAGCTCCGGCGGACCCCTCCTGTGTCCCGCTGGCCATGCCGTGGCATTTCAGAGCCGCT

HepC1a #32

D F D Q G W G P I S Y A N G S G P D Q R P Y C W H Y P P K P
GACTTTGACCAAGGCTGGGGCCCTATCTCTACGCTAACGGAAGCGGACCCGATCAGAGACCCTATTGCTGGCACTATCCCCCTAAGCCT

HepC1a #128

R H V G P G E G A V Q W M N R L I A F A S R G N H V S P T H
AGGCATGTGGGACCCGGAGAGGGAGCCGTCCAGTGGATGAATAGGCTCATCGCTTTCGCTAGCAGAGGCAATCACGTCAGCCCTACCCAT

HepC1a #50

C L W M M L L I S Q A E A A L E N L V I L N A A S L A G T H
TGCCTCTGGATGCTCCTGATTAGCCAAGCCGAAGCCGCTCTGGAACCTCGTGATTCTGAATGCCGCTAGCCTCGCCGGAACCCAT

HepC1a #114

I I P D R E V L Y R E F D E M E E C S Q H L P Y I E Q G M M
ATCATTCCCGATAGGGAAGTGCTCTACAGAGAGTTTGACGAAATGGAAGAGTGTAGCCAACACCTCCCCCTATATCGAACAGGGAATGATG

HepC1a #47

L I H L H Q N I V D V Q Y L Y G V G S S I A S W A I K W E Y
CTGATTCACCTCCACCAAAACATTGTGGATGTGCAATACCTCTACGGAGTGGGAAGCTCCATCGCTAGCTGGGCCATTAAGTGGGAGTAT

HepC1a #200

V S H A R P R W F W F C L L L L A A G V G I Y L L P N R A A
GTGTCCACGCTAGGCCTAGGTGTTCTGTTCTGTCTGCTCGCCGCTGGCGTCGGCATTACCTCCTGCCTAACAGAGCCGCT

HepC1a #85

A A T L G F G A Y M S K A H G I D P N I R T G V R T I T T G
GCCGCTACCCTCGGCTTTGGCGCTTACATGAGCAAAGCCCATGGCATTGACCCTAACATTAGGACAGGCGTCAGGACAATCACAACCGGA

HepC1a #62

R V Q G L L R I C A L A R K M I G G H Y V Q M A I I K L G A
AGGGTCCAGGACTGCTCAGGATTTGCGCTCTGGCTAGGAAAATGATTGGCGGACACTATGTGCAAATGGCTATCATTAAAGCTCGGCGCT

HepC1a #153

R R F A Q A L P V W A R P D Y N P P L V E T W K K P D Y E P
AGGAGATTCTGCTCAGGCTCTGCCTGTGTGGGCCAGACCCGATTACAATCCCCCTCTGGTCGAGACATGGAAAAGCCTGACTATGAGCCT

HepC1a #72

T A A Q T F L A T C I N G V C W T V Y H G A G T R T I A S P
ACCGCTGCCCAAACCTTTCTGGCTACCTGTATCAATGGCGTCTGCTGGACCGCTACCATGGCGCTGGCACAAGGACAATCGCTAGCCCT

HepC1a #65

Figure 26 (Cont)

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W A H N G L R D L A V A V E P V V F S Q M E T K L I T W G A
TGGGCTCACAATGGCCTCAGGGATCTGGCTGTGGCTGTGGAACCCGTCGTGTTTAGCCAAATGGAAACAAACTGATTACCTGGGGCGCT

HepC1a #74
K G P V I Q M Y T N V D Q D L V G W P A P Q G S R S L T P C
AAGGGACCCGTCATCCAAATGTATACCAATGTGGATCAGGATCTGGTCGGCTGGCCCGCTCCCCAAGGCTCCAGGTCCCTGACACCCGT

HepC1a #151
K V V I L D S F D P L V A E E D E R E I S V P A E I L R K S
AAGGTCGTGATTCTGGATAGCTTTGACCCTCTGGTCGCCGAAGAGGATGAGAGAGAGATTAGCGTCCCCGCTGAGATTCTGAGAAAGTCC

HepC1a #64
L T G T Y V Y N H L T P L R D W A H N G L R D L A V A V E P
CTGACAGGCACATACGTCTACAATCACCTCACCCCTCTGAGAGACTGGGCCCATACGGACTGAGAGACCTCGCCGTCGCCGTCGAGCCT

HepC1a #80
V C T R G V A K A V D F I P V E N L E T T M R S P V F T D N
GTGTGTACCAGAGGCGTCGCCAAAGCCGTCGACTTTATCCCTGTGGAACCTCGAGACAACCATGAGGTCCCCCGCTCTTACAGACAAT

HepC1a #95
A L G I N A V A Y Y R G L D V S V I P T S G D V V V V A T D
GCCCTCGGCATTACGCTGTGGCTTACTATAGGGGACTGGATGTGTCCGTGATTCCACAAAGCGGAGACGTCGTGGTCGTGGCTACCGAT

HepC1a #111
M S A D L E V V T S T W V L V G G V L A A L A A Y C L S T G
ATGTCCGCGCATCTGGAAGTGGTCACCTCCACCTGGGTGCTCGTGGGAGGCGTCTGGCTGCCCTCGCCGCTTACTGTCTGTCCACCGGA

HepC1a #97
A L M T G Y T G D F D S V I D C N T C V T Q T V D F S L D P
GCCCTCATGACAGGCTATACCGGAGACTTTGACTCCGTGATTGACTGTAACACATGCGTCACCCAAACCGTCGACTTTAGCCTCGACCT

HepC1a #2
N T N R R P Q D V K F P G G G Q I V G G V Y L L P R R G P R
AACACAAACAGAAGGCCCTCAGGATGTGAAATTCCTGGCGGAGGCCAAATCGTCGGCGGAGTGTATCTGCTCCCAAGGGGACCCAGA

HepC1a #11
R A L A H G V R V L E D G V N Y A T G N L P G C S F S I F L
AGGGCTCTGGCTCACGGAGTGAGAGTGCTCGAGGATGGCGTCAACTATGCCACAGGCAATCTGCCTGGCTGTAGCTTTAGCATTTTCCTC

HepC1a #169
S K F G Y G A K D V R C H A R K A V A H I N S V W K D L L E
AGCAAATTCGATACGGAGCCAAAGACGTCAGGTGTCACGCTAGGAAAGCCGTCGCCCATATCAATAGCGTCTGGAAGACCTCCTGGAA

HepC1a #28
T P G A K Q N I Q L I N T N G S W H I N S T A L N C N E S L
ACCCCTGGCGCTAAGCAAAACATTGAGCTCATCAATACCAATGGCTCCTGGCATATCAATAGCAAGCCCTCAACTGTAACGAAAGCCTC

HepC1a #30
N T G W L A G L F Y Q H K F N S S G C P E R L A S C R R L T
AACACAGGCTGGCTGGCTGGCTCTTCTATCAGCATAAGTTTAACCTCCAGCGGATGCCCTGAGAGACTGGCTAGCTGTAGGAGACTGACA

HepC1a #49
V V L L F L L L A D A R V C S C L W M M L L I S Q A E A A L
GTGGTCCTGCTCTTCTCCTGCTCGCCGATGCCAGAGTGTGTAGCTGTCTGTGGATGATGCTGCTCATCTCCAGGCTGAGGCTGCCCTC

HepC1a #192
D C E I Y G A C Y S I E P L D L P P I I Q R L H G L S A F S
GACTGTGAGATTTACGGAGCCTGTTACTCCATCGAACCCCTCGACCTCCCCCTATCATTCAGAGACTGCATGGCCTCAGCGCTTTCTCC

HepC1a #73
W T V Y H G A G T R T I A S P K G P V I Q M Y T N V D Q D L
TGGACAGTGTATACCGGAGCCGGAACCAAGAACCATGCTCCCCCAAGGCCCTGTGATTGAGATGTACACAAACGTCGACCAAGACCTC

HepC1a #101
Y R F V A P G E R P S G M F D S S V L C E C Y D A G C A W Y
TACAGATTGCTCGCCCTGGCGAAAGGCTAGCGGAATGTTTGACTCCAGCGTCTGTGTGAGTGTACGATGCCGGATGCGCTTGGTAT

HepC1a #45
R S E L S P L L L S T T Q W Q V L P C S F T T L P A L S T G
AGGTCCGAGCTCAGCCCTCTGCTCCTGTCCACCACACAGTGGCAGGTCTGCTTGTCTCTTACAACCCCTCCCCGCTCTGTCCACCGGA

HepC1a #195
L R K L G V P P L R A W R H R A R S V R A R L L A R G G R A

Figure 26 (Cont)

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CTGAGAAAGCTCGGCGTCCCCCTCTGAGAGCCTGGAGGCATAGGGCTAGGTCCGTGAGAGCCAGACTGCTCGCCAGAGGCGGAAGGGCT

HepC1a #121

S P L T T S Q T L L F N I L G G W V A A Q L A A P G A A T A
AGCCCTCTGACAACCTCCAGACACTGCTCTTCAATATCCTCGGCGGATGGGTGCGCGCTCAGCTCGCCGCTCCCGAGCCGCTACCGCT

HepC1a #61

L W I L Q A S L L K V P Y F V R V Q G L L R I C A L A R K M
CTGTGGATCCTCCAGGCTAGCCTCCTGAAAGTGCCTTACTTTGTGAGAGTGCAAGGCCTCCTGAGAATCTGTGCCCTCGCCAGAAAGATG

HepC1a #137

V K N G T M R I V G P R T C R N M W S G T F P I N A Y T T G
GTGAAAAACGGAACCATGAGGATTGTGGGACCCAGAACCTGTAGGAATATGTGGAGCGGAACCTTTCCCATTAACGCTTACACAACCGGA

HepC1a #92

E V A L S T T G E I P F Y G K A I P L E V I K G G R H L I F
GAGGTGCGCCTCAGCACAAACCGAGAGATTCCCTTTTACGGAAAGGCTATCCCTCTGGAAGTGATTAAGGGAGGCAGACACCTCATCTTT

HepC1a #188

L T R D P T T P L A R A A W E T A R H T P V N S W L G N I I
CTGACAAGGGATCCCACAACCCCTCTGGCTAGGGCTGCCTGGGAGACAGCCAGACACACACCCGTCAACTCCTGGCTCGGCAATATCATTT

HepC1a #140

R V S A E E Y V E I R R V G D F H Y V T G M T T D N L K C P
AGGGTCAGCGCTGAGGAATACGTCGAGATTAGGAGAGTGGGAGACTTTCATATGTGACAGGCATGACCACAGACAATCTGAAATGCCTT

HepC1a #155

P V V H G C P L P P P R S P P V P P P R K K R T V V L T E S
CCCGTCGTGCTAGGCTGTCCCCTCCCCCTCCCAAGCCCTCCCGTCCCCCTCCCAAGAAAAGGACAGTGGTCTGACAGAGTCC

HepC1a #157

T L S T A L A E L A T K S F G S S S T S G I T G D N T T T S
ACCCTCAGCACAGCCCTCGCCGAAGTGGCTACCAAAAGCTTTGGCTCCAGCTCCACCTCCGGCATTACCGGAGACAATACCACAACCTCC

HepC1a #135

V S C Q R G Y K G V W R G D G I M H T R C H C G A E I T G H
GTGTCTGCCAAAGGGGATACAAAGGCGTCTGGAGAGGCGATGGCATTATGCATACCAGATGCCATTGCGGAGCCGAAATCACAGGCCAT

HepC1a #20

V F L V G Q L F T F S P R R H W T T Q G C N C S I Y P G H I
GTGTTTCTGTGCGGCCAACTGTTTACCTTTAGCCCTAGGAGACACTGGACCACACAGGGATGCAATTGCTCCATCTATCCCGGACACATT

HepC1a #123

F V G A G L A G A A I G S V G L G K V L V D I L A G Y G A G
TTCGTGCGCGCTGGCCTCGCCGAGCCGCTATCGGAAGCGTCGGCCTCGGCAAAGTGCTCGTGGATATCCTCGCCGGATACGGAGCCGGA

HepC1a #133

D I W D W I C E V L S D F K T W L K A K L M P Q L P G I P F
GACATTTGGGATTGGATTGCGAAGTGCTCAGCGATTTCAAACCTGGCTGAAAGCCAACTGATGCCCCAACTGCCTGGCATTTCCCTTT

HepC1a #15

N S S I V Y E A A D A I L H T P G C V P C V R E G N A S R C
AACTCCAGCATTTGTATGAGGCTGCCGATGCCATTCTGCATACCCCTGGCTGTGTGCCCTTGCCTCAGGGAAGGCAATGCCTCCAGGTGT

HepC1a #31

S S G C P E R L A S C R R L T D F D Q G W G P I S Y A N G S
AGCTCCGGCTGTCCCGAAAGGCTCGCCTCCTGCAGAAGGCTCACCGATTTGATCAGGGATGGGGACCCATTAGCTATGCCAATGGCTCC

HepC1a #178

R T E E A I Y Q C C D L D P Q A R V A I K S L T E R L Y V G
AGGACAGAGGAAGCCATTTACCAATGCTGTGACCTCGACCCTCAGGCTAGGGTCGCCATTAAAGTCCCTGACAGAGAGACTGTATGTGGGA

HepC1a #69

V S K G W R L L A P I T A Y A Q Q T R G L L G C I I T S L T
GTGTCCAAGGGATGGAGACTGCTCGCCCCTATCACAGCCTATGCCCAACAGACAAGGGGACTGCTCGGCTGTATCATTACCTCCCTGACA

HepC1a #191

F F S V L I A R D Q L E Q A L D C E I Y G A C Y S I E P L D
TTCTTTAGCGTCTGATTGCCAGAGACCAACTGGAACAGGCTCTGGATTGCGAAATCTATGGCGCTTGCTATAGCATTGAGCCTCTGGAT

HepC1a #142

C Q V P S P E F F T E L D G V R L H R F A P P C K P L L R E
TGCCAAGTGCCTAGCCCTGAGTTTTTACAGAGCTCGACGGAGTGAGACTGCATAGGTTTGCCCCCTCCCTGTAAGCCTCTGCTCAGGGAA

Figure 26 (Cont)

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HepC1a #182

T C Y I K A R A A C R A A G L Q D C T M L V C G D D L V V I
ACCTGTTACATTAAGGCTAGGGCTGCCGTGTAGGGCTGCCGGACTGCAAGACTGTACCATGCTGGTCTGCGGAGACGATCTGGTCGTGATT

HepC1a #86

I D P N I R T G V R T I T T G S P I T Y S T Y G K F L A D G
ATCGATCCCAATATCAGAACCGGAGTGAGAACCATTACCACAGGCTCCCCATTACCTATAGCACATACGGAAGTTTCTGGCTGACGGA

HepC1a #44

C N W T R G E R C D L E D R D R S E L S P L L L S T T Q W Q
TGCAATTGGACAAGGGGAGAGAGATGCGATCTGGAAGACAGAGACAGAAGCGAACTGTCCCCCTCCTGCTCAGCACAAACCAATGGCAA

HepC1a #22

T G H R M A W D M M M N W S P T A A L V M A Q L L R I P Q A
ACCGGACACAGAATGGCTTGGGATATGATGATGAATTGGTCCCCACAGCCGCTCTGGTCATGGCTCAGCTCCTGAGAATCCCTCAGGCT

HepC1a #127

P G A L V V G V V C A A I L R R H V G P G E G A V Q W M N R
CCCGGAGCCCTCGTGGTCGGCGTCGTGTGTGCCGTATCCTCAGGAGACACGTCGGCCCTGGCGAAGGCGCTGTGCAATGGATGAACAGA

HepC1a #149

H D S P D A E L I E A N L L W R Q E M G G N I T R V E S E N
CAGATAGCCCTGACGCTGAGCTCATCGAAGCAATCTGCTCTGGAGACAGGAAATGGGAGGCAATATACAAGGGTCGAGTCCGAGAAT

HepC1a #105

E G V F T G L T H I D A H F L S Q T K Q S G E N F P Y L V A
GAGGGAGTGTTTACCGGACTGACACACATTGACGCTCACTTCTGTGCCAGACAAAGCAAAGCGGAGAGAATTTCCCTTACCTCGTGGCT

HepC1a #5

R G R R Q P I P K A R R P E G R T W A Q P G Y P W P L Y G N
AGGGGAAGGAGACAGCCTATCCCTAAGGCTAGGAGACCCGAAGGCAGAACCTGGGCCCAACCCGGATACCTTGGCCTCTGTATGGCAAT

HepC1a #173

L I V F P D L G V R V C E K M A L Y D V V S K L P L A V M G
CTGATTGTGTTTCCCGATCTGGGAGTGAGAGTGTTGTGAGAAAATGGCTCTGTATGACGTCGTGTCCAAGCTCCCCCTCGCCGTCATGGGA

HepC1a #12

Y A T G N L P G C S F S I F L L A L L S C L T V P A S A Y Q
TACGCTACCGGAAACCTCCCCGATGCTCCTTCTCCATCTTCTGCTCGCCCTCCTGTCTGCTCACCCTCCCCGCTAGCGCTTACCAA

HepC1a #124

L G K V L V D I L A G Y G A G V A G A L V A F K I M S G E V
CTGGGAAAGGTCTGTGCGACATTCTGGCTGGCTATGGCGCTGGCGTCGCCGGAGCCCTCGTGGCTTTCAAATCATGAGCGGAGAGGTC

HepC1a #160

S Y S S M P P L E G E P G D P D L S D G S W S T V S S E A G
AGCTATAGCTCCATGCCTCCCCCTCGAGGGAGAGCCTGGCGATCCCGATCTGTCCGACGGAAGCTGGAGCACAGTGTCCAGCGAAGCCGGA

HepC1a #150

R Q E M G G N I T R V E S E N K V V I L D S F D P L V A E E
AGGCAAGAGATGGGCGGAAACATTACCAGAGTGGAAGCGAAACAAAGTGGTCATCCTCGACTCCTTCGATCCCTCGTGGCTGAGGAA

HepC1a #75

V G W P A P Q G S R S L T P C T C G S S D L Y L V T R H A D
GTGGGATGGCTGCCCTCAGGGAAGCAGAAGCCTCACCCCTTGACATGCGGAAGCTCCGACCTCTACCTCGTGACAAGGCATGCCGAT

HepC1a #88

G C S G G A Y D I I I C D E C H S T D A T S I L G I G T V L
GGCTGTAGCGGAGGCGCTTACGATATCATATCTGTGACGAATGCCATAGCACAGACGCTACCTCCATCCTCGGCATTGGCACAGTGCTC

HepC1a #99

T F T I E T T T L P Q D A V S R T Q R R G R T G R G K P G I
ACTTTACCATTTAGACAACCACACTGCCTCAGGATGCCGTGAGCAGAACCCAAAGGAGAGGAGAGAACCGGAAGGGGAAAGCCCTGGCATT

HepC1a #40

D C F R K H P E A T Y S R C G S G P W I T P R C L V D Y P Y
GACTGTTTCAGAAAGCATCCCGAAGCCACATACTCCAGGTGTGGCTCGGCCCTTGGAATTACCCCTAGGTGTCTGGTCGACTATCCCTAT

HepC1a #201

L A A G V G I Y L L P N R A A
CTGGCTGCCGGAGTGGGAATCTATCTGCTCCCAATAGGGCTGCC

Figure 26 (Cont)

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HepC1a #163

A L V T P C A A E E Q K L P I N A L S N S L L R H H N L V Y
GCCCTCGTGACACCTGTGCCGTGAGGAACAGAACTGCTATCAATGCCCTCAGCAATAGCCTCCTGAGACACCATAACCTCGTGTAT

HepC1a #132

I S S E C T T P C S G S W L R D I W D W I C E V L S D F K T
ATCTCCAGCGAATGCACAACCCCTTGCTCGGCTCCTGGCTCAGGGATATCTGGGACTGGATCTGTGAGGTCTGTCCGACTTTAAGACA

HepC1a #134

W L K A K L M P Q L P G I P F V S C Q R G Y K G V W R G D G
TGGCTCAAGGCTAAGCTCATGCTCAGCTCCCGGAATCCCTTTCGTGAGCTGTGAGAGGCTATAAGGGAGTGTGAGGGGAGACGGA

HepC1a #41

S G P W I T P R C L V D Y P Y R L W H Y P C T I N Y T I F K
AGCGGACCCTGGATCACACCAGATGCCCTCGTGGATTACCTTACAGACTLGGGCACTATCCCTGTACCATTAACTATACCATT'TTCAA

Artificial Protein:

VIPVRRRGDSRGSLLSPRPISYLLKSSSGGPARRGREILLGPADGMVSKGWRLAPITAYARLHRFAPPCKPLLREEVSFRVGLHHEYVPGSVVFSQMET
KLITWGADTAACGDIINGLPVSLLCFAGHAVGIFRAAVCTRGVAKAVDFIPVCCVIVGRIVLSGKPAIIPDREVLYREFDEMPCTPLPAPNYTFALWR
VSAHEYVEIRRVGDALYDVVSKLPLAVMGSSYGFQYSPGQQRVEFISWCLWWLQYFLTRVEAQLHVWVPLNVVRGENLVILNAASLAGTHGLVSFLVFF
CFAWYLLPPIIQRLHGLSAFSLHSYSPGEINRVAACNPPLVETWKKPDYEPFVVHGCPLPPRSPFGVSSIASWAIKWEYVVLFLLLADARVCSLN
NTRPPLGNWFGCTWMNSTGFTKVCGAPPFTEAMTRYSAAPPDPPQPEYDLELITSCSSWPLLLLALLALPQRAYALDTEVAASCGGVVLQQTRGLLGCI
ITSLTGRDNKQVEGEVQIVSSSPPAVPQSFQVAHLHAPTGSKSTKVPAANPGLPVCQDHLDFWEGVFTGLTHIDAHFVLVLLFAGVDAETHVTGGN
AGRTTSGLVSLLEVLTLHPVTKYIMTMSADLEVVSTWVVLVGLMALTLSPYKRYISWCLWWLQYFLTRVAICGKYLFWNAVTRTKLKLTPIAAAGR
LDLSIAYFMSVGNWAKVLVLLLFAGVDAETHVTRLARGSPSSMASSASQLSAPSLKATCTANGLVSFVFFCFWYLLKGRWVPGAVYALYGMQLPC
EPEPDVAVLTSMLTDPESHITAEAGRDSVTPIDTTIMAKNEVFCVQPEKGGKRPARYAAQGYKVLVLPNSVAATLFGGAYMSKAHGVRNSTGLYHVTN
DCPNSSIVYEADAILHTSSYGFQYSPGQQRVEFLVQAWKSKKTPMGFSDTAACGDIINGLPVSARRGREILLGPADGMSQLSAPSLKATCTANHDS
AELIEANLLWNPATASLMAFTAATVTSPLTTSQTLFFNLILGLVQAWKSKKTPMGFSYDTRCFDSTVTESDIDERISVPAEILRKSRRFAQALPVWARP
DYMFAPTLWARMILMTHFFSVLIARDQLEQALSIVPTSGDVVVVATDALMTGYTGDGDSVIDCHSKKCCDELAAKLVALGINAVAYIRGLDVLVPCSF
TTLPALSTGLIHLHQNIVDVQYLYKGRWVPGAVYALYGMWPLLLLALLALPQRAYSPITYSTYGYKFLADGGCSGGAYDIIICDECARSVRARLLARGGR
AAICGKYLFWNAVTRTKKAVAHINSVWKDLLEDVTPIDTTIMAKNEFTSPVVGTTDRSGAPTYSWGANDDTVFVPGVPCVREGNASRCVWAMTPT
VATRDGKLQDCTMLVCGDDLVVICESAGVQEDAAASLRAVAGALVAFKIMSGEVPSTEDLVNLLPALLSYDTRCFDSTVTESDIRTEEAITYCCDLDPQ
ELTPAETTURLRAYMNTPLGPVCQDHLFWPQPEYDLELITSCSSNVSVAHGAGKRVYYLGVKVIDTLTCGFADLMGYIPLVGAPLGGAAIPLLEVIK
GGRHLIFCHSKKCCDELAAKLVGGVLAALAAVCLSTGCVVIVGRIVLSGKPACESAGVQEDAAASLRAFTAMTRYSAAPPDPCWFTAGYSGGDIYHSV
SHARPRWFVCLLLSSSTSGITGDNITTSSEAPSPGCPDSDAERTQRRGRGTGRGKPGIYRFPVAPGERPSGMFDMVRMYGVEHRELAACNWRGERC
DLEDREDAQLHVWVPLNVRRGGRDAVILLMCVHPTLGVRAIRKTSERSQPRGRQPIPKARRPEGNVSVAHGAGKRVYYLFRDPTTFLARAWESE
PAPSGCPDSDAESYSSMPLEGBPGDPGGHYVQMAIILKALGTGYVNYHLTLPLRDPSTEDLVNLLPALLSGALVGVVCAAILTRILDMAGAHW
GVLAGIATLWARMILMTHFFSVLIARDQLEQALSIVPTSGDVVVVATDALMTGYTGDGDSVIDCHSKKCCDELAAKLVALGINAVAYIRGLDVLVPCSF
QLRRHIDLVLGSRWLHYPCTINYTIFKVRMYVGGVEHRELAAVFCVQPEKGGKRPARLIVFPDLGVRVCEKMMGYIPLVGAPLGGAAIPLLEVIK
DGVNGGNAGRTTSGLVSLTLPGAKQNIQLINTNGLALLSCLTVPASAYQVRNSTGLYHVTNDCPGRDNKQVEGEVQIVSTAQTFLATCINGVCPATQ
LRRHIDLVLGSRWLHYPCTINYTIFKVRMYVGGVEHRELAAVFCVQPEKGGKRPARLIVFPDLGVRVCEKMMGYIPLVGAPLGGAAIPLLEVIK
WTGALVTPCAAEQKLPALDTEVAASCGGVVLVGLMALTLSPYKRYWMNSTGFTKVCGAPPCVIGGAGNNTLHCPTSVEEACSLTPPHSAKSGFGY
GAKDVRCHARISGQYLAGLSTLPGNPAIASLMAFTAATVTVGGVYLLPRRGPRLGVRAIRKTSERSQPLHSYSPGETNRVAACCLRLGVPPLRAWR
HRTARHTPWNMSWGLNIIIMFAPTLWARMILMTHENLETTMRSVFTDNSSPAPVQSFQVAHLATPPGSVTVPHPNIEEVALSTTGEIPFYKGLVFDIT
KLLAVFGLPWLILQASLLKVYPVFTAALVMAQLLRIPQAILDMAGAHWGLVAGCNTCTVQTVDLSDPTFTIETTLTPQDAVSHGPTPLLLYRLGAVQ
NEVTLTHPVTKYIMTCAVAIKSLTERLYVGGPLTNSRGENGCGYRRCVIGGAGNNTLHCPTDCFRKHPATYSRCGCTCGSSDLVYLVTRHADVIVPVR
GDSRGLLNMWSGTFFINAYTTGPCTPLPAPNYTFALWHSTDATSLIGITVLDQAEAGARLVVLAATVVPESDAAARVTAISSLTTLVTLQLLRRLH
RPSWGPTDPRRRSRNLGKVIDTLTCGFADLGPDRPYCWHYFPKPGCIVPAKSVCEGQVYCEGQHLPIEQQMMLIAEQFKALGLLQTYQATVCA
AQAPPPSWDQMWKCLIRLKPCLGIVPAKSVCGPVYCTPSPVVGTTDRSGSSLTVTQLLRRLHQLWISSECTTPCPSGSLRDLSDGWSWTVSSEAGT
EDVVCSSMSYSWTGDMQMWKCLIRLKPCLGIVPAKSVCGPVYCTPSPVVGTTDRSGSSLTVTQLLRRLHQLWISSECTTPCPSGSLRDLSDGWSWTVSSEAGT
LSTLPLGLIAFASRGNHVSPTHYVPESDAAARVTAIATLCSALVAGDLGCVSVFLVQGLPFTFSPRRHSSVLCEDYDAGCAWYELTPAETTVRLRAYMGW
VAAQLAAPGAATAFVGAGLAGAAIGSVGSHWINTALNCNESLNTGWLGLFYQHKFNALSNLLRHHNLVYSTTSRSACQKQKVTAAMSTNPKPQ
RKTNRNTNRRPQDVKFPFGGSGTQKQSGENFFYLVAQATVCARAQAPPSAPTYSWGANDTDVFLNNTRPPLGNWFGCTVPPRKRRTVVLTSTLS
TALAELATKSGFSTTSRSACQKQKVTFDRQLVLDVSHYQVLDQAEAGARLVVLAATVPPGSVTVPHNIEFYHYVTGMTNDNLKCPQVPSPEFFTE
LDGVLKLTPIAAAGRLDLSGWFTAGYSGGDIYHSASRQAEVIAPAVQTNWQKLEVFVWAKHMMNFCRASGVLTSCGNTLTCTYIKARAACRAAGLFDRL
QVLDVSHYQVLDVKEVKAAASKVKANLLGPLTNSRGENGCGYRRCRASGVLTSCGNTLIMHTRCHCGAEITGHVKNGTMRIVGPRTCREVSFRVGLH
VGSQPLPCEPDPDVAVLTSEVKAAASKVKANLLSVEEACSLTPPHSAKGRDAVILLMCVHPTLVFDITKLLAVFGLPMLTDPSHITAEAAAGRRRLAR
SPSSMASSASPRPISYLLKSSSGGPPLCPAGHAVGIFRAADFQGWGPISYANGSGPDQRPYCWYHPKPRHVGPGEGAVQWMNRLIAFASRGNHVS
THCLWMLLIISQAEAALENLVIINAASLAGTHIIPDREVLYREFDEMEECQHLPIEQQMMLIHLHQNIVDVQYLYGVSSIASWAIKWEYVSHARP
RWFVFCLLLLAAGVGITYLLPNRAAAATLFGGAYMSKAHGIDPNIRTGVRTITTRGVQGLLRICALARKMIGGHYVQMAIILKAGRRFAQALPVWARP
YNPPLVETWKKPDYEPTEAAQTFLATCINGVCTVYHGAGTRTIAFPWAHNGRLDLAVAVEPVVFSQMETKLI TWGAKGPVIQMYTNVDQDLVGWPAPQ
GSRSLTPCKVVILDSFDPLVAEEDEREISVPAEILRKSLSLTGYVNYHLTLPLRDWAHNGRLDLAVAVEPVCTRGVAKAVDFIPVENLETTMRSVFTDN
ALGINAVAYYRGLDVSVIPTSGDVVVVATDMSADLEVVSTWVVLVGGVLAALAAVCLSTGALMTGYTGDGDSVIDCNCTVDTGLSDPNTNRPQD
VKFEGGGQIVGGVYLLPRRGPRLALAHGVRVLEDGVNYATGNLPSCSFSIFLSKPGYGAKDVRCHARKAVAHINSVWKDLLETGKAKQNIQLINTNGS
WHINSTALNCNESLNTGWLGLFYQHKFNSSSGCPELASCRLTLVLLFLLADARVCSLWMLLIISQAEAAALDCEYACACYSIEPLDLPPIIQRLH
GLASFSTVYHGAGTRTIAFPKGPVIQMYTNVDQDLRYFVAPGERPSGMFDDSVLCECYDAGCAWYRSELSPLLSSTQWQVLPDPSFTLTPALSTGLR
KLGVPLRAWRRARSVRARLLARGGRASPLTTSQTLFFNLILGWWAAQLAAPGAATLWILQASLLKVYPFVRVQGLLRICALARKMVKNGTMRIVG
PRTCRNMWSGTFFINAYTTGEVALSTTGEIPFYKKAIPLEVIKGRHLLIFLTRDPTPLARAWEETARHTPVMSWGLNIIIRVSAEEYVEIRRVGDPHY
VTGMTNDNLKCPVVGHCPLPPRSPVPPRKRRTVVLTSTLSTALAEALATKSGSSSTSGITGDNITTSVSCQRGYKGVWGRGDGIMHTRCHCGAE
ITGHVFLVGQLFTFSPRRHWTQGCNCSIYPGHIFVAGLAGAAIGSVGLGKVLVDILAGYGAGDIWDWICEVLSDFKTLWAKALMPQLPGIPFNSSI
VYBAADAILHTPGCVPCVREGNASRCSGCPERLASCRLTDFDQGWGPISYANGSRTEEAITYCCDLDPQARVAIKSLTERLYVGVSKGWRLAPIT
AYAQQTRGLLGCIITSLTFFSVLIARDQLEQALDCEIYGACYSIEPLDQCVPSPEFFTELDGVRHLRFAPPCKPLLRETCYIKARAACRAAGLQDCTM

Figure 26 (Cont)

LVCGDDLVVIIIDPNIRITGVRTITITGSPITYSTYKGLADGCNWRGERCDLEDRDRSELSPLLLSTTQWQTGHRMAWDMMMNWSPTAALVMAQLLRIP
QAPGARLVGVVCAAILRRHVPGEGAVQWMNRHDSFDAELLEANLLWRQEMGNGNITRVESENGSVFTGLTHIDAHFLSQTQKSGENFPYLVARGRRQP
IPKARPEBGTWAPQPGYPLWGLNIVFDLGRVRCEKMALYDVVSKLPLAVMGYATGNLPGCSFSIFLLALLSCLTVPASAYQKGLVLDILAGYA
GVAGALVAFKIMSGEVSYSMPPLEGEPDPLDSGWSVTSSAGRGQEMGNITRVESENKUVILDSFDPLVAEEVWGAPQGRSLTPTCTGSSDL
YLVTIRHADGCSGGAYDIIICDECHSTDATSILGIGTVLFTPTIETTTLPQDAVSRTQRRGRTGRGKPGIDCFRKHPEATYRCSGSPWITPRCLVDYPY
LVAGVGIIYLLPNRAAALLIPTCAEEQKLPINALSNSLLRRHNLVYISSECTTPCSGSWLRLDWDWICEVLSDFKTLWKAKLMPQLPGIIPFVSCQRGYK
GVWRGDGSGPWITPRCLVDYPYRLWHXYLPTCINTYITFK

1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2808

Figure 26 (Cont)

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CAGCTCAGGAGACACATTGACCTCCTGGTCGGCTCCAGGCTCTGGCATTACCTTTGCAACAATCAATTACACAATCTTTAAGGTCAGGATGTACGTCGG
CGGAGTGGAAACACAGACTGGAAGCCGCTGTGTTTTCGCTCCAGCTAGAGAAAGCGGAAGGAAACCCGCTAGGCTCATCGTCTTCCCTGACCTCGGCG
TCAGGCTCTGCGAAAAGATGATGGGATACATTCCCTCTGTTGGAGCCCTCTGGGAGGCGCTGCCAGAGCCCTCGCCCATGGCGTCAGGGTCTTGAA
GACGGAGTGAATGGCGGAAACGCTGGCAGAACCAAGCGGACTGGTCAGCCTCTGACACCCGAGGCGAAACAGAATATCCAACTGATTAAACACAA
CGGACTGGCTCTGCTCAGCTGTCTGACAGTGCCTGCCTCCGCTATCAGGTGAGGAATAGCACAGGCTCTTACCATGTGACAAACGATTGCCCTGGC
GAGACAAAAACCAAGTGGAGGCGAAGTGCAAATCGTCAGCACAGCCCTCAGCATTCTCGCCACATGCAATTAACGGAGTGTGTCCGCTACCCAA
CTGAGAAGGCATATCGATCTGCTCGTGGGAAGCGCTACCTCTGCTCGGCCCTTACGTCGGCGATCTGTGTGGCTCCACGCTCCACAGGCTCCGG
CAAAAGCACAAAGGTCCTCGCTATGCGGCTCAGGGATACAAAGTGTCTGCTCAACCCTAGCGTCAGGACATGGGCTCAGCCTGGCTATTCCT
GGCCCTCTACGGAACGAAGGCTGTGGCTGGGCGGATGGCTCTGTGCCCCAGAGGCTCCACCGAAGACGTCGTGTGTTGCTCCATGTCCTACTCC
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GGTCGGCTCATGGCTCTGACACTGTCCCCCTATTACAAAGGTATTGGATGAATCCACCGGATTCACAAAGGCTGCGGAGCCCTCCCTGTGTGA
TTGGCGGAGCGGAACATAACCTCCACTGTGCCCAAGCGTCGAGGAAGCTGTAGCCTCACCCCTCCGCATAGCGCTAAGTCCAAGTTTGGCTAT
GGCGCTAAGGATGTGAGATGCCATGCCAGAATCTCCGCTTCAGTATCTGGCTGGCCCTCAGCACACTGCCTGGCAATCCGCTAGCTAGCTCAT
GGCTTTACAGCGCTGTGACACAGATTGTGGGAGGCGTCTACCTCTGCTCCTAGGAGAGGCGCTAGGCTCGGCGTACAGGCTACCAGAAAGACAGCG
AAAGGTCACAGCTCTGCATAGCTATAGCCCTGGCGAAATCAATAGGTCGCGCTTGCCTCAGGAACTGGGAGTGCCTCCCTCAGGGCTGTGGAG
CACAAACCGCTAGGCATACCTGTGAATAGCTGGCTGGGAAACATTTATCATGTGCCAATCTCCACACTGTGGGCGCAAGATGATTCTGATGACCTATGA
GAATCTGGAACCAACATGAGAAGCCCTGTGTTTACCATAACTCCAGCCCTCCGCTGTGCTCAGTCTTCCAAGTGGCTCACCTCGCCACACCCCT
CTGGCTCCGTGACAGTGCCTCACCTTAACATTAGGAGAGTGGCTCTGTCCACACAGGCGAAATCCCTTTCTATGGCAACTGGTCTTCGATATCACA
AAGCTCTGTCTGCGCTCTTGGACCCCTCTGGATTCTGCAAGCTCCCTGTCAAGTCCCTTATTTCTGTCACCGCTGCCCTCGTGATGGCCCACT
GCTCAGGATTTCCCAAGCCATTCTGGATATGATTGCCGAGGCCATTGGGGAGTCTGCCCGGATGCAATACCTGTGTGACACAGACAGATGGATTCT
CCCTGGATCCACATTCAATCGAAACCAACCCCTCCCAAGAGCGCTGTGTCCACAGGACCCACACCCCTCCTGTATAGGCTCGGCGCTGTGCAA
AACGAAGTGACACTGACACACCTGTGACAAAGTATATGATGACCTGTGCGAGAGTGGCTATCAAAAGCCTCACCGAAAGGCTCTACGTCGGCGGAGC
CCTCACAATAGCAGAGGCGCAAACTGTGGCTATAGGATGCGTCTCAGGAGCGCTGGCAATAACACACTGCTATTTGCCATACCGATTGCTTTAGGA
AACCCCTGAGGCTACCTATAGCAGATGCGGAACCTGTGGCTCCAGCGATCTGTATCTGGTCCACAGACAGCTGACGTCATCCCTGTGAGAAGGAGA
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AATGGATTAGCTCCGAGTGTACCAACCCCTGTAGCGGAAGCTGGCTGAGAGACCTCAGCGATGGCTCCTGGTCCACCGCTCAGCTCGGAGCTGGCACA
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CTGTCCACCCTCCCGGACTGATTGCTTTGCCCTCAGGAGAAACCATGCTGTCCCAACACACTATGTGCTGAGTCCGAGCTGCCGCTGAGCTCAC
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GTGGCTCCCAACTGGCTGCCCTGGCGCTGCCACAGCCCTTTGTGGAGCGGACTGTGGCTGGCGCTGCCATTGGCTCCTGGTCCGAGAGGCTGGCATTAA
CTCCACCGCTCTGAATTGCAATGAGTCCCTGAATACCGGATGGCTCGCCGAGCTGTTTTACCAACACAAATTAATAACGCTCTGTCCAATCCCTGC
TCAGGATCACAATCTGGTCTACTCCACCAAGCAGAGCGCTGTGCCAAGGCAAAAGAGTGACAGCCGCTATGTCCACCAATCCCAACCCCAA
AGGAAACCAAAAGGAATACCAATAGGAGACCCCAAGACCTCAAGTTTTCGGGAGGCGGAAGCCAAACCAACAGTCCGCGGAAACCTTCCCTATCT
GGTCGCTATCAGGCTACCGTCTGCGCTAGGGCTCAGGCTCCCTCCCTCCGCCCCCTACCTATAGCTGAGGCGCTAACGATACCGATGTGTGTG
TCAACAATACAGACCCCTCTGGGAAGTGGTTCGGATGACAGTGCCTCCCTAGGAAAAAGAGAACCGTCTGCTCACCGAAGCAGACTGTCC
ACCGCTCTGGCTGAGCTCGCCACAAGTCTTCCGAAGCACAACCTCCAGGTCGCGCTCTGAGAGACAGAAAAAGGTCACCTTTGACAGACTGCAAGT
GCTCGACTCCCACTATCAGGATGTGCTCGACCAAGCGGAAACCGCTCCAGCTAGGCTCTGGCTCCTGGCTACCGCTACCCCTCCCGGAAGCGTCAACG
TCCCCATCCCAATATCGAATTCCATTACGTCACCGGAATGACAAACCGATAACCTCAAGTGTCCCTGTGAGTCCCTCCCGCAATTCTTTACCGAA
CTGGATGGCGCTCTGAACTGACACCCATTGCCGCTCGCGGAAGGCTCGAGCTCAGCGGATGGTTCACCGCTGGCTATAGCGGAGGCGATATCTATCA
CTCCGCTCCAGGCAAGCGAAGTGTGCCCCGCTGCGCTCGACAACTGGCAGAACTGGAAGTGTGTTGGGCTATAGCATATGTGCACTTTTGCA
GAGCCTCCGCGCTCTGACAACTCTGCGGAAACACACTGACATGCTATATCAAGCCAGAGCCGCTTGACAGAGCCGCTGGCTCTTCGATAGGCTC
CAGGTCCTGGATAGCCATTACCAAGAGCTCTGAAAGAGGTCAAGGCTGCGCTAGCAAAAGTGAAGCCAATCTGCTCGGCCCTCTGACAACTCCAG
GGGAGAGAAATTGCGGATACAGAAGGTGTAGGCTAGCGAGTGTCCACCAAGCTGTGGCAATACCCTCATCATGACACAAAGGTGTCACTGTGGCG
CTGAGATTACCGGACAGCTCAAGATGGCAATGAGATCTGTCGCGCTTAGGACATGACAGAGGTCAGCTTTAGGGTGGCGCTCCACGAATACCCT
GTGGGAAGCCAACTGCTTGGCAACCGAACCAGATGTGGCTGTGCTCACCTCAAGGAAGTGAAGCCGCTGCTCCTCAAGGTCAAGGCTAACCTCCT
GTCCGTGGAGAGGCTGTCTCCCTGACACCCCTCACTCCGCCAAGGCGAGAGCGCTGTGATTCTGCTCATGTGTGTGGTCCACCTACCTCGTGT
TTGACATTACCAAACTGCTCCTGGCTGTGTTTGGCCCTATGCTCAACCGATCCCTCCCAATTAACCGCTGAGGCTGCGGGAAGGAGACTGGCTAGGGGA
AGCCCTCCCTCCATGGCTAGCTCCAGCGCTAGCCCTAGGCTATCTCCTACCTCAAGGAAGCTCCGGCGGACCCCTCCTGTGTCCCGTGGCCATGC
CGTCGGCATTTTACAGGCGCTGACTTTGACCAAGGCTGGGGCCCTATCTCCTACGCTAACGGAAGCGGACCCGATCAGAGACCTATTGCTGGCACT
ATCCCCCTAAGCTAGGCTATGTGGACCCGAGAGGAGCGCTCCAGTGGATGAATAGGCTCATCGCTTTGCTAGCAGAGGCAATCAGCTGACGCCCT
ACCCATTGCTCTGATGATGCTCCTGATTAGCCAAAGCCGAGCCGCTCTGGAATAACCTCGTGATTCTGAATGCCGCTGAGCTCCCGGAAACCCATAT
CATTCCCGATAGGGAAGTGTCTACAGAGAGTTTACGAAATGGAAGAGTGTAGCCAACCTCCCTATATCGAACAGGGAATGATGCTGATTACCC
TCCACAAAAACATTGTGGATGTGCAATACCTCTACGGAGTGGGAAGTCCATCGTATGCTGGGCCATTAAAGTGGGAGTATGTGTCCACCGCTAGGCTC
AGTGTGTTCTGTTCTGTCTGCTCTGCTCGCGCTGGCGCTGGCAATTAACCTCTGCTGCTTAAACAGAGCCGCTGCGCTGAGCTGTGGCTGTGGCTTA
CATGAGCAAAAGCCCATGGCATTGACCCTAACATTAGGACAGGCGTCAGGACAATCAACCGGAAGGTCAGGAGCTGCTCAGGATTGTGGCTCTGG
CTAGGAAATGATTGGCGGACACTATGTGCAAAATGGCTATCATTAAGCTCGGCGCTAGGAGATTGCTCAGGCTCTGCTGTGTGGGCGAGACCCGAT
TACAACTCCCTCTGGTCTGAGACATGGAAGGCTGACTATGAGCTACCGCTGCCAAACCTTTCTGGCTACCTGTATCAATGGCGCTGTGGAC
CGTCTACCATGGCTGGCAACAGGCAATCGCTAGCCCTTGGGCTCAACATGGCTCAGGAGTCTGGCTGTGGTGTGGGACCCGCTGTGTTAGCC
AAATGGAACCAAACTGATTACCTGGGGCGCTAAGGACCCGCTCATCAAATGTATACCAATGTGGATCAGGATCTGTGTCGGCTGGCCGCTCCCAA
GGCTCCAGGTCCTGACACCCCTGTAGGTCGTGATTCTGGATAGCTTTGACCTCTGCTGCGGAGAGGATGAGAGAGAGATTAGCGTCCCGCTGGA
GATTCTGAGAAACTCCTGACAGGCAATACGCTTACAATCACCTCACCTCTGAGAGACTGGGCCCCATACCGGACTGAGAGCTCGCCCTCGCGCT
TCGAGCCTGTGTGTACCAGAGGCGCTGCCAAAGCCGCTCGACTTTATCCCTGTGGAAACCTCGAGACAACCATGAGGTCCTCCGCTCTTACAGACAAT
GCCCTCGGCATTAACGCTGTGGCTTACTATAGGGGACTGGATGTGTCCGTGATTCCCAAGCGGAGAGCTGCTGGTCTGGCTACCGATATGTCCG

Figure 26 (Cont)

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CGATCTGGAAGTGGTCACTCCACCTGGGTGCTCGTGGGAGGCGTCTGGGTGCCCTCGCCGCTTACTGTCTGTCCACCGAGCCCTCATGACAGGCT
 ATACCGGAGACTTTGACTCCGTGATTGACTGTAACACATGCGTCACCCAAACCGTCGACTTTAGCCTCGACCCCTAACACAAACAGAGGCTCAGGAT
 GTGAAATTCCTGGCGGAGGCCAAATCGTCGGCGGAGTGTATCTGCTCCCCAGAAAGGGGACCCAGAAAGGCTCTGGCTCAGCGAGTGAGAGTGTCTCGA
 GGATGGCGTCAACTATGCCACAGGCAATCTGCCTGGCTGTAGCTTTAGCATTTTCTCAGCAAATTCGAGATACGGAGCCAAAGACGTGAGGTGTACG
 CTAGGAAAGCCGTCGCCCATATCAATAGCGTCTGGAAGACCTCTGGAACCCCTGGCGCTAAGCAAAACATTGAGCTCATCAATACCAATGGCTCC
 TGGCATATCAATAGCACAGCCCTCAACTGTAAACGAAAGCCTCAACACAGGCTGGCTGGCTGGCTCTTCTATCAGCATAAGTTTAACTCCAGCGGATG
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 TCATCTCCAGGCTGAGGCTGCCCTCGACTGTGAGATTTACGGAGCTGTACTCCATCGAACCCCTCGACCTCCCCCTATCATTACAGAGCTGCAT
 GGCTCAGCGCTTTCTCTGGACAGTGTATCACGGAGCCGGAACCAAGCAACATTGCTCTCCCCAAAGGCCCTGTGATTGAGATGTACACAAACGTGGA
 CCAAGACCTCTACAGATTCTGTGCCCCCTGGCGAAAGGCCCTAGCGGAATGTTTGAATCCAGCGTCTGTGTGAGTGTACGATGCCGGATGCCCTTGGT
 ATAGGTCGAGCTCAGCCCTCTGCTCTCTGTCCACCACACAGTGGCAGGTCTCTGCTCTTCTCACAACCCCTCCCCGCTCTGTCCACCGGACTGAGA
 AAGCTCGGCGTCCCCCTCTGAGAGCCTGGAGGCATAGGGCTAGGTCCGTGAGAGCCAGACTGCTCGCCAGAGGCGGAAGGGCTAGCCCTCTGACAAAC
 CTCCAGACACTGCTCTTCAATATCTCTGGCGGATGGGTGCGCGCTCAGCTCGCCGCTCCCGGAGCCGCTACCGCTCTGTGGATCTCCAGGCTAGCC
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 CCCAGAACCTGTAGGAATATGTGGAGCGGAACCTTTCCCATTAACGCTTACACAAACCGGAGAGGTGCGCTCAGCACAACCCGAGAGATTCCTTTTA
 CGGAAAGGCTATCCCTCTGGAAGTGATTAAGGGAGGCAGACACCTCATCTTTCTGACAAGGGATCCCAACCCCTCTGGCTAGGGCTGCTGGGAGA
 CAGCCAGACACACCCGCTCAACTCTGGCTCGGCAATATCATATTAGGCTCAGCGTGAAGAAATACGTCGAGATTAGGAGAGTGGGAGACTTTCACTAT
 GTGACAGGCATGACACAGCAATCTGAAATGCCCTCCGCTCGTGATGCTCTCCCTCCCCCTCCAGAACCCCTCCGTCCTCCCTCCAGAAA
 GAAAGGACAGTGGTCTGACAGAGTCCACCTCAGCACAGCCCTCGCCGAAGTGGCTACCAAAAGCTTTGGCTCCAGCTCCACCTCCGGCATTACCG
 GAGACAATACCAACACCTCCGTGTCTGCCAAAGGGGATACAAAGGCGTCTGGAGAGGCGATGGCATTATGCATACAGATGCCATTGCGGAGCCGAA
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 GTGACCTCGACCCCTCAGGCTAGGGTCCGCAATTAAGTCCCTGACAGAGAGACTGTATGTGGAGTGTCCAAGGGATGGAGACTGCTCGCCCTATCACA
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 GGATTGCGAAATCTATGGCGCTTGCTATAGCATTGAGCCTCTGGATTGCCAAGTGCTTAGCCCTGAGTTTTTTACAGAGCTCGACGGAGTGAGACTGC
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 CAACCAATGGTCAAAACCGGACACAGAATGGCTTGGGATATGATGATGAATTTGCTCCCCACAGCCGCTCTGGTCTAGGCTCAGCTCTGAGAATCCCT
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 ATCCCTAAGGCTAGGAGACCCGAAGGACAGCTGGGCCAACCCCGGATACCTTTGGCTCTGTATGGCAATCTGATTGTGTTTCCCGATCTGGGAGT
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 CATTGGCACAGTGTCTACCTTTTACCATTGAGACAACCACTGCTCAGGATGCGCTCAGCAGAACCCAAAGGAGAGGCAACCGGAAGGGAAGG
 CTGGCATTGACTGTTTCAGAAAGCATCCCGAAGCCACATACTCCAGGTGTGGCTCCCGCCCTTGATTACCCCTAGTGTGTGGTCTGACTATCCCTAT
 CTGGCTGCGGAGTGGGAATCTATCTGCTCCCCAATAGGGCTGCGCCCTCTGTGACACCTGTGCGCTGAGGAACAGAAATGCTTATCAATGCCCT
 CAGCAATAGCCTCTGAGACACCAATAACCTCGTGTATATCTCCAGCAATGCAACACCCCTTGCTCCGGCTCTGGCTCAGGATATCTGGGACTGGA
 TCTGTGAGGTCTGTCCGACTTTAAGACATGGCTCAAGGCTAAGCTCATGCTCAGCTCCCGGAATCCCTTTCTGTGAGTGTGAGAGGCTATAAG
 GGAGTGTGGAGGGGAGACGGAAGCGGACCCCTGGATCACACCCAGATGCTCTGTGGATTACCTTTACAGACTGTGGCACTATCCCTGTACCATTAACTA
 TACCATTTCCTCAA

HepC Savine Cassette Sequences (A+B+C) with specific restriction sites removed which can be joined to generate a single expressible open reading frame that encodes the hepc Savine protein above

Cassette A

ggcggatccccaccATGGTGAATTCCTGTCAGGAGAGGGGAGACTCCAGGGGAAGCCTCTGTCCCCAGACCCATTAGC
 TATCTGAAAGGCTCCAGCGAGGCCCTGCGAGAAGGGGAAGGGAATCCTCTTGGGACCCGCTGACGGAATGGTCAGCAA
 AGGCTGGAGGCTCCTGGCTCCCATACCGCTTACGCTAGGCTCCACAGATTGCTCTCCCTTTGCAACCCCTCCTGAGAG
 AGGAAGTGTCTCTCAGAGTGGGACTCATGAGTATCCGCTCGGTGGTCTTCTCCAGATGGAGACAAAGCTCATC
 ACATGGGGAGCCGATACCGCTGCTGTGGCGATATCATTACCGACTGCTGTGTCTCTGCTCTGCTGCTGCGGACACGC
 TGTGGGAATCTTTAGGCTGCGCTGTGCAACAAGGGGAGTGGCTAAGGCTGTGGATTTTATTCCCGTCTGCGTCTGTATTG
 TGGGAAGGATTGTCTCAGCGGAAGCCCTGCCATTATCCCTGACAGAGAGGTCCTGTATAGGGAATTTGATGAGATGCCC
 TGTACCCCTCTGCTGCCCCCTAACTATACCTTTGCCCTCTGGAGAGTGTCCGCCGAAGAGTATGTGGAATCAGAGGGT
 CGCGGATGCCCTCTACGATGTGTGTCAGCAAACTGCTCTGGCTGTGATGGGCTCAGCTATGGCTTTTCACTATAGCCCTG
 GCCAAGGGCTCGAGTTTATCTCTGGTGTCTGTGGTGGCTCCAGTATTTCTCACCAGAGTGGAGCCCAACTGCTATGT
 TGGTGGCTCCCTCAACCTCAGGGGAGAGAATCTGGTCTATCTCAACGCTGCTCCCTGGCTGGCACACAGGATGGT
 CAGCTTTCTGGTCTTCTTTTGGCTTTGGCTGGTACCTCTGCTCCCTTATCCAAAGGCTCCACGGACTGTCCGCTTTA
 GCCTCCACTCTCTCTCCCGGAGAGATTAAAGAGTGGCTGCTGTAAACCTCCCTCGTGGAAACCTGGGAAGAAACCC
 GATTACGAACCCCTGTGGTCCAGGATGCCCTCTGCTCCCCCTAGGTCCCCCTGGCGTGGCTCCAGCATTTGCTC

Figure 26 (Cont)

CTGSGCTATCAAATGGGAAATACGTCTGCTCCTGTTTCTGCTCTCGGCTGACGCTAGGGTCTGCTCCCTGAATAACACAA
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ACAGAGGCTATGACAAGGTATAGCGTCTCCCCCGGCGATCCCCCTCAGGCTGAGTATGACCTCATCAACAAGCTG
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GCGGAGGCGTCTGCTGCTCCAGCAAACAGAGGCCCTCTGGGATGCATTATCAACAAGCTTACCAGGAAGGAGATAAGAATCAG
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CTCAGGAAAGAGCAGAGTTTGGCCAAAGCCCTCCCGCTGTGGCTAGGCTGACTATGTTTGGCTTACCCTTACCCTCTGGG
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ACAGAAAAGGTACCTTTGACAGACTGCAAGTGTCTGACTCCCACTATCAGGATGTGCTCGACCAAGCCGAAACCGCTG
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Figure 26 (Cont)

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Cassette C

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 GCGCTTACCAACTGGGAAAGGTCCTGGTgGatATTCTGCTGGCTATGGCGCTGGCGTCCCGGAGCCCTCGTGGCTTTT
 AAAATCATGAGCGGAGAGGTGAGCTATAGCTCCATGCCCTCCCTCGAGGAGAGGCTGGCGATCCGATCTGTGCGGAG
 AAGCTGGAGCACAGTGTCCAGCGAAGCCGGAAGGCAAGAGATGGGCGGAAACATTACCAAGTGGAAAGCGAAAAACAAAG
 TGGTTCATCTCGATCTCTCGATCCCTCGTGGCTGAGGAAGTGGGATGGCCTGCCCTCAGGGAAGCAGAAGCCTCACC
 CTTGACATGCGGAAGCTCCGACCTTACCTCGTGACAAGGCATGCCGATGGCTGTAGCGGAGGCGCTTACGATATCAT
 TATCTGTGACGAATGCCATAGCAGACGCTACCTCCCTCGGATTTGGCAGATGGCAGTGTCTCACTTTACATTTAGACAA
 CCACATGCTCAGGATGCCGTGAGCAGAACCCAAAGGAGAGGAGAACCCGAAGGGGAAAGCCTGGCATTTGACTGTTTC
 AGAAAGCATCCCGAAGCCACATACTCCAGGTGTGGCTCCGGCCCTTGGATTACCCCTAGGTGTCTGGTgGATATCCCTA
 TCTGGCTGCGGAGTGGGAATCTATCTGCTCCCAATAGGGCTGCCGCCCTCGTGACACCTGTGCGGCTGAGGAACAGA

Figure 26 (Cont)

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AACTGCCTATCAATGCCCTCAGCAATAGCCTCCTGAGACACCATAACCTCGTGTATATCTCCAGCGAATGCACAACCCCT
TGCTCCGGCTCCTGGCTCAGGGATATCTGGGACTGGATCTGTGAGGTCCTGTCCGACTTTAAGACATGGCTCAAGGCTAA
GCTCATGCCTCAGCTCCCCGGAATCCCTTTCGTGAGCTGTCAGAGAGGCTATAAGGGAGTGTGGAGGGGAGACGGAAGCG
GACCCTGGATCACACCCAGATGCCTCGTGGATTACCCTTACAGACTGTGGCACTATCCCTGTACCATTAACTATACCATT
TCAAAGatctTGAgtcgacgaattcgcc

Figure 26 (Cont)

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Melanoma Savine design

Two savines - one containing scrambled melanocyte differentiation Ags
 - one containing scrambled melanoma cancer specific Ags

Genes in melanocyte differentiation Savine

gp100

MDLVLRKCLLHLAVIGALLAVGATKVPNRQDWLGVSRQLRTKAWNRLYPEWTEAQRLLDCWRGGQVSLKVSNDGPTLI
 GANASFSIALNFFPGSQKVLDPDGQVIWVNNTIINGSQVWGGQPVYPQETDDACIFPDGGPCPSGWSQKRSFVYVWKTW
 GQYWQVLGGPVSGLSIGTGRAMLGTHTMEVTVYHRRGSRSYVPLAHSSSAFTITDQVPFVSVSQRLRALDGGNKHFLR
 NQPLTFALQLHDPGSGYLAEADLSYTWDFGDSSGTLISRALVVTHTYLEPGPVTAAQVVLQAAIPLTSCGSSPVPGTDDG
 HRPTAEAPNTTAGQVPTTEVVGTTTPGQAPTAEPSTTSVQVPTTEVISTAPVQMPSTAESTGMTPEKVPVSEVMGTTLA
 EMSTPEATGMTPAEVSIVVLSGTTAAQVTTTEWVETTARELPIPEPEGPDASSIMSTESITGSLGPLLDGTATLRLVK
 RQVPLDCVLRYGSGFSVTLDIVQGIESAEILQAVPSGEGDAFELTVSCQGGPLKEACMEISSPGCQPPAQRLLCQPVLP
 SPACQLVLHQILKGGSGTYCLNVSLADTNSLAVVSTQLIMPQGEAGLGQVPLIVGILLVLMVVLASLIYRRRLMKQD
 FSVPLPHSSSHWLRLPRIFCSCPIGENSPLLSGQQV

MART

MPREDAHFYGYPPKKGHGHSYTTAEAAAGIGILTIVILGVLLLLIGCWYCRNRNGYRALMDKSLHVGTTQCALTRRCPOEG
 FDHRDSKVSLLQEKNCPEVVPNAPPAYEKLKSAEQSPPPYSP

TRP-1

PAFLTWHRYHLLRLLEKDMQEMLQEPFSFLPYWNFATGKNVCDICTDDLMGSRSNFDSLISPNVSFVSQWRVVCDSLED
 YDTLGTLCNSTEDGPIRRNPAGNVARPMVQRLPEPQDVAQCLEVGLEFDTPPFYNSNSTNSFRNTVEGYSDPTGKYDPAV
 RSLHNLHLFLNGTGGQTHLSSQDPIFVLLHTFTDAVFDEWLRRYNADISTFPLENAPIGHNRYNMVFPFWPPVTNTE
 MFVTAPDNLGYTYE

Tyros

MLLAVLYCLLWSFQTSAGHFPRACVSSKNLMEKECCPPWSGDRSPCGQLSGRGSCQNILLSNAPLGPQFPFTGVDDRE
 SWPSVFYNRTCQCSGNFMGFNCGNCKFGFWGPNCTERRLLVRNIFDLSAFEKDKFFAYLTLAKHTISSDYVIPIGTY
 GQMKNGSTPMFNDINIYDLFVWMHYVSMALLGGSEIWRDIDFAHEAPAFPLPWHRLFLRLWEQEIQKLTGDENFTIP
 YDWRDAEKCDICTDEYMGQHPPTNPPLLSPASFSSWQIVCSRLEEYNHSHQSLCNGTPEGPLRRNPGNHDKSRTPLR
 PSSADVEFCLSLTQYESGSMKKAANFSFRNTLEGFASPLTGIADASQSSMHNALHIYMNGTMSQVQGSANDPIFLLHH
 AFVDSIFEQWLQRHRPLQEVYPEANAPIGHNRESYMVPFIPLYRNGDFFISSKDLGYDYSYLQSDSDPSFQDYIKSYL
 EQASRIWSWLLGAAMVGAULTALLAGLVSLLCRHKRQQLPEEKQPLLMEKEDYHSLYQSHL

TRP2

MSPLWWGFLLSCLGCKILPGAQQGFPRVCMTVDSLNVKECCPRLGAESANVCGSQQGRGQCTEVRADTRPWSGPYILR
 NQDDRELWPRKFFHRTCKCTGNFAGYNCGDCKFGWTGPNCERKKPPVIRQNIHSLSPQEREQFLGALDLAKRVHPDY
 VITTQHWLGLLGPNGTQPPQFANCSVYDFFVWLHYYSVRDITLLGPGRPYRAIDFSHQGPAFVTWHRYHLLCLERDLQRL
 IGNESFALPYWNFATGRNECDVCTDQLFGAARPDPTLISRNSRFSSWETVCDSDDDYNHLVTLNCTYEGLLRNQM
 GRNSMKLPITLKDIRDCLSLQKFDNPPFFQNSTFSFRNALEGFDKADGTLDSQVMSLHNLVHSLNCTNALPHSAANDP
 IFVVLHSFTDAIFDEWMKRFNPPADAWPQELAPIGHNRMYNMVPFFPPVTNEELFLTSDQLGYSYALDLPVSVEETPG
 WPTLLVVMGTLVALVGLFVLLAFLQYRRRLKGYTPLMETHLSSKRYTEEA

MC1R

MAVQGSQRLLGSLNSTPTAIPQLGLAANQTGARCLEVSISDGLFSLGLVSLVENALVVATIAKNRNLHSPMYCFIC
 CLALSDLLVSGTNVLETAVILLLEAGALVARAAVLQQLDNVIDVITCSSMLSSLCLFLGAIIVDRIYISIFYALRYHSIV
 TLPRAPRAVAIIWVASVVFSTLFIAYYDHVAVLLCLVVFFLAMLVLMVAVLYVHMLARACQHAQGIARLHKRQRPVHQG
 FGLKGAVTLTILLGIFFLCWGPFFLHLTLIVLCPEHPTCGCIFKNFNLFLALIICNAIIDPLIYAFHSQELRRTLKEV
 LTCSW

MUC1F

MTPGTQSPFFLLLLLTIVLTVVTGSGHASSTPGGEKETSATQRSSVPSSTEKNAVSMTSSVLSSHSPGSGSSTTQGDV
 TLAPATEPASGSAATWGQDVTSVPVTRPALGSTTPPAHDVTSAPDNK

Figure 27

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MUC1R

NRPALGSTAPPVHNVTASGSASGSASTLVHNGTSARATTTTPASKSTPFSIPSHHSDTPTTLASHSTKTDASSTHHSS
 VPPLTSSNHSTSPQLSTGVSFFFLSFHISNLQFNSSLEDPSTDYYQELQRDISEMFLQIYKQGGFLGLSNIKFRPGSV
 VVQLTLAFREGTINVHDVETQFNQYKTEAASRYNLTISDVSVDVPPFSAQSGAGVPGWGIALLVLCVLVALAIVY
 LIALAVCQCRKKNYGQLDIFPARDTYHPMSEYPTYHTHGRYVPPSSSTRSPYEKVSAGNGGSSLSYTNPAVAAAANL

NB Muc 1 Repeat sequences in the middle of the gene were removed

Genes in melanoma specific Savine

BAGE

MAARAVFLALSAQLLQARLMKEESPVVSWRLEPEDGTALCFIF

GAGE-1

MSWRGRSTYRPRRRYVEPPMIGPMRPEQFSDEVEPATPEEGEPATQRQDPAAQEGEGASAGQGPKPEADSQEQ
 GHPQTGCECEDGPDGQEMDPPNPEEVKTPEEEMRSHYVAQTGILWLLMNNCFNLSPRKP

gp100In4

SWSQKRSFVYVWKTWGEGLPSQPIIHTCVYFFLPDHLFGRPFHLNFCDFL

MAGE-1

MSLEQRSLSHCKPEEALAEAQOEALGLVCVQAATSSSSPLVLGTLLEEVPTAGSTDPQPQSGASAFPTTINFTRQRPSE
 GSSSREEEGPSTSCILESIFRAVITKKVADLVGFLLKRYRAREPVTKAEMLESVIKKNYKHCPEIFGKASESLQLVFG
 IDVKEADPTGHSYVLVTCGLSYDGLLDGNQIMPKTGFLIIIVLVMIAMEGGHAPEEEEIWEELSVMEVYDGREHSAYGE
 PRKLLTQDLVQEKYLEYRQVPDSDPARYEFLWGPRLAETSIVKVLEYVIKVSARVRFFFPFSLREALREEEEGV

MAGE-3

MPLEQRSQHCKPEEGLEARGEALGLVGAQAPATEEQEAASSSTLVEVTLGEVPAAESDPDPQPQSGASSLPTTMNYP
 LWSQSYEDSSNQEEEGPSTFPDLESEFQAALSARKVAELVHFLLLKRYRAREPVTKAEMLGSVVGNWQYFFPVIKSKASS
 SLQLVFGIELMEVDPIGHLYIFATCLGLSYDGLLDGNQIMPAGLLIIIVLAIAREGDCAPEEKIWEELSVLEVFEGR
 EDSILGDPKLLTQHFVQENYLEYRQVPDSDPACYEFLWGPRLVETSYVKVLHMHVKISGGPHISYPPLHEWVLREG
 EE

PRAME

MERRRLWGSIQSRYISMSVWTSPPRLVELAGQSLLKDEALAIAALELLPRELFPPLFMAAFDGRHSQTLKAMVQAWPF
 TCLPLGVLMMKGQHLHLETFAVLDGLDVLLAQEVRPRRWKLQVLDLRKNSHQDFWTVWSGNRSLSYFPEPEAAQPMT
 KKRKVDGLSTEAEQPFIPVEVLVDLFLKEGACDELFSYLIEKVKRKNVLRRLCCKKLKIFAMPMDIKMILKMOVQLDS
 IEDLEVCTCWKLPTLAKFSPYLGQMINLRLLLSHIHASSYISPEKEEQYIAQFTSQFLSLQCLQALYVDSLFFLRGR
 LDQLLRHVMNPLETSLITNCRLSEGDMHLSQSPSVSLSVLSLSGVMLTDVSPEPLQALLERASATLQDLVFDECGI
 TDDQLLALLPSLSHCSQLTTLSTFYGNSSISALQSLLOHLIGLSNLTHVLYVPVPLESYEDIHGTLHLERLAYLHARLR
 ELLCELGRPSMVWLSANPCPHCGDRFTFYDPEPILCPCFMPN

TRP2IN2

LMETHLSSKRYTEEAGGFFPWLKVVYRFFVIGLRVWQWEVISCCLKIKRATTRQP

NYNSO1a

MQAEGRGTTGGSTGDADGPGGPGIPDGPGGNAGGPGEAGATGGRGPRGAGAARASGPGGGAPRGPHGGAASGLNGCCRC
 GARGPESRLLEFYLAMPFATPMEAELARRSLAQDAPPLVPVGVLLKEFTVSGNILTIRLTAADHRQLQLSISCLQQL
 SLLMWITQCFLPVFLAQPPSGQRR

NYNSO1b

MLMAQEALAFMLAQGAMLAQERRVPRAAEVPGAQGGQGGPRGREGAPRGVRMAARLQG

LAGE1

Figure 27 (Cont)

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MQAEGQGTGGSTGDADGPGGPGIPDGPGGNAGGPGGEAGATGGRGPRGAGAARASGPRGGAPRGPHGGAASAQDGRCP
 GARRPDSRLLQLHITMPFSSPMEAELVRRILSRDAAPLPRGAVLKDFTVSGNLLFIRLTAADHRQLQLSISSCLQQL
 SLLMWITQCFLPVFLAQAPSGQRR

Differentiation Savine Scramble process

Disease name : melanoma
 Input filename : Diffmucg.txt
 Output filename : Diffmucs.txt
 Number genes : 8
 Number segments : 187
 Segment length : 30
 Segment overlap : 15

Segments in original order:

 Gene : gp100
 Segment# : 1
 Offset : 1
 1st Codon : 1
 A A M D L V L K R C L L H L A V I G A L L A V G A T K V P R
 GCCGCTATGGATCTGGTCCTGAAAAGGTGTCTGCTCCACCTCGCCGTCATCGGAGCCCTCCTGGCTGTGGGAGCCACAAAGGTCCCCAGA

Gene : gp100
 Segment# : 2
 Offset : 16
 1st Codon : 1
 V I G A L L A V G A T K V P R N Q D W L G V S R Q L R T K A
 GTGATTGGCGCTCTGCTCGCGCTCGGCGCTACCAAAGTGCTTAGGAATCAGGATTGGCTCGGCGTCAGCAGACAGCTCAGGACAAAGGCT

Gene : gp100
 Segment# : 3
 Offset : 31
 1st Codon : 1
 N Q D W L G V S R Q L R T K A W N R Q L Y P E W T E A Q R L
 AACCAAGACTGGCTGGGAGTGTCCAGGCAACTGAGAACCAAAGCCTGGAACAGACAGCTCTACCCTGAGTGGACCGAAGCCCAAAGGCTC

Gene : gp100
 Segment# : 4
 Offset : 46
 1st Codon : 1
 W N R Q L Y P E W T E A Q R L D C W R G G Q V S L K V S N D
 TGGAATAGGCAACTGTATCCCGAATGGACAGAGGCTCAGAGACTGGATTGCTGGAGGGGAGGCCAAGTGTCCCTGAAAGTGTCCAACGAT

Gene : gp100
 Segment# : 5
 Offset : 61
 1st Codon : 1
 D C W R G G Q V S L K V S N D G P T L I G A N A S F S I A L
 GACTGTGGAGAGGCGGACAGGTGAGCCTCAAGGTGAGCAATGACGGACCCACACTGATTGGCGCTAACGCTAGCTTTAGCATTGCCCTC

Gene : gp100
 Segment# : 6
 Offset : 76
 1st Codon : 1
 G P T L I G A N A S F S I A L N F P G S Q K V L P D G Q V I
 GGCCCTACCCTCATCGGAGCCAATGCCTCCTTCTCCATCGCTCTGAATTTCCCTGGCTCCAGAAAGTGTCCCCGATGGCCAAGTGATT

Gene : gp100
 Segment# : 7
 Offset : 91
 1st Codon : 1
 N F P G S Q K V L P D G Q V I W V N N T I I N G S Q V W G G
 AACTTTCCCGAAGCCCAAAGGTCTGCCTGACGGACAGGTGATCTGGGTGAATAACACAATCATTACGGAAGCCAAGTGTGGGGCGGA

Gene : gp100
 Segment# : 8
 Offset : 106
 1st Codon : 1

Figure 27 (Cont)

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W V N N T I I N G S Q V W G G Q P V Y P Q E T D D A C I F P
TGGGTCAACAATACCATTATCAATGGCTCCCAGGTCTGGGGAGGCCAACCCGTCTACCCTCAGGAAACCGATGACGCTTGCATTTTCCTC

Gene : gp100
Segment# : 9
Offset : 121
1st Codon : 1

Q P V Y P Q E T D D A C I F P D G G P C P S G S W S Q K R S
CAGCCTGTGTATCCCCAAGAGACAGACGATGCCTGTATCTTCCCGATGGCGGACCCTGTCCCTCCGGCTCCTGGTCCCAGAAAAGGTCC

Gene : gp100
Segment# : 10
Offset : 136
1st Codon : 1

D G G P C P S G S W S Q K R S F V Y V W K T W G Q Y W Q V L
GACGGAGGCCCTTGCCCTAGCGGAAGCTGGAGCCAAAAGAGAAGCTTTGTGTATGTGTGGAAGACATGGGGACAGTATTGGCAAGTGCTC

Gene : gp100
Segment# : 11
Offset : 151
1st Codon : 1

F V Y V W K T W G Q Y W Q V L G G P V S G L S I G T G R A M
TTCGTCTACGTCTGGAACCTGGGGCCAATACTGGCAGGTCTGGGAGGCCCTGTGTCCGGCCTCAGCATTTGGCACAGGCAGAGCCATG

Gene : gp100
Segment# : 12
Offset : 166
1st Codon : 1

G G P V S G L S I G T G R A M L G T H T M E V T V Y H R R G
GGCGGACCCTCAGCGGACTGTCCATCGGAACCGGAAGGGCTATGCTCGGCACACACAATGGAAGTGACAGTGTATCACAGAAGGGGA

Gene : gp100
Segment# : 13
Offset : 181
1st Codon : 1

L G T H T M E V T V Y H R R G S R S Y V P L A H S S S A F T
CTGGGAACCCATACCATTGAGGTACCCGTCTACCATAGGAGAGGCTCCAGGTCTACGTCCCCCTCGCCCATAGCTCCAGCGCTTTTACA

Gene : gp100
Segment# : 14
Offset : 196
1st Codon : 1

S R S Y V P L A H S S S A F T I T D Q V P F S V S V S Q L R
AGCAGAAGCTATGTGCCTCTGGCTCACTCCAGCTCCGCCTTTACCATTACCGATCAGGTCCCCTTTAGCGTCAGCGTCAGCCAACCTGAGA

Gene : gp100
Segment# : 15
Offset : 211
1st Codon : 1

I T D Q V P F S V S V S Q L R A L D G G N K H F L R N Q P L
ATCACAGACCAAGTGCCCTTTCTCCGTGTCCGTGTCCAGCTCAGGCTCTGGATGGCGGAAACAAACACTTTCTGAGAAACCAACCCCTC

Gene : gp100
Segment# : 16
Offset : 226
1st Codon : 1

A L D G G N K H F L R N Q P L T F A L Q L H D P S G Y L A E
GCCCTCGACGAGGCAATAAGCATTTCTCAGGAATCAGCCTCTGACATTGCTCTGCAACTGCATGACCCTAGCGGATACCTCGCCGAA

Gene : gp100
Segment# : 17
Offset : 241
1st Codon : 1

T F A L Q L H D P S G Y L A E A D L S Y T W D F G D S S G T
ACCTTTGCCCTCCAGCTCCACGATCCCTCCGGCTATCTGGCTGAGGCTGACCTCAGCTATACCTGGGACTTTGGCGATAGCTCCGGCACA

Gene : gp100
Segment# : 18
Offset : 256
1st Codon : 1

A D L S Y T W D F G D S S G T L I S R A L V V T H T Y L E P
GCCGATCTGTCTACACATGGGATTTCCGAGACTCCAGCGGAACCCCTCATCTCCAGGGCTCTGGTCGTGACACACACATACCTCGAGCCT

Figure 27 (Cont)

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Gene : gp100
Segment# : 19
Offset : 271
1st Codon : 1
L I S R A L V V T H T Y L E P G P V T A Q V V L Q A A I P L
CTGATTAGCAGAGCCCTCGTGGTCACCCATACCTATCTGGAACCCGGACCCGTCACCGCTCAGGTCGTGCTCCAGGCTGCCATTCCCCTC

Gene : gp100
Segment# : 20
Offset : 286
1st Codon : 1
G P V T A Q V V L Q A A I P L T S C G S S P V P G T T D G H
GGCCCTGTGACAGCCCAAGTGGTCCTGCAAGCCGCTATCCCTCTGACAAGCTGTGGCTCCAGCCCTGTGCCTGGCACAACCGATGGCCAT

Gene : gp100
Segment# : 21
Offset : 301
1st Codon : 1
T S C G S S P V P G T T D G H R P T A E A P N T T A G Q V P
ACCTCCTGCGGAAGCTCCCCGTCGCCGAACACAGACGGACACAGACCCACAGCCGAAGCCCTAACACAACCGCTGGCCAAGTGCCT

Gene : gp100
Segment# : 22
Offset : 316
1st Codon : 1
R P T A E A P N T T A G Q V P T T E V V G T T P G Q A P T A
AGGCCTACCGCTGAGGCTCCCAATACCACAGCCGGACAGGTCCCCACAACCGAAGTGGTCCGCACAACCCCTGGCCAAGCCCTACCGCT

Gene : gp100
Segment# : 23
Offset : 331
1st Codon : 1
T T E V V G T T P G Q A P T A E P S G T T S V Q V P T T E V
ACCACAGAGGTCTGGGAACCAACCCGGACAGGCTCCCAAGCCGAACCCCTCCGGCACAACCTCCGTGCAAGTGCCTACCACAGAGGTC

Gene : gp100
Segment# : 24
Offset : 346
1st Codon : 1
E P S G T T S V Q V P T T E V I S T A P V Q M P T A E S T G
GAGCCTAGCGGAACCAAGCGTCCAGGTCCCCACAACCGAAGTGATTAGCAGACCCCTGTGCAAATGCCTACCGCTGAGTCCACCGGA

Gene : gp100
Segment# : 25
Offset : 361
1st Codon : 1
I S T A P V Q M P T A E S T G M T P E K V P V S E V M G T T
ATCTCCACCGTCCCGTCCAGATGCCCACAGCCGAAAGCACAGGCATGACCCCTGAGAAAGTGCTGTGTCAGGTCATGGGAACCACA

Gene : gp100
Segment# : 26
Offset : 376
1st Codon : 1
M T P E K V P V S E V M G T T L A E M S T P E A T G M T P A
ATGACACCCGAAAAGGTCCCCGTGAGCGAAGTGATGGGCACAACCCCTGCCGAAATGTCCACCCCTGAGGCTACCGGAATGACACCCGCT

Gene : gp100
Segment# : 27
Offset : 391
1st Codon : 1
L A E M S T P E A T G M T P A E V S I V V L S G T T A A Q V
CTGGCTGAGATGAGCACACCCGAAGCCACAGGCATGACCCCTGCCGAAGTGTCCATCGTCGTGCTCAGCGGAACCAAGCCGCTCAGGTC

Gene : gp100
Segment# : 28
Offset : 406
1st Codon : 1
E V S I V V L S G T T A A Q V T T T E W V E T T A R E L P I
GAGGTCAGCATGTGGTCCTGTCCGGCACAACCGCTGCCCAAGTGACAACCACAGAGTGGGTGGAAACCAAGCCAGAGAGCTCCCCATT

Gene : gp100

Figure 27 (Cont)

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Segment# : 29
Offset : 421
1st Codon : 1
T T T E W V E T T A R E L P I P E P E G P D A S S I M S T E
ACCACAACCGAATGGGTCGAGACAACCGCTAGGGAACTGCCTATCCCTGAGCCTGAGGGACCCGATGCCTCCAGCATTATGTCCACCGAA

Gene : gp100
Segment# : 30
Offset : 436
1st Codon : 1
P E P E G P D A S S I M S T E S I T G S L G P L L D G T A T
CCCGAACCCGAAGGCCCTGACGCTAGCTCCATCATGAGCACAGAGTCCATCACAGGCTCCCTGGGACCCCTCCTGGATGGCACAGCCACA

Gene : gp100
Segment# : 31
Offset : 451
1st Codon : 1
S I T G S L G P L L D G T A T L R L V K R Q V P L D C V L Y
AGCATTACCGGAAGCCTCGGCCCTCTGCTCGACGGAACCGCTACCCTCAGGCTCGTGAAAAGGCAAGTGCCTCTGGATTGCGTCCTGTAT

Gene : gp100
Segment# : 32
Offset : 466
1st Codon : 1
L R L V K R Q V P L D C V L Y R Y G S F S V T L D I V Q G I
CTGAGACTGGTCAAGAGACAGGTCCCCCTCGACTGTGTGCTCTACAGATACGGAAGCTTTAGCGTCACCCCTCGACATTGTGCAAGGCATT

Gene : gp100
Segment# : 33
Offset : 481
1st Codon : 1
R Y G S F S V T L D I V Q G I E S A E I L Q A V P S G E G D
AGGTATGGCTCCTTCTCCGTGACACTGGATATCGTCCAGGGAATCGAAAGCGCTGAGATTCTGCAAGCCGTCCCTCCGGCGAAGGCGAT

Gene : gp100
Segment# : 34
Offset : 496
1st Codon : 1
E S A E I L Q A V P S G E G D A F E L T V S C Q G G L P K E
GAGTCCGCGAAATCCTCCAGGCTGTGCCTAGCGGAGAGGGAGACGCTTTCGAACTGACAGTGTCTGCCAAGGCGGACTGCCTAAGGAA

Gene : gp100
Segment# : 35
Offset : 511
1st Codon : 1
A F E L T V S C Q G G L P K E A C M E I S S P G C Q P P A Q
GCCTTTGAGCTCACCGTCAGCTGTGAGGAGGCTCCCAAAGAGGCTTGCATGGAGATTAGCTCCCCCGGATGCCAACCCCTGCCCAA

Gene : gp100
Segment# : 36
Offset : 526
1st Codon : 1
A C M E I S S P G C Q P P A Q R L C Q P V L P S P A C Q L V
GCCTGTATGGAAATCTCCAGCCCTGGCTGTGAGCCTCCCGCTCAGAGACTGTGTGAGCCTGTGCTCCCCCTCCCGCTTGCCAACTGGTC

Gene : gp100
Segment# : 37
Offset : 541
1st Codon : 1
R L C Q P V L P S P A C Q L V L H Q I L K G G S G T Y C L N
AGGCTCTGCCAACCCGTCTGCCTAGCCCTGCCTGTGAGCTCGTGCTCCACCAATCCTCAAGGAGGCTCCGGCACATACTGTCTGAAT

Gene : gp100
Segment# : 38
Offset : 556
1st Codon : 1
L H Q I L K G G S G T Y C L N V S L A D T N S L A V V S T Q
CTGCATCAGATTCTGAAAGGCGGAAGCGGAACCTATTGCCTCAACGTGAGCCTCGCCGATACCAATAGCCTCGCCGTCTGTCCACCCAA

Gene : gp100
Segment# : 39
Offset : 571

Figure 27 (Cont)

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1st Codon : 1
V S L A D T N S L A V V S T Q L I M P G Q E A G L G Q V P L
GTGTCCCTGGCTGACACAACTCCCTGGCTGTGGTCAGCACACAGCTCATCATGCCCGGACAGGAAGCCGACTGGGACAGGTCCCCCTC

Gene : gp100
Segment# : 40
Offset : 586
1st Codon : 1
L I M P G Q E A G L G Q V P L I V G I L L V L M A V V L A S
CTGATTATGCCTGGCCAAGAGGCTGGCCTCGGCCAAGTGCCTCTGATTGTGGGAATCCTCCTGGTCCTGATGGCCGTCGTGCTCGCCTCC

Gene : gp100
Segment# : 41
Offset : 601
1st Codon : 1
I V G I L L V L M A V V L A S L I Y R R R L M K Q D F S V P
ATCGTCGGCATTTCTGCTCGTGTCTCATGGCTGTGGTCCTGGCTAGCCTCATCTATAGGAGAAGGCTCATGAAACAGGATTCTCCGTGCCT

Gene : gp100
Segment# : 42
Offset : 616
1st Codon : 1
L I Y R R R L M K Q D F S V P Q L P H S S S H W L R L P R I
CTGATTTACAGAAGGAGACTGATGAAGCAAGACTTTAGCGTCCCCCAACTGCCTCACTCCAGCTCCCACTGGCTGAGACTGCCTAGGATT

Gene : gp100
Segment# : 43
Offset : 631
1st Codon : 1
Q L P H S S S H W L R L P R I F C S C P I G E N S P L L S G
CAGCTCCCCCATAGCTCCAGCCATTGGCTCAGGCTCCCCAGAATCTTTTGCTCCTGCCCTATCGGAGAGAATAGCCCTCTGCTCAGCGGA

Gene : gp100
Segment# : 44
Offset : 646
1st Codon : 1
F C S C P I G E N S P L L S G Q Q V A A
TTCTGTAGCTGTCCCATTTGGCGAAAACCCCCCTCTGTCCGGCCAACAGGTGCGCGCT

Gene : MART
Segment# : 1
Offset : 1
1st Codon : 1
A A M P R E D A H F I Y G Y P K K G H G H S Y T T A E E A A
GCCGCTATGCCTAGGGAAGACGCTCACTTTATCTATGGCTATCCAAAAAGGGACACGGACACTCCTACACAACCGCTGAGGAAGCCGCT

Gene : MART
Segment# : 2
Offset : 16
1st Codon : 1
K K G H G H S Y T T A E E A A G I G I L T V I L G V L L L I
AAGAAAGGCCATGGCCATAGCTATACCACAGCCGAAGAGGCTGCCGAATCGGAATCCTCACCCTCATCCTCGGCGTCTGCTCCTGATT

Gene : MART
Segment# : 3
Offset : 31
1st Codon : 1
G I G I L T V I L G V L L L I G C W Y C R R R N G Y R A L M
GGCATTGGCATTCTGACAGTGATTCTGGGAGTGCTCCTGCTCATCGGATGCTGGTACTGTAGGAGAAGGAATGGCTATAGGGCTCTGATG

Gene : MART
Segment# : 4
Offset : 46
1st Codon : 1
G C W Y C R R R N G Y R A L M D K S L H V G T Q C A L T R R
GGCTGTTGGTATTGCAGAAGGAGAAACGGATACAGAGCCCTCATGGATAAGTCCCTGCATGTGGGAACCAATGCGCTCTGACAAGGAGA

Gene : MART
Segment# : 5
Offset : 61
1st Codon : 1
D K S L H V G T Q C A L T R R C P Q E G F D H R D S K V S L

Figure 27 (Cont)

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GACAAAAGCCTCCACGTCGGCACACAGTGTGCCCTCACCAGAAGGTGTCCCCAAGAGGGATTGATCACAGAGACTCCAAGGTCAGCCTC

Gene : MART

Segment# : 6

Offset : 76

1st Codon : 1

C P Q E G F D H R D S K V S L Q E K N C E P V V P N A P P A
TGCCCTCAGGAAGGCTTTGACCATAGGGATAGCAAAGTGTCCCTGCAAGAGAAAACTGTGAGCCTGTGGTCCCCAATGCCCTCCCGCT

Gene : MART

Segment# : 7

Offset : 91

1st Codon : 1

Q E K N C E P V V P N A P P A Y E K L S A E Q S P P P Y S P
CAGGAAAAGAAATTGCGAACCCTCGTGCCTAACGCTCCCCCTGCCCTATGAGAACTGTCCGCCGAACAGTCCCCCCTCCCTATAGCCCT

Gene : MART

Segment# : 8

Offset : 106

1st Codon : 1

Y E K L S A E Q S P P P Y S P A A
TACGAAAAGCTCAGCGCTGAGCAAAGCCTCCCCCTTACTCCCCGCTGCC

Gene : TRP-1

Segment# : 1

Offset : 1

1st Codon : 1

A A P A F L T W H R Y H L L R L E K D M Q E M L Q E P S , F S
GCCGCTCCCGCTTTCTCACCTGGCACAGATACCATCTGCTCAGGCTCGAGAAAGACATGCAGGAAATGCTCCAGGAACCTCCTTCTCC

Gene : TRP-1

Segment# : 2

Offset : 16

1st Codon : 1

L E K D M Q E M L Q E P S F S L P Y W N F A T G K N V C D I
CTGAAAAGGATATGCAAGAGATGCTGCAAGAGCCTAGCTTTAGCCTCCCTATTGGAATTCGCTACCGAAAGAATGTGTGTGACATT

Gene : TRP-1

Segment# : 3

Offset : 31

1st Codon : 1

L P Y W N F A T G K N V C D I C T D D L M G S R S N F D S T
CTGCCCTTACTGGAACCTTTGCCACAGGCAAAAACGTCTGCGATATCTGTACCGATGACCTCATGGGAAGCAGAAGCAATTCGATAGCACA

Gene : TRP-1

Segment# : 4

Offset : 46

1st Codon : 1

C T D D L M G S R S N F D S T L I S P N S V F S Q W R V V C
TGCACAGACGATCTGATGGGCTCCAGGTCCAACCTTTGACTCCACCCTCATCTCCCCAATAGCGTCTTCTCCCAGTGGAGGGTCTGTGT

Gene : TRP-1

Segment# : 5

Offset : 61

1st Codon : 1

L I S P N S V F S Q W R V V C D S L E D Y D T L G T L C N S
CTGATTAGCCCTAACTCCGTGTTTAGCCAATGGAGAGTGGTCTGCGATAGCCTCGAGGATTACGATACCCTCGGCACACTGTGTAACCTC

Gene : TRP-1

Segment# : 6

Offset : 76

1st Codon : 1

D S L E D Y D T L G T L C N S T E D G P I R R N P A G N V A
GACTCCCTGGAAGACTATGACACACTGGGAACCTCTGCAATAGCACAGAGGATGGCCCTATCAGAAGGAATCCCGCTGGCAATGTGGCT

Gene : TRP-1

Segment# : 7

Offset : 91

1st Codon : 1

T E D G P I R R N P A G N V A R P M V Q R L P E P Q D V A Q
ACCGAAGACGGACCCATTAGGAGAAACCTGCCGGAACGTCCGACAGCCCATGGTGCAGAAAGGCTCCCCGAACCCCAAGACGTGCCCCAA

Figure 27 (Cont)

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Gene : TRP-1
Segment# : 8
Offset : 106
1st Codon : 1
R P M V Q R L P E P Q D V A Q C L E V G L F D T P P F Y S N
AGGCCTATGGTCCAGAGACTGCCTGAGCCTCAGGATGTGGCTCAGTGTCTGGAAGTGGGACTGTTTGACACACCCCTTTCTATAGCAAT

Gene : TRP-1
Segment# : 9
Offset : 121
1st Codon : 1
C L E V G L F D T P P F Y S N S T N S F R N T V E G Y S D P
TGCCTCGAGGTGGGCTCTTCGATACCCCTCCCTTTTACTCCAACCTCCACCAATAGCTTTAGGAATACCGTCGAGGGATACTCCGACCCCT

Gene : TRP-1
Segment# : 10
Offset : 136
1st Codon : 1
S T N S F R N T V E G Y S D P T G K Y D P A V R S L H N L A
AGCACAACTCCTTCAGAAACACAGTGGAGGCTATAGCGATCCACAGGCAAATACGATCCCGCTGTGAGAAGCCTCCACAATCTGGCT

Gene : TRP-1
Segment# : 11
Offset : 151
1st Codon : 1
T G K Y D P A V R S L H N L A H L F L N G T G G Q T H L S S
ACCGGAAAGTATGACCTGCCGTGAGTCCCTGCATAACCTCGCCCATCTGTTTCTGAATGGCACAGGCGGACAGACACACCTCAGCTCC

Gene : TRP-1
Segment# : 12
Offset : 166
1st Codon : 1
H L F L N G T G G Q T H L S S Q D P I F V L L H T F T D A V
CACCTCTTCTCAACGGAACGGAGGCCAAACCCATCTGTCCAGCCAAGACCCTATCTTTGTGCTCCTGCATACCTTTACCGATGCCGTC

Gene : TRP-1
Segment# : 13
Offset : 181
1st Codon : 1
Q D P I F V L L H T F T D A V F D E W L R R Y N A D I S T F
CAGGATCCCATTTTCGTCTCTGCTCCACACATTACAGACGCTGTGTTTGACGAATGGCTCAGGAGATACAATGCCGATATCTCCACCTTT

Gene : TRP-1
Segment# : 14
Offset : 196
1st Codon : 1
F D E W L R R Y N A D I S T F P L E N A P I G H N R Q Y N M
TTTCGATGAGTGGCTGAGAAGGTATAACGCTGACATTAGCACATTCCCTCTGGAAAACGCTCCCATTTGGCCATAACAGACAGTATAACATG

Gene : TRP-1
Segment# : 15
Offset : 211
1st Codon : 1
P L E N A P I G H N R Q Y N M V P F W P P V T N T E M F V T
CCCCTCGAGAATGCCCTATCGGACACAATAGGCAATACAATATGGTCCCCCTTTTGGCCTCCCGTCACCAATACCGAAATGTTTGTGACA

Gene : TRP-1
Segment# : 16
Offset : 226
1st Codon : 1
V P F W P P V T N T E M F V T A P D N L G Y T Y E A A
GTGCCCTTCTGGCCCCCTGTGACAAACACAGAGATGTTTCGTACCGCTCCCGATAACCTCGGCTATACCTATGAGGCTGCC

Gene : Tyros
Segment# : 1
Offset : 1
1st Codon : 1
A A M L L A V L Y C L L W S F Q T S A G H F P R A C V S S K
GCCGCTATGCTCTGGCTGTGCTCTACTGTCTGCTCTGGTCTTCCAAACCTCCGCCGGACACTTTCCCAGAGCCTGTGTGTCCAGCAAA

Gene : Tyros
Segment# : 2

Figure 27 (Cont)

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Offset : 16
1st Codon : 1
Q T S A G H F P R A C V S S K N L M E K E C C P P W S G D R
CAGACAAGCGCTGGCCATTTCCCTAGGGCTTGCCTCAGCTCCAAGAATCTGATGGAGAAAGAGTGTTCCTCCCTGGAGCGGAGACAGA

Gene : Tyros
Segment# : 3
Offset : 31
1st Codon : 1
N L M E K E C C P P W S G D R S P C G Q L S G R G S C Q N I
AACCTCATGAAAAGGAATGCTGTCCCCCTTGGTCCGGCGATAGGTCCCCCTGTGGCCAACTGTCCGGCAGAGGCTCCTGCCAAACATT

Gene : Tyros
Segment# : 4
Offset : 46
1st Codon : 1
S P C G Q L S G R G S C Q N I L L S N A P L G P Q F P F T G
AGCCCTTGGGACAGCTCAGCGGAAGGGGAAGCTGTCAAGATATCTCTGTCCACGCTCCCCTCGGCCCTCAGTTTCCCTTTACCGGA

Gene : Tyros
Segment# : 5
Offset : 61
1st Codon : 1
L L S N A P L G P Q F P F T G V D D R E S W P S V F Y N R T
CTGCTCAGCAATGCCCTCTGGGACCCCAATTCCCTTTCACAGGCGTCGACGATAGGGAAAGCTGGCCCTCCGTGTTTTACAATAGGACA

Gene : Tyros
Segment# : 6
Offset : 76
1st Codon : 1
V D D R E S W P S V F Y N R T C Q C S G N F M G F N C G N C
GTGGATGACAGAGAGTCTTGGCCTAGCGTCTTCTATAACAGAACCTGTCTAGTGTAGCGGAACTTTATGGGATTCAATTGCGGAACTGT

Gene : Tyros
Segment# : 7
Offset : 91
1st Codon : 1
C Q C S G N F M G F N C G N C K F G F W G P N C T E R R L L
TGCCAATGCTCCGGCAATTCATGGGCTTTAACTGTGGCAATTGCAATTCGGATTCTGGGGCCCTAACTGTACCGAAAGGAGACTGCTC

Gene : Tyros
Segment# : 8
Offset : 106
1st Codon : 1
K F G F W G P N C T E R R L L V R R N I F D L S A P E K D K
AAGTTTGGCTTTTGGGGACCAATTGCACAGAGAGAAGGCTCCTGGTCAGGAGAAACATTTTCGATCTGTCCGCCCTGAGAAAGACAAA

Gene : Tyros
Segment# : 9
Offset : 121
1st Codon : 1
V R R N I F D L S A P E K D K F F A Y L T L A K H T I S S D
GTGAGAAGGAATATCTTTGACCTCAGCGCTCCCGAAAAGGATAAGTTTTTCGCTTACCTCACCCCTCGCCAAACACACAATCTCCAGCGAT

Gene : Tyros
Segment# : 10
Offset : 136
1st Codon : 1
F F A Y L T L A K H T I S S D Y V I P I G T Y G Q M K N G S
TTCTTTGCCTATCTGACACTGGCTAAGCATACCATTAGCTCCGACTATGTGATTCCCATTTGGCACATACGGACAGATGAAGAATGGCTCC

Gene : Tyros
Segment# : 11
Offset : 151
1st Codon : 1
Y V I P I G T Y G Q M K N G S T P M F N D I N I Y D L F V W
TACGTCATCCCTATCGGAACCTATGGCCAAATGAAAAACGAAGCACACCCATGTTCATGACATTAACTTTACGATCTGTTTGTGTGG

Gene : Tyros
Segment# : 12
Offset : 166
1st Codon : 1

Figure 27 (Cont)

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T P M F N D I N I Y D L F V W M H Y Y V S M D A L L G G S E
ACCCCTATGTTTAACGATATCAATATCTATGACCTCTTCGTCTGGATGCACTATTACGTCAGCATGGACGCTCTGCTCGGCGGAAGCGAA

Gene : Tyros
Segment# : 13
Offset : 181
1st Codon : 1

M H Y Y V S M D A L L G G S E I W R D I D F A H E A P A F L
ATGCATTACTATGTGTCCATGGATGCCCTCCTGGGAGGCTCCGAGATTTGGAGAGACATTGACTTTGCCCATGAGGCTCCCGCTTTCCTC

Gene : Tyros
Segment# : 14
Offset : 196
1st Codon : 1

I W R D I D F A H E A P A F L P W H R L F L L R W E Q E I Q
ATCTGGAGGATATCGATTTTCGCTCACGAAGCCCTGCCTTTCTGCCTTGGCATAGGCTCTTCCTCCTGAGATGGGAACAGGAAATCCAA

Gene : Tyros
Segment# : 15
Offset : 211
1st Codon : 1

P W H R L F L L R W E Q E I Q K L T G D E N F T I P Y W D W
CCCTGGCAGACTGTTTCTGCTCAGGTGGGAGCAAGAGATTAGAACTGACAGGCGATGAGAATTCACAATCCCTTACTGGGACTGG

Gene : Tyros
Segment# : 16
Offset : 226
1st Codon : 1

K L T G D E N F T I P Y W D W R D A E K C D I C T D E Y M G
AAGCTCACCGGAGACGAAAACCTTTACCATTCCTATTGGGATTTGGAGAGACGCTGAGAAATGCGATATCTGTACCGATGAGTATATGGGA

Gene : Tyros
Segment# : 17
Offset : 241
1st Codon : 1

R D A E K C D I C T D E Y M G G Q H P T N P N L L S P A S F
AGGGATGCCGAAAAGTGTGACATTTGCACAGACGAATACATGGGCGGACAGCATCCCAACAAACCTAACCTCCTGTCCCCGCTAGCTTT

Gene : Tyros
Segment# : 18
Offset : 256
1st Codon : 1

G Q H P T N P N L L S P A S F F S S W Q I V C S R L E E Y N
GGCCAAACCCCTACCAATCCCAATCTGCTCAGCCCTGCCTCCTTCTTTAGCTCCTGGCAAATCGTCTGCTCCAGGCTCGAGGAATACAAT

Gene : Tyros
Segment# : 19
Offset : 271
1st Codon : 1

F S S W Q I V C S R L E E Y N S H Q S L C N G T P E G P L R
TTCTCCAGCTGGCAGATTGTGTGTAGCAGACTGGAAGAGTATAACTCCCACCAAAGCCTCTGCAATGGCACACCCGAAGGCCCTCTGAGA

Gene : Tyros
Segment# : 20
Offset : 286
1st Codon : 1

S H Q S L C N G T P E G P L R R N P G N H D K S R T P R L P
AGCCATCAGTCCCTGTGTAAACGGAACCCCTGAGGGACCCCTCAGGAGAAACCTGGCAATCACGATAAGTCCAGGACACCCAGACTGCCT

Gene : Tyros
Segment# : 21
Offset : 301
1st Codon : 1

R N P G N H D K S R T P R L P S S A D V E F C L S L T Q Y E
AGGAATCCCGGAAACCATGACAAAAGCAGAACCCTAGGCTCCCTCCAGCGCTGACGTCGAGTTTTGCCTCAGCCTCACCCAATACGAA

Gene : Tyros
Segment# : 22
Offset : 316
1st Codon : 1

S S A D V E F C L S L T Q Y E S G S M D K A A N F S F R N T
AGCTCCGCCGATGTGGAATTCTGTCTGTCCCTGACACAGTATGAGTCCGGCTCCATGGATAAGGCTGCCAATTTCTCCTTCAGAAACACA

Figure 27 (Cont)

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Gene : Tyros
Segment# : 23
Offset : 331
1st Codon : 1
S G S M D K A A N F S F R N T L E G F A S P L T G I A D A S
AGCGAAGCATGGACAAAGCCGCTAACTTTAGCTTTAGGAATACCCTCGAGGGATTGCTAGCCCTCTGACAGGCATTGCCGATGCCTCC

Gene : Tyros
Segment# : 24
Offset : 346
1st Codon : 1
L E G F A S P L T G I A D A S Q S S M H N A L H I Y M N G T
CTGGAAGGCTTTGCCCTCCCCCTCACCGGAATCGCTGACGCTAGCCAAAGCTCCATGCATAACGCTCTGCATATCTATATGAATGGCACA

Gene : Tyros
Segment# : 25
Offset : 361
1st Codon : 1
Q S S M H N A L H I Y M N G T M S Q V Q G S A N D P I F L L
CAGTCCAGCATGCACAATGCCCTCCACATTACATGAACGGAACCATGAGCCAAGTGCAAGGCTCCGCCAATGACCCTATCTTTCTGCTC

Gene : Tyros
Segment# : 26
Offset : 376
1st Codon : 1
M S Q V Q G S A N D P I F L L H H A F V D S I F E Q W L Q R
ATGTCCAGGTCCAGGGAAGCGCTAACGATCCCATTTCTCCTGTCATCAGCTTTCTGTCGACTCCATCTTTGAGCAATGGCTCCAGAGA

Gene : Tyros
Segment# : 27
Offset : 391
1st Codon : 1
H H A F V D S I F E Q W L Q R H R P L Q E V Y P E A N A P I
CACCATGCCTTTGTGGATAGCATTTTCGAACAGTGGCTGCAAAGGCATAGGCCTCTGCAAGAGGTCTACCCTGAGGCTAACGCTCCCAT

Gene : Tyros
Segment# : 28
Offset : 406
1st Codon : 1
H R P L Q E V Y P E A N A P I G H N R E S Y M V P F I P L Y
CACAGACCCCTCCAGGAAGTGTATCCCGAAGCCAATGCCCTATCGGACACAATAGGGAAGCTATATGGTCCCTTTATCCCTCTGTAT

Gene : Tyros
Segment# : 29
Offset : 421
1st Codon : 1
G H N R E S Y M V P F I P L Y R N G D F F I S S K D L G Y D
GGCCATAACAGAGAGTCTACATGGTGCCTTTTCATTCCCTCTACAGAAACGGAGACTTTTTCATTAGCTCCAAGGATCTGGGATACGAT

Gene : Tyros
Segment# : 30
Offset : 436
1st Codon : 1
R N G D F F I S S K D L G Y D Y S Y L Q D S D P D S F Q D Y
AGGAATGGCGATTTCTTTATCTCCAGCAAAGACCTCGGCTATGACTATAGCTATCTGCAAGACTCCGACCCTGACTCCTTCCAAGACTAT

Gene : Tyros
Segment# : 31
Offset : 451
1st Codon : 1
Y S Y L Q D S D P D S F Q D Y I K S Y L E Q A S R I W S W L
TACTCTACCTCCAGGATAGCGATCCCAGTAGCTTTCAGGATTACATTAAGTCCCTACCTCGAGCAAGCCTCCAGGATTGGTCTGGCTC

Gene : Tyros
Segment# : 32
Offset : 466
1st Codon : 1
I K S Y L E Q A S R I W S W L L G A A M V G A V L T A L L A
ATCAAAAGCTATCTGGAACAGGCTAGCAGAATCTGGAGCTGGCTGCTCGGCGCTGCCATGGTGGGAGCCGTCTGACAGCCCTCCTGGCT

Gene : Tyros

Figure 27 (Cont)

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Segment# : 33
 Offset : 481
 1st Codon : 1
 L G A A M V G A V L T A L L A G L V S L L C R H K R K Q L P
 CTGGGAGCCGCTATGGTCGGCGCTGTGCTCACCGCTCTGCTCGCCGACTGGTCAGCCTCCTGTGTAGGCATAAGAGAAAGCAACTGCCT

Gene : Tyros
 Segment# : 34
 Offset : 496
 1st Codon : 1
 G L V S L L C R H K R K Q L P E E K Q P L L M E K E D Y H S
 GGCCTCGTGTCCCTGCTCTGCAGACACAAAAGGAAACAGCTCCCCGAAGAGAAACAGCCTCTGCTCATGGAAAAGGAAGACTATCACTCC

Gene : Tyros
 Segment# : 35
 Offset : 511
 1st Codon : 1
 E E K Q P L L M E K E D Y H S L Y Q S H L A A
 GAGGAAAAGCAACCCCTCCTGATGGAGAAAGAGGATTACCATAGCCTCTACCAAAGCCATCTGGCTGCC

Gene : TRP2
 Segment# : 1
 Offset : 1
 1st Codon : 1
 A A M S P L W W G F L L S C L G C K I L P G A Q G Q F P R V
 GCCCGTATGTCCCCCTCTGGTGGGGCTTTCTGCTCAGCTGTCTGGGATGCAAAATCCTCCCGGAGCCCAAGGCCAATTCCTAGGGTC

Gene : TRP2
 Segment# : 2
 Offset : 16
 1st Codon : 1
 G C K I L P G A Q G Q F P R V C M T V D S L V N K E C C P R
 GGCTGTAAGATTCTGCCTGGCGCTCAGGGACAGTTTCCAGAGTGTGTATGACAGTGGATAGCCTCGTGAATAAGGAATGCTGTCCAGA

Gene : TRP2
 Segment# : 3
 Offset : 31
 1st Codon : 1
 C M T V D S L V N K E C C P R L G A E S A N V C G S Q Q G R
 TGCATGACCGTCGACTCCCTGGTCAACAAAGAGTGTGGCCCTAGGCTCGGCGCTGAGTCCGCCAATGTGTGTGGCTCCAGCAAGGCAGA

Gene : TRP2
 Segment# : 4
 Offset : 46
 1st Codon : 1
 L G A E S A N V C G S Q Q G R G Q C T E V R A D T R P W S G
 CTGGGAGCCGAAAGCGCTAACGTCTGCGGAAGCCAAACAGGGAAGGGGACAGTGTACCGAAGTGAGAGCCGATACCAGACCTGGAGCGGA

Gene : TRP2
 Segment# : 5
 Offset : 61
 1st Codon : 1
 G Q C T E V R A D T R P W S G P Y I L R N Q D D R E L W P R
 GGCCAAATGCACAGAGGTGAGGGCTGACACAAGGCCTTGGTCCGGCCCTTACATTCTGAGAAACCAAGACGATAGGGAAGTGTGGCCCGA

Gene : TRP2
 Segment# : 6
 Offset : 76
 1st Codon : 1
 P Y I L R N Q D D R E L W P R K F F H R T C K C T G N F A G
 CCCTATATCCTCAGGAATCAGGATGACAGAGAGCTCTGGCCTAGGAAATTCTTTCACAGAACCTGTAAGTGTACCGGAAACTTTGCCGGA

Gene : TRP2
 Segment# : 7
 Offset : 91
 1st Codon : 1
 K F F H R T C K C T G N F A G Y N C G D C K F G W T G P N C
 AAGTTTTCATAGGACATGCAATGCACAGGCAATTCGCTGGCTATAACTGTGGCGATTGCAATTCGGATGGACAGGCCCTAACTGT

Gene : TRP2
 Segment# : 8
 Offset : 106

Figure 27 (Cont)

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1st Codon : 1
Y N C G D C K F G W T G P N C E R K K P P V I R Q N I H S L
TACAAATTGCGAGACTGTAAGTTTGGCTGGACCGGACCCAATTGCGAAAGGAAAAAGCCTCCCGTCATCAGACAGAATATCCATAGCCTC

Gene : TRP2
Segment# : 9
Offset : 121
1st Codon : 1
E R K K P P V I R Q N I H S L S P Q E R E Q F L G A L D L A
GAGAGAAAGAAACCCCTGTGATTAGGCAAAACATTCACTCCCTGTCCCCCAAGAGAGAGCAATTCCTCGGCGCTCTGGATCTGGCT

Gene : TRP2
Segment# : 10
Offset : 136
1st Codon : 1
S P Q E R E Q F L G A L D L A K K R V H P D Y V I T T Q H W
AGCCCTCAGGAAAGGGAACAGTTTCTGGGAGCCCTCGACCTCGCCAAAAGAGAGTGCATCCCGATTACGTCATCACAACCCCAACTGG

Gene : TRP2
Segment# : 11
Offset : 151
1st Codon : 1
K K R V H P D Y V I T T Q H W L G L L G P N G T Q P Q F A N
AAGAAAAGGGTCCACCCTGACTATGTGATTACCACACAGCATTTGGCTCGGCCTCCTGGGACCCAATGGCACACAGCCTCAGTTTGCCAAT

Gene : TRP2
Segment# : 12
Offset : 166
1st Codon : 1
L G L L G P N G T Q P Q F A N C S V Y D F F V W L H Y Y S V
CTGGGACTGCTCGGCCCTAACGGAACCCAACCCCAATTTCGCTAACTGTAGCGTCTACGATTTCTTTGTGTGGCTGCATTACTATAGCGTC

Gene : TRP2
Segment# : 13
Offset : 181
1st Codon : 1
C S V Y D F F V W L H Y Y S V R D T L L G P G R P Y R A I D
TGCTCCGTTGATGACTTTTTCGTCTGGCTCCACTATTACTCCGTGAGAGACACACTGCTCGGCCCTGGCAGACCCTATAGGGCTATCGAT

Gene : TRP2
Segment# : 14
Offset : 196
1st Codon : 1
R D T L L G P G R P Y R A I D F S H Q G P A F V T W H R Y H
AGGGATACCCTCCTGGGACCCGGAAGGCCCTTACAGAGCCATTGACTTTAGCCATCAGGGACCCGCTTTCGTACCTGGCACAGATACCAT

Gene : TRP2
Segment# : 15
Offset : 211
1st Codon : 1
F S H Q G P A F V T W H R Y H L L C L E R D L Q R L I G N E
TTCTCCACCAAGGCCCTGCCTTTGTGACATGGCATAGGTATCACCTCCTGTGTCTGGAAGGGATCTGCAAAGGCTCATCGGAAACGAA

Gene : TRP2
Segment# : 16
Offset : 226
1st Codon : 1
L L C L E R D L Q R L I G N E S F A L P Y W N F A T G R N E
CTGCTCTGCCTCGAGAGACCTCCAGAGACTGATTGGCAATGAGTCCTTCGCTCTGCCTTACTGGAACCTTGCCACAGGCAGAAACGAA

Gene : TRP2
Segment# : 17
Offset : 241
1st Codon : 1
S F A L P Y W N F A T G R N E C D V C T D Q L F G A A R P D
AGCTTTGCCCTCCCTTATGGAATTTTCGCTACCGGAAGGAATGAGTGTGACGTCTGCACAGACCAACTGTTTGGCGCTGCCAGACCCGAT

Gene : TRP2
Segment# : 18
Offset : 256
1st Codon : 1
C D V C T D Q L F G A A R P D D P T L I S R N S R F S S W E

Figure 27 (Cont)

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TGCGATGTGTGTACCGATCAGCTCTTCGGAGCCGCTAGGCCTGACGATCCACACTGATTAGCAGAACTCCAGGTTTAGCTCCTGGGAA

Gene : TRP2
Segment# : 19
Offset : 271
1st Codon : 1

D P T L I S R N S R F S S W E T V C D S L D D Y N H L V T L
GACCTACCCCTCATCTCCAGGAATAGCAGATTCTCCAGCTGGGAGACAGTGTGTGACTCCCTGGATGACTATAACCATCTGGTCACCCCTC

Gene : TRP2
Segment# : 20
Offset : 286
1st Codon : 1

T V C D S L D D Y N H L V T L C N G T Y E G L L R R N Q M G
ACCGTCTGCGATAGCCTCGACGATTACAATCACCTCGTGACACTGTGTAACGGAACCTATGAGGGACTGCTCAGGAGAAACCAAATGGGA

Gene : TRP2
Segment# : 21
Offset : 301
1st Codon : 1

C N G T Y E G L L R R N Q M G R N S M K L P T L K D I R D C
TGCAATGGCACATACGAAGGCCTCCTGAGAAGGAATCAGATGGGCAGAACTCCATGAAACTGCCTACCCCTCAAGGATATCAGAGACTGT

Gene : TRP2
Segment# : 22
Offset : 316
1st Codon : 1

R N S M K L P T L K D I R D C L S L Q K F D N P P F F Q N S
AGGAATAGCATGAAGCTCCCCACACTGAAAGACATTAGGGATTGCTCAGCCTCCAGAAATTCGATAACCCCTCCCTTTTCCAAAACCTCC

Gene : TRP2
Segment# : 23
Offset : 331
1st Codon : 1

L S L Q K F D N P P F F Q N S T F S F R N A L E G F D K A D
CTGTCCCTGCAAAAGTTTGACAATCCCCCTTCTTTTCAGAATAGCACATTCTCCTTCAGAAACGCTCTGGAAGGCTTTGACAAAGCCGAT

Gene : TRP2
Segment# : 24
Offset : 346
1st Codon : 1

T F S F R N A L E G F D K A D G T L D S Q V M S L H N L V H
ACCTTTTAGCTTTAGGAATGCCCTCGAGGGATTGATAAGGCTGACGGAACCTCGACTCCAGGTCATGTCCCTGCATAACCTCGTGCAT

Gene : TRP2
Segment# : 25
Offset : 361
1st Codon : 1

G T L D S Q V M S L H N L V H S F L N G T N A L P H S A A N
GGCACACTGGATAGCCAAGTGATGAGCCTCCACAATCTGGTCCACTCCTTCTCAACGGAACCAATGCCCTCCTCCATAGCGCTGCCAAT

Gene : TRP2
Segment# : 26
Offset : 376
1st Codon : 1

S F L N G T N A L P H S A A N D P I F V V L H S F T D A I F
AGCTTTCTGAATGGCACAAACGCTCTGCCTCACTCCGCCGCTAACGATCCCATTTTCGTCTGTGCTCCACTCCTTCACAGACGCTATCTTT

Gene : TRP2
Segment# : 27
Offset : 391
1st Codon : 1

D P I F V V L H S F T D A I F D E W M K R F N P P A D A W P
GACCTATCTTTGTGGTCTGCATAGCTTTACCGATGCCATTTTCGATGAGTGGATGAAAAGTTTAAACCTCCCGCTGACGCTTGGCCT

Gene : TRP2
Segment# : 28
Offset : 406
1st Codon : 1

D E W M K R F N P P A D A W P Q E L A P I G H N R M Y N M V
GACGAATGGATGAAGAGATTCAATCCCCCTGCCGATGCCTGGCCCCAAGAGCTCGCCCCCTATCGGACACAATAGGATGTACAATATGGTC

Figure 27 (Cont)

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Gene : TRP2
Segment# : 29
Offset : 421
1st Codon : 1
Q E L A P I G H N R M Y N M V P F F P P V T N E E L F L T S
CAGGAAGTGGCTCCCATTTGGCCATAACAGAATGTATAACATGGTGCCTTTCTTTCCCTGTGACAAACGAAGAGCTCTTCCTCACCTCC

Gene : TRP2
Segment# : 30
Offset : 436
1st Codon : 1
P F F P P V T N E E L F L T S D Q L G Y S Y A I D L P V S V
CCCTTTTCCCTCCCGTCACCAATGAGGAAGTCTTCTGACAAGCGATCAGCTCGGCTATAGCTATGCCATTGACCTCCCGTCAGCGTC

Gene : TRP2
Segment# : 31
Offset : 451
1st Codon : 1
D Q L G Y S Y A I D L P V S V E E T P G W P T T L L V V M G
GACCAACTGGGATACTCCTACGCTATCGATCTGCCTGTGTCCGTGGAAGAGACACCCGGATGGCCTACCACACTGCTCGTGGTCATGGGA

Gene : TRP2
Segment# : 32
Offset : 466
1st Codon : 1
E E T P G W P T T L L V V M G T L V A L V G L F V L L A F L
GAGGAAACCCCTGGCTGGCCCAACCCCTCCTGGTCGTGATGGGCACACTGGTCGCCCTCGTGGGACTGTTTGTGCTCCTGGCTTTCCTC

Gene : TRP2
Segment# : 33
Offset : 481
1st Codon : 1
T L V A L V G L F V L L A F L Q Y R R L R K G Y T P L M E T
ACCTCGTGGCTCTGGTCGGCCTCTTCGTCTGCTCGCCTTTCTGCAATACAGAAGGCTCAGGAAAGGCTATACCCCTCTGATGGAGACA

Gene : TRP2
Segment# : 34
Offset : 496
1st Codon : 1
Q Y R R L R K G Y T P L M E T H L S S K R Y T E E A A A
CAGTATAGGAGACTGAGAAAGGGATACACACCCCTCATGGAAACCATCTGTCCAGCAAAAGGTATACCGAAGAGGCTGCCGCT

Gene : MC1R
Segment# : 1
Offset : 1
1st Codon : 1
A A M A V Q G S Q R R L L G S L N S T P T A I P Q L G L A A
GCCGCTATGGCTGTGCAAGGCTCCAGAGAAGGCTCCTGGGAAGCCTCAACTCCACCCCTACCGCTATCCCTCAGCTCGGCCTCGCCGCT

Gene : MC1R
Segment# : 2
Offset : 16
1st Codon : 1
L N S T P T A I P Q L G L A A N Q T G A R C L E V S I S D G
CTGAATAGCACACCCACAGCCATTCCCCAACTGGGACTGGCTGCCAATCAGACAGGCGCTAGGTGTCTGGAAGTGTCATCTCCGACGGA

Gene : MC1R
Segment# : 3
Offset : 31
1st Codon : 1
N Q T G A R C L E V S I S D G L F L S L G L V S L V E N A L
AACCAAACCGAGCCAGATGCCCTCGAGGTCAGCATTAGCGATGGCCTCTTCTCAGCCTCGGCCTCGTGTCCCTGGTCGAGAATGCCCTC

Gene : MC1R
Segment# : 4
Offset : 46
1st Codon : 1
L F L S L G L V S L V E N A L V V A T I A K N R N L H S P M
CTGTTTCTGTCCCTGGGACTGGTCAGCCTCGTGAAAACGCTCTGGTCTGGCTACCATGCCCCAACAGAACTCCACTCCCCCATG

Gene : MC1R
Segment# : 5

Figure 27 (Cont)

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Offset : 61
1st Codon : 1
V V A T I A K N R N L H S P M Y C F I C C L A L S D L L V S
GTGGTCGCCACAATCGCTAAGAATAGGAATCTGCATAGCCCTATGTATTGCTTTATCTGTTGCCTCGCCCTCAGCGATCTGCTCGTGTCC

Gene : MC1R
Segment# : 6
Offset : 76
1st Codon : 1
Y C F I C C L A L S D L L V S G T N V L E T A V I L L L E A
TACTGTTTCATTGCTGTCTGGCTCTGTCCGACCTCCTGGTCAGCGGAACCAATGTGCTCGAGACAGCCGTCATCCTCCTGCTCGAGGCT

Gene : MC1R
Segment# : 7
Offset : 91
1st Codon : 1
G T N V L E T A V I L L L E A G A L V A R A A V L Q Q L D N
GGCACAAACGTCTGGAAACCGCTGTGATTCTGCTCCTGGAAGCCGGAGCCCTCGTGGCTAGGGCTGCCGTCCTGCAACAGCTCGACAAT

Gene : MC1R
Segment# : 8
Offset : 106
1st Codon : 1
G A L V A R A A V L Q Q L D N V I D V I T C S S M L S S L C
GGCGCTCTGGTCGCCAGAGCCGCTGTGCTCCAGCAACTGGATAACGTATCGATGTGATTACCTGTAGCTCCATGCTCAGCTCCCTGTGT

Gene : MC1R
Segment# : 9
Offset : 121
1st Codon : 1
V I D V I T C S S M L S S L C F L G A I A V D R Y I S I F Y
GTGATTGACGTATCACATGCTCCAGCATGCTGTCCAGCCTCTGCTTTCTGGGAGCCATTGCCGTCGACAGATACATTAGCATTCTCTAT

Gene : MC1R
Segment# : 10
Offset : 136
1st Codon : 1
F L G A I A V D R Y I S I F Y A L R Y H S I V T L P R A P R
TTCCTCGGCGCTATCGCTGTGGATAGGTATATCTCCATCTTTTACGCTCTGAGATACCATAGCATTGTGACACTGCCTAGGGCTCCAGCA

Gene : MC1R
Segment# : 11
Offset : 151
1st Codon : 1
A L R Y H S I V T L P R A P R A V A A I W V A S V V F S T L
GCCCTCAGGTATCATCCATCGTCACCCTCCCCAGAGCCCCCTAGGGCTGTGGCTGCCATTGCGCTCGCCTCCGTGGTCTTCTCCACCCTC

Gene : MC1R
Segment# : 12
Offset : 166
1st Codon : 1
A V A A I W V A S V V F S T L F I A Y Y D H V A V L L C L V
GCCGTCGCCGCTATCTGGGTGGCTAGCGTCGTGTTTAGCACACTGTTTATCGCTTACTATGACCATGTGGCTGTGCTCCTGTGTCTGGTC

Gene : MC1R
Segment# : 13
Offset : 181
1st Codon : 1
F I A Y Y D H V A V L L C L V V F F L A M L V L M A V L Y V
TTCATTGCTTATTACGATCACGTCGCCGTCCTGCTCTGCCTCGTGGTCTTCTTTCTGGCTATGCTCGTGTCTCATGGCTGTGCTCTACGTC

Gene : MC1R
Segment# : 14
Offset : 196
1st Codon : 1
V F F L A M L V L M A V L Y V H M L A R A C Q H A Q G I A R
GTGTTTTCCTCGCCATGCTGGTCTGATGGCCGTCCTGTATGTGCATATGCTCGCCAGAGCCTGTGAGCATGCCCAAGGCATTGCCAGA

Gene : MC1R
Segment# : 15
Offset : 211
1st Codon : 1

Figure 27 (Cont)

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H M L A R A C Q H A Q G I A R L H K R Q R P V H Q G F G L K
CACATGCTGGCTAGGGCTTGCCAAACACGCTCAGGGAATCGCTAGGCTCCACAAAAGGCAAAGGCCTGTGCATCAGGGATTGGACTGAAA

Gene : MC1R
Segment# : 16
Offset : 226
1st Codon : 1

L H K R Q R P V H Q G F G L K G A V T L T I L L G I F F L C
CTGCATAAGAGACAGAGACCCGTCCACCAAGGCTTTGGCCTCAAGGGAGCCGTCACCCTCACCATTCTGCTCGGCATTTTCTTTCTGTGT

Gene : MC1R
Segment# : 17
Offset : 241
1st Codon : 1

G A V T L T I L L G I F F L C W G P F F L H L T L I V L C P
GGCGCTGTGACACTGACAATCCTCCTGGGAATCTTTTCTCTGCTGGGGCCCTTTCTTTCTGCATCTGACACTGATTGTGCTCTGCCCT

Gene : MC1R
Segment# : 18
Offset : 256
1st Codon : 1

W G P F F L H L T L I V L C P E H P T C G C I F K N F N L F
TGGGGACCTTTTCTCTCCACCTCACCTCATCGTCTGTGTCCGAACACCCCTACCTGTGGCTGTATCTTTAAGAATTTCAATCTGTTT

Gene : MC1R
Segment# : 19
Offset : 271
1st Codon : 1

E H P T C G C I F K N F N L F L A L I I C N A I I D P L I Y
GAGCATCCACATGCGGATGCATTTTCAAAAACCTTTAACCTCTTCTCGCCCTCATCATTGCAATGCCATTATCGATCCCTCATCTAT

Gene : MC1R
Segment# : 20
Offset : 286
1st Codon : 1

L A L I I C N A I I D P L I Y A F H S Q E L R R T L K E V L
CTGGCTCTGATTATCTGTAAAGCTATCATTGACCCTCTGATTACGCTTTCCATAGCCAAGAGCTCAGGAGAACCCTCAAGGAAGTGCTC

Gene : MC1R
Segment# : 21
Offset : 301
1st Codon : 1

A F H S Q E L R R T L K E V L T C S W A A
GCCTTTCACTCCAGGAACCTGAGAAGGACACTGAAAGAGGTCCTGACATGCTCCTGGGCTGCC

Gene : MUC1F
Segment# : 1
Offset : 1
1st Codon : 1

A A M T P G T Q S P F F L L L L L T V L T V V T G S G H A S
GCCGCTATGACACCCGGAACCCAAAGCCCTTCTTTCTGCTCCTGCTCCTGACAGTGCTCACCCTCGTGACAGGCTCCGGCCATGCCTCC

Gene : MUC1F
Segment# : 2
Offset : 16
1st Codon : 1

L L T V L T V V T G S G H A S S T P G G E K E T S A T Q R S
CTGCTCACCCTCCTGACAGTGCTCACCAGGAGCGGACACGCTAGCTCCACCCCTGGCGGAGAGAAAGAGACAAGCGCTACCCAAAGGTCC

Gene : MUC1F
Segment# : 3
Offset : 31
1st Codon : 1

S T P G G E K E T S A T Q R S S V P S S T E K N A V S M T S
AGCACACCCGAGGCGAAAAGGAAACCTCCGCCACACAGAGAAGCTCCGTGCTAGCTCCACCGAAAAGAAATGCCGTACGATGACCTCC

Gene : MUC1F
Segment# : 4
Offset : 46
1st Codon : 1

S V P S S T E K N A V S M T S S V L S S H S P G S G S S T T
AGCGTCCCCTCCAGCACAGAGAAAAACGCTGTGTCCATGACAAGCTCCGTGCTCAGCTCCCACTCCCCCGGAAGCGGAAGCTCCACCACA

Figure 27 (Cont)

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Gene : MUC1F
Segment# : 5
Offset : 61
1st Codon : 1
S V L S S H S P G S G S S T T Q G Q D V T L A P A T E P A S
AGCGTCCTGTCCAGCCATAGCCCTGGCTCCGGCTCCAGCACAAACCAAGCCAAGACGTCACCCTCGCCCTGCCACAGAGCCTGCCTCC

Gene : MUC1F
Segment# : 6
Offset : 76
1st Codon : 1
Q G Q D V T L A P A T E P A S G S A A T W G Q D V T S V P V
CAGGGACAGGATGTGACACTGGCTCCCGCTACCGAACCCGCTAGCGGAAGCGCTGCCACATGGGGACAGGATGTGACAAGCGTCCCGTC

Gene : MUC1F
Segment# : 7
Offset : 91
1st Codon : 1
G S A A T W G Q D V T S V P V T R P A L G S T T P P A H D V
GGCTCCGCCGCTACCTGGGGCCAAGACGTCACCTCCGTGCTGTGACAAGGCCTGCCCTCGGCTCCACCACACCCCTGCCCATGACGTC

Gene : MUC1F
Segment# : 8
Offset : 106
1st Codon : 1
T R P A L G S T T P P A H D V T S A P D N K A A
ACCAGACCCGCTCTGGGAAGCACAAACCCCTCCCGCTCAGGATGTGACAAGCGCTCCCGATAACAAAGCCGCT

Gene : MUC1R
Segment# : 1
Offset : 1
1st Codon : 1
A A N R P A L G S T A P P V H N V T S A S G S A S G S A S T
GCCGCTAACAGACCCGCTCTGGGAAGCACAGCCCTCCCGCTCCACAATGTGACAAGCGCTAGCGGAAGCGCTAGCGGAAGCGCTAGCACA

Gene : MUC1R
Segment# : 2
Offset : 16
1st Codon : 1
N V T S A S G S A S G S A S T L V H N G T S A R A T T T P A
AACGTCACCTCCGCTCCGGCTCCGCTCCGGCTCCGCTCCACCCTCGTGCATAACGGAACCTCCGCCAGAGCCACAACCACACCCGCT

Gene : MUC1R
Segment# : 3
Offset : 31
1st Codon : 1
L V H N G T S A R A T T T P A S K S T P F S I P S H H S D T
CTGGTCCACAATGGCACAAGCGCTAGGGCTACCACAACCCCTGCCTCCAAGTCCACCCCTTTCTCCATCCCTAGCCATCACTCCGACACA

Gene : MUC1R
Segment# : 4
Offset : 46
1st Codon : 1
S K S T P F S I P S H H S D T P T T L A S H S T K T D A S S
AGCAAAGCACACCCCTTTAGCATTCCTCCACCATAGCGATACCCCTACCACACTGGCTAGCCATAGCACAAAGACAGACGCTAGCTCC

Gene : MUC1R
Segment# : 5
Offset : 61
1st Codon : 1
P T T L A S H S T K T D A S S T H H S S V P P L T S S N H S
CCCACAACCCCTCGCCTCCCACTCCACAAAACCGATGCCTCCAGCACACACCATAGCTCCGTGCCTCCCTCACCTCCAGCAATCACTCC

Gene : MUC1R
Segment# : 6
Offset : 76
1st Codon : 1
T H H S S V P P L T S S N H S T S P Q L S T G V S F F F L S
ACCATCACTCCAGCGTCCCCCTCTGACAAGCTCCAACCATAGCACAAAGCCCTCAGCTCAGCACAGGCGTCAGCTTTTCTTTCTGTCTCC

Gene : MUC1R

Figure 27 (Cont)

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Segment# : 7
Offset : 91
1st Codon : 1
T S P Q L S T G V S F F F L S F H I S N L Q F N S S L E D P
ACCTCCCCCAACTGTCCACCGAGTGTCCCTCTTTTCTCTCAGCTTTCACATTAGCAATCTGCAATTCAATAGCTCCCTGGAAGACCCCT

Gene : MUC1R
Segment# : 8
Offset : 106
1st Codon : 1
F H I S N L Q F N S S L E D P S T D Y Y Q E L Q R D I S E M
TTCCATATCTCCAACCTCCAGTTTAACTCCAGCCTCAGGATCCCTCCACCGATTACTATCAGGAAGTCAAAGGGATATCTCCGAGATG

Gene : MUC1R
Segment# : 9
Offset : 121
1st Codon : 1
S T D Y Y Q E L Q R D I S E M F L Q I Y K Q G G F L G L S N
AGCACAGACTATTACCAAGAGCTCCAGAGAGACATTAGCGAAATGTTTCTGCAAATCTATAAGCAAGGCGGATTCTCGGCCTCAGCAAT

Gene : MUC1R
Segment# : 10
Offset : 136
1st Codon : 1
F L Q I Y K Q G G F L G L S N I K F R P G S V V V Q L T L A
TTCTCCAGATTACAAACAGGGAGGCTTCTGGGACTGTCCAACATTAAGTTTAGGCCTGGCTCCGTGGTTCGTGCAACTGACACTGGCT

Gene : MUC1R
Segment# : 11
Offset : 151
1st Codon : 1
I K F R P G S V V V Q L T L A F R E G T I N V H D V E T Q F
ATCAAATTACAGACCCGGAAGCGTTCGTGGTCCAGCTCACCTCGCCTTAGGGAAGGCACAATCAATGTGCATGACGTCGAGACACAGTTT

Gene : MUC1R
Segment# : 12
Offset : 166
1st Codon : 1
F R E G T I N V H D V E T Q F N Q Y K T E A A S R Y N L T I
TTCAGAGAGGGAACCATTAACGTCCACGATGTGGAAACCAATTCAATCAGTATAAGACAGAGGCTGCCTCCAGGTATAACCTCACCATT

Gene : MUC1R
Segment# : 13
Offset : 181
1st Codon : 1
N Q Y K T E A A S R Y N L T I S D V S V S D V P F P F S A Q
AACCAATACAAAACCGAAGCCGCTAGCAGATACAATCTGCAATCTCCGACGTCAGCGTCAGCGATGTGCCTTTCCCTTTCTCCGCCCAA

Gene : MUC1R
Segment# : 14
Offset : 196
1st Codon : 1
S D V S V S D V P F P F S A Q S G A G V P G W G I A L L V L
AGCGATGTGTCCGTGTCCGACGTCCCTTTCCCTTAGCGCTCAGTCCGGCGTGGCGTCCCGGATGGGGAATCGCTCTGCTCGTGCTC

Gene : MUC1R
Segment# : 15
Offset : 211
1st Codon : 1
S G A G V P G W G I A L L V L V C V L V A L L A I V Y L I A L
AGCGGAGCCGGAGTGCCTGGCTGGGGCATTGCCCTCCTGGTCTGGTCTGCGTCTGGTTCGCCCTCGCCATTGTGTATCTGATTGCCCTC

Gene : MUC1R
Segment# : 16
Offset : 226
1st Codon : 1
V C V L V A L A I V Y L I A L A V C Q C R R K N Y G Q L D I
GTGTGTGTGCTCGTGGCTCTGGCTATCGTCTACCTCATCGCTCTGGCTGTGTGTAGTGTAGGAGAAAGAATTACGGACAGCTCGACATT

Gene : MUC1R
Segment# : 17
Offset : 241
1st Codon : 1

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Figure 27 (Cont)

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1st Codon : 1
 A V C Q C R R K N Y G Q L D I F P A R D T Y H P M S E Y P T
 GCCGTCTGCCAATGCAGAAGGAAAACTATGGCCAAGTGGATATCTTTCCCGCTAGGGATACCTATCACCTATGTCCGAGTATCCCACA

Gene : MUC1R
 Segment# : 18
 Offset : 256
 1st Codon : 1

F P A R D T Y H P M S E Y P T Y H T H G R Y V P P S S T D R
 TTCCCTGCCAGAGACACATACCATCCCATGAGCGAATACCCTACCTATCACACACACGGAAGGTATGTGCCTCCCTCCAGCACAGACAGA

Gene : MUC1R
 Segment# : 19
 Offset : 271
 1st Codon : 1

Y H T H G R Y V P P S S T D R S P Y E K V S A G N G G S S L
 TACCATACCATGGCAGATACGTCCCCCTAGCTCCACCGATAGTCCCCCTATGAGAAAGTGTCCGCCGAAACGGAGGCTCCAGCCTC

Gene : MUC1R
 Segment# : 20
 Offset : 286
 1st Codon : 1

S P Y E K V S A G N G G S S L S Y T N P A V A A A S A N L A
 AGCCCTTACGAAAAGGTGAGCGCTGGCAATGGCGGAAGTCCCTGTCTACACAAACCTGCCGTGCGCGTGCCTCCGCCAATCTGGCT

Gene : MUC1R
 Segment# : 21
 Offset : 301
 1st Codon : 1

S Y T N P A V A A A S A N L A A
 AGCTATACCAATCCCGCTGTGGCTGCCGCTAGCGCTAACCTCGCCGCT

Segments in scrambled order:

 gp100 #4
 W N R Q L Y P E W T E A Q R L D C W R G G Q V S L K V S N D
 TGGAATAGGCAACTGTATCCCGAATGGACAGAGGCTCAGAGACTGGATTGCTGGAGGGGAGGCCAAGTGTCCCTGAAAGTGTCCAACGAT

TRP2 #6
 P Y I L R N Q D D R E L W P R K F F H R T C K C T G N F A G
 CCCTATATCCTCAGGAATCAGGATGACAGAGAGCTCTGGCCTAGGAAATCTTTACAGAACCTGTAAGTGTACCGGAACTTTGCCGGA

Tyros #30
 R N G D F F I S S K D L G Y D Y S Y L Q D S D P D S F Q D Y
 AGGAATGGCGATTCTTTATCTCCAGCAAAGACCTCGGCTATGACTATAGCTATCTGCAAGACTCCGACCTGACTCCTTCCAAGACTAT

TRP-1 #1
 A A P A F L T W H R Y H L L R L E K D M Q E M L Q E P S F S
 GCCGCTCCCGCTTTCTCCTCACCTGGCACAGATACCATCTGCTCAGGCTCGAGAAAGACATGCAGGAAATGCTCCAGGAACCTCCTTCTCC

Tyros #29
 G H N R E S Y M V P F I P L Y R N G D F F I S S K D L G Y D
 GGCCATAACAGAGAGTCTTACATGGTGCTTTTCATTCCCCTCTACAGAAACGGAGACTTTTTCATTAGCTCCAAGGATCTGGGATACGAT

TRP2 #16
 L L C L E R D L Q R L I G N E S F A L P Y W N F A T G R N E
 CTGCTCTGCCTCGAGAGAGACCTCCAGAGACTGATGGCAATGAGTCCTTCGCTCTGCCTTACTGGAACCTTGCCACAGGCAGAAAACGAA

gp100 #23
 T T E V V G T T P G Q A P T A E P S G T T S V Q V P T T E V
 ACCACAGAGGTCGTGGGAACACACCCGGACAGGCTCCACAGCCGAACCTCCGGCACAACCTCCGTGCAAGTGCCTACCACAGAGGTC

MUC1R #9
 S T D Y Y Q E L Q R D I S E M F L Q I Y K Q G G F L G L S N
 AGCACAGACTATTACCAAGAGCTCCAGAGAGACATTAGCGAAATGTTTCTGCAAATCTATAAGCAAGGCGGATTCTCGGCCTCAGCAAT

gp100 #36
 A C M E I S S P G C Q P P A Q R L C Q P V L P S P A C Q L V
 GCCTGTATGGAAATCTCCAGCCCTGGCTGTCAGCTCCCCTCAGAGACTGTGTAGCCTGTGCTCCCTCCCCGCTTGCCAACCTGGTC

TRP2 #31
 D Q L G Y S Y A I D L P V S V E E T P G W P T T L L V V M G

Figure 27 (Cont)

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GACCAACTGGGATACTCCTACGCTATCGATCTGCCTGTGTCCGTGGAAGAGACACCCGGATGGCCTACCACACTGCTCGTGGTCATGGGA

TRP-1 #7

T E D G P I R R N P A G N V A R P M V Q R L P E P Q D V A Q
ACCGAAGACGGACCCATTAGGAGAAACCTGCCGAAACGTCGCCAGACCCATGGTGCAAAGGCTCCCCGAACCCCAAGACGTCGCCCAA

TRP2 #3

C M T V D S L V N K E C C P R L G A E S A N V C G S Q Q G R
TGCATGACCGTCGACTCCCTGGTCAACAAAGAGTGTTGCCCTAGGCTCGGCGCTGAGTCCGCCAATGTGTGTGGCTCCAGCAAGGCAGA

MUC1R #13

N Q Y K T E A A S R Y N L T I S D V S V S D V P F P F S A Q
AACCAATACAAAACCGAAGCCGCTAGCAGATACAATCTGACAATCTCCGACGTCAGCGTCAGCGATGTGCCTTTCCCTTCTCCGCCCAA

TRP2 #1

A A M S P L W W G F L L S C L G C K I L P G A Q G Q F P R V
GCCGCTATGTCCCCCTCTGGTGGGGCTTTCTGCTCAGCTGTCTGGGATGCAAAATCCTCCCGGAGCCCAAGGCCAATTCCCTAGGGTC

gp100 #18

A D L S Y T W D F G D S S G T L I S R A L V V T H T Y L E P
GCCGATCTGTCTACACATGGGATTTTCGGAGACTCCAGCGGAACCTCATCTCCAGGGCTCTGGTCTGTGACACACACATACCTCGAGCCT

gp100 #27

L A E M S T P E A T G M T P A E V S I V V L S G T T A A Q V
CTGGCTGAGATGAGCACACCCGAAGCCACAGGCATGACCCCTGCCGAAGTGTCCATCGTCTGTCTCAGCGGAACACAGCCGCTCAGGTC

MUC1R #11

I K F R P G S V V V Q L T L A F R E G T I N V H D V E T Q F
ATCAAATTCAGACCCGGAAGCGTCGTGGTCCAGCTCACCCCTCGCCTTTAGGGAAGGCACAATCAATGTGCATGACGTCGAGACACAGTTT

MUC1F #7

G S A A T W G Q D V T S V P V T R P A L G S T T P P A H D V
GGCTCCGCCGCTACCTGGGGCCAAGACGTCACCTCCGTGCCTGTGACAAGGCCCTGCCCTCGGCTCCACCACACCCCTGCCCATGACGTC

MC1R #16

L H K R Q R P V H Q G F G L K G A V T L T I L L G I F F L C
CTGCATAAGAGACAGAGACCCGTCCACCAAGGCTTTGGCCTCAAGGGAGCCGTCACCCCTACCATTTCTGTCTCGGCATTTTCTTTCTGTGT

MC1R #20

L A L I I C N A I I D P L I Y A F H S Q E L R R T L K E V L
CTGGCTCTGATTATCTGTAACGCTATCATTGACCCTCTGATTACGCTTTCCATAGCCAAGAGCTCAGGAGAACCCTCAAGGAAGTGCTC

TRP2 #7

K F F H R T C K C T G N F A G Y N C G D C K F G W T G P N C
AAGTTTTTCCATAGGACATGCAAATGCACAGGCAATTTTCGTGGCTATAACTGTGGCGATTGCAAATTCGGATGGACAGGCCCTAACTGT

TRP2 #23

L S L Q K F D N P P F F Q N S T F S F R N A L E G F D K A D
CTGTCCCTGCAAAAGTTTGACAAATCCCCCTTTCTTTTCAGATAGCACATTCTCCTTCAGAAACGCTCTGGAAGGCTTTGACAAAGCCGAT

MUC1R #4

S K S T P F S I P S H H S D T P T T L A S H S T K T D A S S
AGCAAAAGCACACCCCTTTAGCATTCCCTCCACCATAGCGATACCCCTACCACACTGGCTAGCCATAGCACAAAGACAGACGCTAGCTCC

MUC1R #1

A A N R P A L G S T A P P V H N V T S A S G S A S G S A S T
GCCGCTAACAGACCCGCTCTGGGAAGCACAGCCCTCCCGTCCACAATGTGACAAGCGCTAGCGGAAGCGCTAGCGGAAGCGCTAGCACA

TRP2 #21

C N G T Y E G L L R R N Q M G R N S M K L P T L K D I R D C
TGCAATGGCACATACGAAGGCCTCTGAGAAGGAATCAGATGGGCAGAACTCCATGAACTGCCTACCCCTCAAGGATATCAGAGACTGT

MUC1R #6

T H H S S V P P L T S S N H S T S P Q L S T G V S F F F L S
ACCCATCACTCCAGCGTCCCCCTCTGACAAGCTCCAACCATAGCACAAAGCCCTCAGCTCAGCACAGGCGTCAGCTTTTTCTTTCTGTCC

MC1R #13

F I A Y Y D H V A V L L C L V V F F L A M L V L M A V L Y V
TTCATTGCCTATTACGATCAGTCGCCGTCCTGCTCTGCCTCGTGGTCTTCTTTCTGGCTATGCTCGTGTCTCATGGCTGTGCTCTACGTC

Tyros #16

K L T G D E N F T I P Y W D W R D A E K C D I C T D E Y M G

Figure 27 (Cont)

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AAGCTCACCGGAGACGAAAACTTTACCATTCCCTATTGGGATTGGAGAGACGCTGAGAAATGCGATATCTGTACCGATGAGTATATGGGA

gp100 #32
L R L V K R Q V P L D C V L Y R Y G S F S V T L D I V Q G I
CTGAGACTGGTCAAGAGACAGGTCCCCCTCGACTGTGTGCTCTACAGATACGGAAGCTTTAGCGTCACCCCTCGACATTGTGCAAGGCATT

MClR #10
F L Q I Y K Q G G F L G L S N I K F R P G S V V V Q L T L A
TTCCTCCAGATTTACAAACAGGGAGGCTTTCTGGGACTGTCCAACATTAAGTTTAGGCCTGGCTCCGTGGTCTGCAACTGACACTGGCT

MClR #9
V I D V I T C S S M L S S L C F L G A I A V D R Y I S I F Y
GTGATTGACGTCATCACATGCTCCAGCATGCTGTCCAGCCTCTGCTTTCTGGGAGCCATTGCCGTGACAGATACATTAGCATTTTCTAT

Tyros #21
R N P G N H D K S R T P R L P S S A D V E F C L S L T Q Y E
AGGAATCCCGAAACCATGACAAAAGCAGAACCCTAGGCTCCCCCTCCAGCGCTGACGTCGAGTTTTCCTCAGCCTCACCCAATACGAA

TRP-1 #14
F D E W L R R Y N A D I S T F P L E N A P I G H N R Q Y N M
TTCGATGAGTGGCTGAGAAGGTATAACGCTGACATTAGCACATTCCCTCTGGAAAACGCTCCCATTGGCCATAACAGACAGTATAACATG

gp100 #39
V S L A D T N S L A V V S T Q L I M P G Q E A G L G Q V P L
GTGTCCCTGGCTGACACAACTCCCTGGCTGTGGTCAGCACACAGCTCATCATGCCCGACAGGAAGCCGGACTGGGACAGGTCCCCCTC

gp100 #20
G P V T A Q V V L Q A A I P L T S C G S S P V P G T T D G H
GGCCCTGTGACAGCCCAAGTGGTCTGCAAGCCGCTATCCCTCTGACAAGCTGTGGCTCCAGCCCTGTGCCTGGCACAACCGATGGCCAT

Tyros #8
K F G F W G P N C T E R R L L V R R N I F D L S A P E K D K
AAGTTTGGCTTTTGGGGACCCAATTGCACAGAGAGAAGGCTCCTGGTCAGGAGAAACATTTTCGATCTGTCCGCCCCCTGAGAAAGACAAA

gp100 #13
L G T H T M E V T V Y H R R G S R S Y V P L A H S S S A F T
CTGGGAACCCATACCATGGAGGTACCGCTCTACCATAGGAGAGGCTCCAGGTCTACGTCCCCCTCGCCCATAGCTCCAGCGCTTTTACA

MClR #12
A V A A I W V A S V V F S T L F I A Y Y D H V A V L L C L V
GCCGTGCGCGCTATCTGGGTGGCTAGCGTCGTGTTTAGCACACTGTTTATCGCTTACTATGACCATGTGGCTGTGCTCCTGTGTCTGGTC

TRP2 #25
G T L D S Q V M S L H N L V H S F L N G T N A L P H S A A N
GGCACACTGGATAGCCAAGTGATGAGCCTCCACAATCTGGTCCACTCCTTCTCAACGGAACCAATGCCCTCCCCCATAGCGCTGCCAAT

MART #4
G C W Y C R R R N G Y R A L M D K S L H V G T Q C A L T R R
GGCTGTTGGTATTGCAAGGAGAAACGGATACAGAGCCCTCATGGATAAGTCCCTGCATGTGGGAACCAATGCCTCTGACAAGGAGA

Tyros #15
P W H R L F L L R W E Q E I Q K L T G D E N F T I P Y W D W
CCCTGGCACAGACTGTTTCTGCTCAGGTGGGAGCAAGAGATTGAGAACTGACAGGCGATGAGAATTTACAATCCCTTACTGGGACTGG

MClR #1
A A M A V Q G S Q R R L L G S L N S T P T A I P Q L G L A A
GCCGCTATGGCTGTGCAAGGCTCCCAGAGAAGGCTCCTGGGAAGCCTCAACTCCACCCTACCGCTATCCCTCAGCTCGGCCTCGCCGCT

MClR #5
V V A T I A K N R N L H S P M Y C F I C C L A L S D L L V S
GTGTGCGCCACAATCGCTAAGAATAGGAATCTGCATAGCCCTATGTATTGCTTTATCTGTTGCCTCGCCCTCAGCGATCTGCTCGTGTCTC

Tyros #25
Q S S M H N A L H I Y M N G T M S Q V Q G S A N D P I F L L
CAGTCCAGCATGCACAATGCCCTCCACATTTACATGAACGGAACCATGAGCCAAGTGCAAGGCTCCGCCAATGACCCTATCTTTCTGCTC

Tyros #18
G Q H P T N P N L L S P A S F F S S W Q I V C S R L E E Y N
GGCCAACACCCTACCAATCCCAATCTGCTCAGCCCTGCCTCCTTCTTTAGCTCCTGGCAAATCGTCTGCTCCAGGCTCGAGGAATACAAT

MClR #6
Y C F I C C L A L S D L L V S G T N V L E T A V I L L L E A

Figure 27 (Cont)

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TACTGTTTCATTGCTGTCTGGCTCTGTCCGACCTCCTGGTCAGCGGAACCAATGTGCTCGAGACAGCCGTCATCCTCCTGCTCGAGGCT

TRP2 #19
D P T L I S R N S R F S S W E T V C D S L D D Y N H L V T L
GACCCTACCCTCATCTCCAGGAATAGCAGATTCTCCAGCTGGGAGACAGTGTGTGACTCCCTGGATGACTATAACCATCTGGTCACCCCTC

MUC1F #8
T R P A L G S T T P P A H D V T S A P D N K A A
ACCAGACCCGCTCTGGGAAGCACAAACCCCTCCCGCTCACGATGTGACAAGCGCTCCCGATAACAAAGCCGCT

Tyros #17
R D A E K C D I C T D E Y M G G Q H P T N P N L L S P A S F
AGGGATGCCGAAAAGTGTGACATTTGCACAGACGAATACATGGGCGGACAGCATCCCACAAACCTAACCTCCTGTCCCCGCTAGCTTT

gp100 #17
T F A L Q L H D P S G Y L A E A D L S Y T W D F G D S S G T
ACCTTTGCCCTCCAGCTCCACGATCCCTCCGGCTATCTGGCTGAGGCTGACCTCAGCTATACCTGGGACTTTGGCGATAGCTCCGGCACA

Tyros #22
S S A D V E F C L S L T Q Y E S G S M D K A A N F S F R N T
AGCTCCGCCGATGTGGAATTCTGTCTGTCCCTGACACAGTATGAGTCCGGCTCCATGGATAAGGCTGCCAATTCTCCTTCAGAAACACA

gp100 #6
G P T L I G A N A S F S I A L N F P G S Q K V L P D G Q V I
GGCCCTACCTCATCGGAGCAATGCCTCCTTCTCCATCGCTCTGAATTTCCCTGGCTCCCAGAAAGTGCTCCCCGATGGCCAAGTGATT

MC1R #18
W G P F F L H L T L I V L C P E H P T C G C I F K N F N L F
TGGGGACCCCTTTTCTCCACCTCACCTCATCGTCTGTGTCCGAACACCTTACCTGTGGCTGTATCTTTAAGAATTTCAATCTGTTT

Tyros #7
C Q C S G N F M G F N C G N C K F G F W G P N C T E R R L L
TGCCAATGCTCCGGCAATTTTCATGGGCTTTAACTGTGGCAATTGCAAATTCGGATTCTGGGGCCCTAACTGTACCGAAAGGAGACTGCTC

TRP2 #34
Q Y R R L R K G Y T P L M E T H L S S K R Y T E E A A A
CAGTATAGGAGACTGAGAAAGGGATACACACCCCTCATGGAACCCATCTGTCCAGCAAAGGTATACCGAAGAGGCTGCCGCT

TRP-1 #15
P L E N A P I G H N R Q Y N M V P F W P P V T N T E M F V T
CCCCTCGAGAATGCCCTATCGGACACAATAGGCAATACAATATGTTCCCTTTTGGCTCCCGTCACCAATACCGAAATGTTTGTGACA

gp100 #7
N F P G S Q K V L P D G Q V I W V N N T I I N G S Q V W G G
AACTTTCCCGGAAGCCAAAAGGTCTGCTGACGGACAGGTATCTGGGTGAATAACACAATCATTAACGGAAGCCAAGTGTGGGGCGGA

gp100 #22
R P T A E A P N T T A G Q V P T T E V V G T T P G Q A P T A
AGGCCTACCGCTGAGGCTCCCAATACCACAGCCGACAGTCCCCACAACCGAAGTGGTCGGCACAACCCCTGGCCAAGCCCTACCGCT

MUC1F #3
S T P G G E K E T S A T Q R S S V P S S T E K N A V S M T S
AGCACACCCGGAGGCGAAAAGGAAACCTCCGCCACACAGAGAAGCTCCGTGCCTAGCTCCACCGAAAAGAATGCCGTGAGCATGACCTCC

gp100 #42
L I Y R R R L M K Q D F S V P Q L P H S S S H W L R L P R I
CTGATTTACAGAAGGAGACTGATGAAGCAAGACTTTAGCGTCCCCCACTGCCTCACTCCAGCTCCCACTGGCTGAGACTGCCTAGGATT

TRP2 #12
L G L L G P N G T Q P Q F A N C S V Y D F F V W L H Y Y S V
CTGGGACTGCTCGGCCCTAACGGAACCCAACCCCAATTCGCTAACTGTAGCGTCTACGATTTCTTTGTGTGGCTGCATTACTATAGCGTC

TRP-1 #9
C L E V G L F D T P P F Y S N S T N S F R N T V E G Y S D P
TGCCCTCGAGGTCGGCTCTTCGATACCCCTCCCTTTTACTCCAACCTCCACCAATAGCTTTAGGAATACCGTCGAGGGATACTCCGACCCCT

gp100 #1
A A M D L V L K R C L L H L A V I G A L L A V G A T K V P R
GCCGCTATGGATCTGGTCTGAAAAGGTGTCTGCTCCACCTCGCCGTCATCGGAGCCCTCCTGGCTGTGGGAGCCACAAAGGTCCCCAGA

MC1R #3
N Q T G A R C L E V S I S D G L F L S L G L V S L V E N A L

Figure 27 (Cont)

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AACCAAACCGGAGCCAGATGCCTCGAGGTCAGCATTAGCGATGGCCTCTTCCTCAGCCTCGGCCTCGTGTCCTGGTCGAGAATGCCCTC

Tyros #23

S G S M D K A A N F S F R N T L E G F A S P L T G I A D A S
AGCGGAAGCATGGACAAAGCCGCTAACTTTAGCTTTAGGAATACCCTCGAGGGATTGCTAGCCCTCTGACAGGCATTGCCGATGCCCTC

Tyros #4

S P C G Q L S G R G S C Q N I L L S N A P L G P Q F P F T G
AGCCCTTGCGGACAGCTCAGCGGAAGGGGAAGCTGTGAGAATATCCTCCTGTCCAACGCTCCCCTCGGCCCTCAGTTTCCCTTTACCGGA

Tyros #13

M H Y Y V S M D A L L G G S E I W R D I D F A H E A P A F L
ATGATTACTATGTGTCCATGGATGCCCTCCTGGGAGGCTCCGAGATTTGGAGAGACATTGACTTTGCCCATGAGGCTCCCGCTTTCCTC

Tyros #35

E E K Q P L L M E K E D Y H S L Y Q S H L A A
GAGGAAAAGCAACCCCTCCTGATGGAGAAAGAGGATTACCATAGCCTCTACCAAAGCCATCTGGCTGCC

TRP2 #5

G Q C T E V R A D T R P W S G P Y I L R N Q D D R E L W P R
GGCCAATGCACAGAGGTGAGGGCTGACACAAGGCCTTGGTCCGGCCCTTACATTCTGAGAAACCAAGACGATAGGGAAGTGTGGCCAG

MUC1F #4

S V P S S T E K N A V S M T S S V L S S H S P G S G S S T T
AGCGTCCCCTCCAGCACAGAGAAAAACGCTGTGTCCATGACAAGCTCCGTGCTCAGCTCCCCTCCCGGAAGCGGAAGCTCCACCACA

Tyros #12

T P M F N D I N I Y D L F V W M H Y Y V S M D A L L G G S E
ACCCCTATGTTTAAAGATATCAATATCTATGACCTCTTCGTCTGGATGCACTATTACGTCAGCATGGACGCTCTGCTCGGCGGAAGCGAA

gp100 #9

Q P V Y P Q E T D D A C I F P D G G P C P S G S W S Q K R S
CAGCCTGTGTATCCCAAGAGACAGACGATGCCTGTATCTTTCCCGATGGCGGACCCTGTCCCTCCGGCTCCTGGTCCCAGAAAAGGTCC

TRP-1 #6

D S L E D Y D T L G T L C N S T E D G P I R R N P A G N V A
GACTCCCTGGAAGACTATGACACACTGGGAACCCCTCTGCAATAGCACAGAGGATGGCCCTATCAGAAGGAATCCCGCTGGCAATGTGGCT

gp100 #8

W V N N T I I N G S Q V W G G Q P V Y P Q E T D D A C I F P
TGGGTCAACAATACCATTATCAATGGCTCCAGGTCTGGGGAGGCCAACCCGCTACCTCAGGAAACCGATGACGCTTGCAATTTTCCCT

MART #7

Q E K N C E P V V P N A P P A Y E K L S A E Q S P P P Y S P
CAGGAAAAGAATTGCGAACCCGTCGTGCCTAACGCTCCCCCTGCCTATGAGAACTGTCCGCCGAACAGTCCCCCCTCCCTATAGCCCT

gp100 #14

S R S Y V P L A H S S S A F T I T D Q V P F S V S V S Q L R
AGCAGAAGCTATGTGCTCTGGCTCACTCCAGCTCCGCCCTTACCATTACCGATCAGGTCCCCTTTAGCGTCAGCGTCAGCCAAGTGA

TRP-1 #2

L E K D M Q E M L Q E P S F S L P Y W N F A T G K N V C D I
CTGGAAGAGGATATGCAAGAGATGCTGCAAGAGCCTAGCTTTAGCCTCCCCTATTGGAATTTGCTACCGAAAGAATGTGTGTGACATT

TRP-1 #16

V P F W P P V T N T E M F V T A P D N L G Y T Y E A A
GTGCCCTTCTGGCCCCCTGTGACAAACACAGAGATGTTTCGTACCGCTCCCGATAACCTCGGCTATACCTATGAGGCTGCC

TRP2 #13

C S V Y D F F V W L H Y Y S V R D T L L G P G R P Y R A I D
TGCTCCGTGTATGACTTTTTCGTCTGGCTCCACTATTACTCCGTGAGAGACACACTGCTCGGCCCTGGCAGACCCTATAGGCTATCGAT

Tyros #9

V R R N I F D L S A P E K D K F F A Y L T L A K H T I S S D
GTGAGAAGGAATATCTTTGACCTCAGCGCTCCCGAAAAGGATAAGTTTTTCGCTTACCTCACCTCGCAAACACACAATCTCCAGCGAT

MART #2

K K G H G H S Y T T A E E A A G I G I L T V I L G V L L L I
AAGAAAGGCCATGGCCATAGCTATACCACAGCCGAAGAGGCTGCCGAATCGGAATCCTCACCGTCATCCTCGGCGTCTGCTCCTGATT

gp100 #11

F V Y V W K T W G Q Y W Q V L G G P V S G L S I G T G R A M

Figure 27 (Cont)

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TTCGTCTACGTCTGGAAAACCTGGGGCCAATACTGGCAGGTCCTGGGAGGCCCTGTGTCCGGCCTCAGCATTGGCACAGGCAGAGCCATG

gp100 #12
G G P V S G L S I G T G R A M L G T H T M E V T V Y H R R G
GGCGGACCCGTCAGCGGACTGTCCATCGGAACCGGAAGGGCTATGCTCGGCACACACACAATGGAAGTGACAGTGTATCAGAGAAGGGGA

gp100 #25
I S T A P V Q M P T A E S T G M T P E K V P V S E V M G T T
ATCTCCACCGCTCCCGTCCAGATGCCCACAGCCGAAAGCACAGGCATGACCCCTGAGAAAGTGCCTGTGTCCGAGGTCTATGGGAACCACA

Tyros #19
F S S W Q I V C S R L E E Y N S H Q S L C N G T P E G P L R
TTCCTCAGCTGGCAGATTGTGTGTAGCAGACTGGAAGAGTATAACTCCACCAAAGCCTCTGCAATGGCACACCCGAAGGCCCTCTGAGA

TRP2 #27
D P I F V V L H S F T D A I F D E W M K R F N P P A D A W P
GACCCATCTTTGTGGTCTGCATAGCTTTACCGATGCCATTTTCGATGAGTGGATGAAAGGTTTAAACCCTCCCGCTGACGCTTGGCCT

MC1R #15
H M L A R A C Q H A Q G I A R L H K R Q R P V H Q G F G L K
CACATGCTGGCTAGGGCTTGCCAAACAGCTCAGGGAATCGCTAGGCTCCACAAAAGGCAAAGGCCCTGTGCATCAGGGATTCCGACTGAAA

MUC1F #2
L L T V L T V V T G S G H A S S T P G G E K E T S A T Q R S
CTGCTCACCGTCTGACAGTGGTACCCGGAAGCGGACAGCTAGCTCCACCCCTGGCGGAGAGAAAAGAGACAAGCGCTACCCAAAGGTCC

gp100 #44
F C S C P I G E N S P L L S G Q Q V A A
TTCTGTAGCTGTCCCATTTGGCGAAAACCTCCCCCTCCTGTCCGGCCAACAGGTCGCCGCT

TRP2 #24
T F S F R N A L E G F D K A D G T L D S Q V M S L H N L V H
ACCTTTAGCTTTAGGAATGCCCTCGAGGGATTGATAAGGCTGACGGAACCCCTCGACTCCAGGTCAATGTCCCTGCATAACCTCGTGCAT

Tyros #20
S H Q S L C N G T P E G P L R R N P G N H D K S R T P R L P
AGCCATCAGTCCCTGTGTAAACGGAACCCCTGAGGGACCCCTCAGGAGAAACCCCTGGCAATCACGATAAGTCCAGGACACCCAGACTGCCT

TRP2 #30
P F F P P V T N E E L F L T S D Q L G Y S Y A I D L P V S V
CCCTTTTCCCTCCCGTCACCAATGAGGAACCTGTTCGTGACAAGCGATCAGTCCGGCTATAGCTATGCCATTGACCTCCCGCTCAGCGTC

TRP2 #9
E R K K P P V I R Q N I H S L S P Q E R E Q F L G A L D L A
GAGAGAAAGAAACCCCTGTGATTAGGCAAAACATTCACCTCCCTGTCCCCCAAGAGAGAGCAATTCCTCGGCGCTCTGGATCTGGCT

TRP2 #29
Q E L A P I G H N R M Y N M V P F F P P V T N E E L F L T S
CAGGAACCTGGCTCCCATTTGGCCATAACAGAATGTATAACATGGTGCCTTTCTTTCCCTGTGACAAACGAAGAGCTCTTCCTCACCTCC

gp100 #28
E V S I V V L S G T T A A Q V T T T E W V E T T A R E L P I
GAGGTCAGCATTGTGGTCTGTCCGGCACAACCGCTGCCCAAGTGACAACCACAGAGTGGGTGGAAACCACAGCCAGAGAGCTCCCCATT

MUC1R #7
T S P Q L S T G V S F F F L S F H I S N L Q F N S S L E D P
ACCTCCCCCAACTGTCCACCGAGTGTCTTCTTTTCTCAGCTTTTACATTAGCAATCTGCAATTCAATAGCTCCCTGGAAGACCTT

MUC1R #19
Y H T H G R Y V P P S S T D R S P Y E K V S A G N G G S S L
TACCATACCCATGGCAGATACGTCCCCCTAGCTCCACCGATAGTCCCCCTATGAGAAAGTGTCCGCCGGAACCGAGGCTCCAGCCTC

MC1R #4
L F L S L G L V S L V E N A L V V A T I A K N R N L H S P M
CTGTTTCTGTCCCTGGGACTGGTCAGCCTCGTGGAAAACGCTCTGGTCTGGCTACCATTGCCAAAACAGAAACCTCCACTCCCCCATG

TRP2 #26
S F L N G T N A L P H S A A N D P I F V V L H S F T D A I F
AGCTTTCTGAATGGCACAACGCTCTGCCTCACTCCGCCGCTAACGATCCCATTTTCGTCTGTCTCCACTCCTTCACAGACGCTATCTTT

MUC1R #17
A V C Q C R R K N Y G Q L D I F P A R D T Y H P M S E Y P T

Figure 27 (Cont)

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GCCGCTCTGCCAATGCAGAAGGAAAACTATGGCCAACTGGATATCTTTCCCGCTAGGGATACCTATCACCTATGTCCGAGTATCCCACA

MC1R #14

V F F L A M L V L M A V L Y V H M L A R A C Q H A Q G I A R
GTGTTTTTCTCGCCATGCTGGTCTGTATGGCCGTCTGTATGTGCATATGCTCGCCAGAGCCTGTCAGCATGCCCAAGGCATTGCCAGA

TRP-1 #10

S T N S F R N T V E G Y S D P T G K Y D P A V R S L H N L A
AGCACAACTCCTTCAGAAACACAGTGGAAAGGCTATAGCGATCCACAGGCAAATACGATCCCGCTGTGAGAAGCCTCCACAATCTGGCT

TRP-1 #3

L P Y W N F A T G K N V C D I C T D D L M G S R S N F D S T
CTGCCTTACTGGAACCTTGCCACAGGCAAAACGTCTGCGATATCTGTACCGATGACCTCATGGGAAGCAGAAGCAATTTGATAGCACA

gp100 #15

I T D Q V P F S V S V S Q L R A L D G G N K H F L R N Q P L
ATCAGACCAAGTGCTTTTCTCCGTGTCCGTGTCCAGCTCAGGCTCTGGATGGCGGAAACAAACACTTTCTGAGAAACCAACCCCTC

MUC1R #8

F H I S N L Q F N S S L E D P S T D Y Y Q E L Q R D I S E M
TTCCATATCTCCAACCTCCAGTTTAACTCCAGCCTCGAGGATCCCTCCACCGATTACTATCAGGAAGTCAAAGGGATATCTCCGAGATG

MUC1R #20

S P Y E K V S A G N G G S S L S Y T N P A V A A A S A N L A
AGCCCTTACGAAAAGGTGAGCGCTGGCAATGGCGGAAGTCCCTGTCTACACAAACCCTGCCGTGCGCGCTGCCCTCCGCAATCTGGCT

Tyros #11

Y V I P I G T Y G Q M K N G S T P M F N D I N I Y D L F V W
TACGTCATCCCTATCGGAACCTATGGCCAAATGAAAACGGAAGCACACCCATGTTCAATGACATTAACATTTACGATCTGTTTGTGTGG

gp100 #37

R L C Q P V L P S P A C Q L V L H Q I L K G G S G T Y C L N
AGGCTCTGCCAACCCGTCTGCCTAGCCCTGCCTGTGAGCTCGTGCTCCACCAATCTCAAGGGAGGCTCCGGCACATACTGTCTGAAT

gp100 #33

R Y G S F S V T L D I V Q G I E S A E I L Q A V P S G E G D
AGGTATGGCTCCTTCTCCGTGACACTGGATATCGTCCAGGGAATCGAAAGCGCTGAGATTCTGCAAGCCGTCCCTCCGGCGAAGGCGAT

Tyros #27

H H A F V D S I F E Q W L Q R H R P L Q E V Y P E A N A P I
CACCATGCCTTTGTGGATAGCATTTTTCGAACAGTGGCTGCAAAGGCATAGGCCCTCTGCAAGAGGTCTACCCCTGAGGCTAACGCTCCCAT

TRP-1 #4

C T D D L M G S R S N F D S T L I S P N S V F S Q W R V V C
TGCACAGACGATCTGATGGGCTCCAGGTCCAACTTTGACTCCACCTCATCTCCCCAATAGCGTCTTCTCCAGTGGAGGGTCTGTGTGT

MUC1R #18

F P A R D T Y H P M S E Y P T Y H T H G R Y V P P S S T D R
TTCCCTGCCAGAGACACATACCATCCCATGAGCGAATACCCTACCTATCACACACAGGAAGGTATGTGCTCCCTCCAGCACAGACAGA

MUC1R #21

S Y T N P A V A A A S A N L A A
AGCTATACCAATCCCGCTGTGGCTGCCGCTAGCGCTAACCTCGCCGCT

MC1R #19

E H P T C G C I F K N F N L F L A L I I C N A I I D P L I Y
GAGCATCCACATGCGGATGCATTTTCAAAAACCTTTAACCTCTTCTCGCCCTCATCATTTGCAATGCCATTATCGATCCCTCATCTAT

Tyros #26

M S Q V Q G S A N D P I F L L H H A F V D S I F E Q W L Q R
ATGTCCAGGTCCAGGGAAGCGCTAACGATCCCATTTTCTCTGTCATCAGCTTTTCGTGACTCCATCTTTGAGCAATGGCTCCAGAGA

TRP2 #22

R N S M K L P T L K D I R D C L S L Q K F D N P P F F Q N S
AGGAATAGCATGAAGCTCCCACTGAAAGACATTAGGGATTGCCTCAGCCTCCAGAAATTCGATAACCTCCCTTTTCCAAAACCTCC

gp100 #19

L I S R A L V V T H T Y L E P G P V T A Q V V L Q A A I P L
CTGATTAGCAGAGCCCTCGTGGTCACCCATACCTATCTGGAACCCGGACCCGTCACCGCTCAGGTCTGTCTCCAGGCTGCCATTCCCTCT

TRP2 #17

S F A L P Y W N F A T G R N E C D V C T D Q L F G A A R P D

Figure 27 (Cont)

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AGCTTTGCCCTCCCCTATTGGAATTTTCGCTACCGGAAGGAATGAGTGTGACGTCTGCACAGACCAACTGTTTGGCGCTGCCAGACCCGAT

gp100 #2
V I G A L L A V G A T K V P R N Q D W L G V S R Q L R T K A
GTGATTGGCGCTCTGCTCGCCGTCGGCGCTACCAAAGTGCCTAGGAATCAGGATTGGCTCGGCGTCAGCAGACAGCTCAGGACAAAGGCT

gp100 #16
A L D G G N K H F L R N Q P L T F A L Q L H D P S G Y L A E
GCCCTCGACGGAGGCAATAAGCATTTCCTCAGGAATCAGCCTCTGACATTGCTCTGCAACTGCATGACCCTAGCGGATACCTCGCCGAA

TRP2 #18
C D V C T D Q L F G A A R P D D P T L I S R N S R F S S W E
TGCATGTGTGTACCGATCAGCTCTTCGGAGCCGCTAGGCCTGACGATCCCACTGATTAGCAGAACTCCAGGTTTAGCTCCTGGGAA

MART #1
A A M P R E D A H F I Y G Y P K K G H G H S Y T T A E E A A
GCCCTATGCTAGGGAAGACGCTCACTTTATCTATGGCTATCCAAAAAGGGACACGGACACTCCTACACAACCGCTGAGGAAGCCGCT

TRP-1 #11
T G K Y D P A V R S L H N L A H L F L N G T G G Q T H L S S
ACCGAAAAGTATGACCCTGCCGTGAGTCCCTGCATAACCTCGCCCATCTGTTTCTGAATGGCACAGGCGGACAGACACCTCAGCTCC

MUC1R #14
S D V S V S D V P F P F S A Q S G A G V P G W G I A L L V L
AGCGATGTGTCCGTGTCCGACGTCCCCTTTCCCTTTAGCGCTCAGTCCGGCGCTGGCGTCCCGGATGGGGAATCGCTCTGCTCGTGTCTC

TRP2 #10
S P Q E R E Q F L G A L D L A K K R V H P D Y V I T T Q H W
AGCCCTCAGGAAAGGGAACAGTTTCTGGGAGCCCTCGACCTCGCCAAAAGAGAGTGCATCCCGATTACGTATCACAAACCAACACTGG

Tyros #10
F F A Y L T L A K H T I S S D Y V I P I G T Y G Q M K N G S
TTCTTTGCTATCTGACACTGGCTAAGCATAACCATTAGCTCCGACTATGTGATTCCCATTTGGCACATACGGACAGATGAAGAATGGCTCC

MC1R #7
G T N V L E T A V I L L L E A G A L V A R A A V L Q Q L D N
GGCACAACGTCCTGGAAACCGCTGTGATTCTGCTCCTGGAAGCCGGAGCCCTCGTGGCTAGGGCTGCCGTCTGCAACAGCTCGACAAT

MUC1R #16
V C V L V A L A I V Y L I A L A V C Q C R R K N Y G Q L D I
GTGTGTGTGCTCGTGGCTCTGGCTATCGTCTACCTCATCGCTCTGGCTGTGTGTGTCAGTGTAGGAGAAAGATTACGGACAGCTCGACATT

MART #6
C P Q E G F D H R D S K V S L Q E K N C E P V V P N A P P A
TGCCCTCAGGAAGGCTTTTGACCATAGGGATAGCAAAGTGTCCCTGCAAGAGAAAACTGTGAGCCTGTGGTCCCCAATGCCCTCCCGCT

MUC1F #5
S V L S S H S P G S G S S T T Q G Q D V T L A P A T E P A S
AGCGTCTGTCTCAGCCATAGCCCTGGCTCCGGCTCCAGCACAACCAAGGCCAAGACGTACCCCTCGCCCTGCCACAGAGCTGCCTCC

TRP2 #28
D E W M K R F N P P A D A W P Q E L A P I G H N R M Y N M V
GACGAATGGATGAAGAGATTCAATCCCCCTGCCGATGCTGGCCCCAAGAGCTCGCCCTATCGGACACAATAGGATGTACAATATGGTC

MC1R #21
A F H S Q E L R R T L K E V L T C S W A A
GCCTTTCACTCCCAGGAAGTGAAGAGGACACTGAAAGAGGTCTGACATGCTCCTGGGCTGCC

TRP2 #15
F S H Q G P A F V T W H R Y H L L C L E R D L Q R L I G N E
TTCTCCCAAGGCCCTGCCTTTGTGACATGGCATAGGTATCACCTCCTGTGTCTGGAAAGGGATCTGCAAAGGCTCATCGGAAACGAA

TRP-1 #8
R P M V Q R L P E P Q D V A Q C L E V G L F D T P P F Y S N
AGGCATATGTTCCAGAGACTGCCTGAGCCTCAGGATGTGGCTCAGTGTCTGGAAGTGGGACTGTTTGTACACACCCCTTCTATAGCAAT

TRP-1 #13
Q D P I F V L L H T F T D A V F D E W L R R Y N A D I S T F
CAGGATCCCATTTTCGTCTGCTCCACATTACAGACGCTGTGTTTGACGAATGGCTCAGGAGATACAATGCCGATATCTCCACCTTT

TRP2 #4
L G A E S A N V C G S Q Q G R G Q C T E V R A D T R P W S G

Figure 27 (Cont)

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CTGGGAGCCGAAAGCGCTAACGTCTGCGGAAGCCAAACAGGGAAGGGGACAGTGTACCGAAGTGAGAGCCGATACCAGACCCTGGAGCGGA

TRP2 #8

Y N C G D C K F G W T G P N C E R K K P P V I R Q N I H S L
TACAATTGCGGAGACTGTAAGTTTGGCTGGACCGGACCCAATTGCGAAAGGAAAAAGCCTCCCGTCATCAGACAGAATATCCATAGCCTC

TRP-1 #12

H L F L N G T G G Q T H L S S Q D P I F V L L H T F T D A V
CACCTCTTCTCAACGGAACCGGAGGCCAAACCCATCTGTCCAGCCAAGACCCTATCTTTGTGCTCCTGCATACCTTTACCGATGCCGTC

Tyros #34

G L V S L L C R H K R K Q L P E E K Q P L L M E K E D Y H S
GGCCTCGTGTCCCTGTCTGTGACAGACACAAAAGGAAACAGCTCCCCGAAGAGAAACAGCCTCTGCTCATGGAAGGAAGACTATCACTCC

TRP2 #2

G C K I L P G A Q G Q F P R V C M T V D S L V N K E C C P R
GGCTGTAAGATTCTGCTGGCGCTCAGGGACAGTTTCCAGAGTGTGTATGACAGTGGATAGCCTCGTGAATAAGGAATGCTGTCCAGA

gp100 #43

Q L P H S S S H W L R L P R I F C S C P I G E N S P L L S G
CAGTCCCCCATAGCTCCAGCCATTGGCTCAGGCTCCCCAGAATCTTTTGTCTGCCCTATCGGAGAGAATAGCCCTCTGCTCAGCGGA

gp100 #10

D G G P C P S G S W S Q K R S F V Y V W K T W G Q Y W Q V L
GACGGAGGCCCTTGCCCTAGCGGAAGCTGGAGCCAAAAGAGAAGCTTTGTGTATGTGTGGAAGACATGGGGACAGTATTGGCAAGTGCTC

gp100 #3

N Q D W L G V S R Q L R T K A W N R Q L Y P E W T E A Q R L
AACCAAGACTGGCTGGGAGTGTCCAGGCAACTGAGAACCAAGCCTGGAACAGACAGCTCTACCCTGAGTGGACCGAAGCCCAAGGCTC

Tyros #14

I W R D I D F A H E A P A F L P W H R L F L L R W E Q E I Q
ATCTGGAGGGATATCGATTTTCGCTCACGAAGCCCCTGCCTTTCTGCCTTGGCATAGGCTCTTCCTCCTGAGATGGGAACAGGAAATCCAA

MUC1F #1

A A M T P G T Q S P F F L L L L L T V L T V V T G S G H A S
GCCGCTATGACACCCGGAACCCAAAGCCCTTTCTTTCTGCTCCTGCTCCTGACAGTGTCTACCGTCTGACAGGCTCCGGCCATGCCCTC

MART #5

D K S L H V G T Q C A L T R R C P Q E G F D H R D S K V S L
GACAAAAGCCTCCAGCTCGGCACACAGTGTGCCTCACCAGAAGGTGTCCCCAAGAGGGATTTCGATCACAGAGACTCCAAGGTCAGCCTC

MUC1R #2

N V T S A S G S A S G S A S T L V H N G T S A R A T T T P A
AACGTACCTCCGCCTCCGGCTCCGCCTCCGCCTCCACCCTCGTGCATAACGGAACCTCCGCCAGAGCCACAACCACACCCGCT

Tyros #24

L E G F A S P L T G I A D A S Q S S M H N A L H I Y M N G T
CTGGAAGGCTTTTGCTCCCCCTCACCGGAATCGCTGACGCTAGCCAAAGCTCCATGCATAACGCTCTGCATATCTATATGAATGGACA

TRP2 #14

R D T L L G P G R P Y R A I D F S H Q G P A F V T W H R Y H
AGGGATACCCTCCTGGGACCCGGAAGGCCTTACAGAGCCATTGACTTTAGCCATCAGGGACCCGCTTTTCGTACCTGGCACAGATACCAT

Tyros #1

A A M L L A V L Y C L L W S F Q T S A G H F P R A C V S S K
GCCGCTATGCTCCTGGCTGTGCTCTACTGTCTGCTCTGGTCTTCCAAACCTCCGCCGGACACTTTCCAGAGCCTGTGTGTCCAGCAA

gp100 #35

A F E L T V S C Q G G L P K E A C M E I S S P G C Q P P A Q
GCCTTTGAGCTACCGTCTAGCTGTCTAGGGAGGCCTCCCCAAGAGGCTTGATGGAGATTAGCTCCCCCGGATGCCAACCCCTGCCCAA

Tyros #6

V D D R E S W P S V F Y N R T C Q C S G N F M G F N C G N C
GTGGATGACAGAGAGTCTTGGCCTAGCGTCTTCTATAACAGAACCTGTCTAGTGTAGCGGAACTTTATGGGATTCAATTGCGGAAAGTGT

gp100 #34

E S A E I L Q A V P S G E G D A F E L T V S C Q G G L P K E
GAGTCCGCCGAAATCTCCAGGCTGTGCCTAGCGGAGAGGGAGACGCTTTGAACTGACAGTGTCTGCCAAGGCGGACTGCCTAAGGAA

TRP2 #20

T V C D S L D D Y N H L V T L C N G T Y E G L L R R N Q M G

Figure 27 (Cont)

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ACCGTCTGCGATAGCCTCGACGATTACAATCACCTCGTGACACTGTGTAACGGAACCTATGAGGGACTGCTCAGGAGAAACCAAATGGGA

Tyros #5

L L S N A P L G P Q F P F T G V D D R E S W P S V F Y N R T
CTGCTCAGCAATGCCCTCTGGGACCCCAATTCCCTTTCACAGGCGTCGACGATAGGGAAAGCTGGCCCTCCGTGTTTTACAATAGGACA

MART #8

Y E K L S A E Q S P P P Y S P A A
TACGAAAAGCTCAGCGCTGAGCAAAGCCCTCCCCCTTACTCCCCGCTGCC

gp100 #41

I V G I L L V L M A V V L A S L I Y R R R L M K Q D F S V P
ATCGTCGGCATTCTGCTCGTGTCTCATGGCTGTGGTCTGGCTAGCCTCATCTATAGGAGAAGGCTCATGAAACAGGATTCTCCGTGCCCT

MART #3

G I G I L T V I L G V L L L I G C W Y C R R R N G Y R A L M
GGCATTGGCATTCTGACAGTGATTCTGGGAGTGCTCTGCTCATCGGATGCTGGTACTGTAGGAGAAGGAATGGCTATAGGGCTCTGATG

Tyros #31

Y S Y L Q D S D P D S F Q D Y I K S Y L E Q A S R I W S W L
TACTCCTACCTCCAGGATAGCGATCCCGATAGCTTTCAGGATTACATTAAGTCCTACCTCGAGCAAGCCTCCAGGATTGGTCTGGCTC

MUC1F #6

Q G Q D V T L A P A T E P A S G S A A T W G Q D V T S V P V
CAGGGACAGGATGTGACACTGGCTCCCGCTACCGAACCGCTAGCGGAAGCGTGCCACATGGGGACAGGATGTGACAAGCGTCCCGCTC

gp100 #21

T S C G S S P V P G T T D G H R P T A E A P N T T A G Q V P
ACCTCCTGCGGAAGCTCCCCGTCCCCGGAACACAGACGGACACAGACCCACAGCCGAAGCCCTAACACACCGCTGGCCAAGTGCCT

MUC1R #3

L V H N G T S A R A T T T P A S K S T P F S I P S H H S D T
CTGGTCCACAATGGCACAAGCGCTAGGGCTACCACAACCCCTGCCTCCAAGTCCACCCCTTCTCCATCCCTAGCCATCACTCCGACACA

TRP2 #32

E E T P G W P T T L L V V M G T L V A L V G L F V L L A F L
GAGGAAACCCCTGGCTGGCCCAACCCCTCCTGGTCGTGATGGGCACACTGGTCGCCCTCGTGGGACTGTTTGTGCTCCTGGCTTTCCCTC

gp100 #29

T T T E W V E T T A R E L P I P E P E G P D A S S I M S T E
ACCACAACCGAATGGGTGAGACAACCGCTAGGGAATGCCTATCCCTGAGCCCTGAGGGACCCGATGCCTCCAGCATATGTCCACCGAA

MUC1R #17

G A V T L T I L L G I F F L C W G P F F L H L T L I V L C P
GGCGCTGTGACACTGACAATCCTCCTGGGAATCTTTTCTCTGCTGGGGCCCTTCTTTCTGCATCTGACACTGATTGTGCTCTGCCCT

Tyros #33

L G A A M V G A V L T A L L A G L V S L L C R H K R K Q L P
CTGGGAGCCGCTATGGTCGGCGCTGTGCTCACCGCTCTGCTCGCCGACTGGTCAGCCTCCTGTGTAGGCATAAGAGAAAGCAACTGCCT

MUC1R #8

G A L V A R A A V L Q Q L D N V I D V I T C S S M L S S L C
GGCGCTCTGGTCGCCAGAGCCGCTGTGCTCCAGCAACTGGATAACGTCATCGATGTGATTACCTGTAGCTCCATGCTCAGCTCCCTGTGT

gp100 #26

M T P E K V P V S E V M G T T L A E M S T P E A T G M T P A
ATGACACCCGAAAAGGTCCCGTCAGCGAAGTGATGGGCACAACCCCTCGCCGAAATGTCCACCCCTGAGGCTACCGAATGACACCCGCT

Tyros #2

Q T S A G H F P R A C V S S K N L M E K E C C P P W S G D R
CAGACAAGCGCTGGCCATTTCCTAGGGCTTGCCTCAGCTCCAAGAATCTGATGGAGAAAGAGTGTGCCCCCTCCCTGGAGCGGAGACAGA

MUC1R #11

A L R Y H S I V T L P R A P R A V A A I W V A S V V F S T L
GCCCTCAGGTATCACTCCATCGTCACCCCTCCCCAGAGCCCTTAGGCTGTGGCTGCCATTTGGGTGCGCCTCCGTGGTCTTCTCCACCCCT

MUC1R #12

F R E G T I N V H D V E T Q F N Q Y K T E A A S R Y N L T I
TTCAGAGAGGGAACCATTAACGTCCACGATGTGGAACCCCAATTCAATCAGTATAAGACAGAGGCTGCCTCCAGGTATAACCTCACCATT

Tyros #3

N L M E K E C C P P W S G D R S P C G Q L S G R G S C Q N I

Figure 27 (Cont)

AACCTCATGAAAAGGAATGCTGTCCCCCTTGGTCCGGCGATAGGTCCCCCTGTGGCCAACTGTCCGGCAGAGGCTCCTGCCAAACATT

I K S Y L E Q A S R I W S W L L G A A M V G A V L T A L L A
ATCAAAGCTATCTGGAACAGGCTAGCAGAATCTGGAGCTGGCTGCTCGGCGCTGCCATGGTGGGAGCCGCTCTGACAGCCCTCTGGCT

P T T L A S H S T K T D A S S T H H S S V P P L T S S N H S
 CCCACAACCCCTCGCCTCCCACTCCACCAAACCGATGCCTCCAGCACACCATAGCTCCGTCGCTCCCCTCACCTCCAGCAATCACTCC

S G A G V P G W G I A L L V L V C V L V A L A I V Y L I A L
AGCGGAGCCGGAGTGCCTGGCTGGGGCATTGCCCTCCTGGTCCTGCTCGTCTGGTCGCCCTCGCCATTGTGTATCTGATTGCCCTC

F L G A I A V D R Y I S I F Y A L R Y H S I V T L P R A P R
TTCTCTGGCGCTATCGCTGTGGATAGGTATATCTCCATCTTTTACGCTCTGAGATACCATAGCATTGTGACACTGCCTAGGGCTCCCAGA

L I M P G Q E A G L G Q V P L I V G I L L V L M A V V L A S
CTGATTATGCCTGGCCAAGAGGCTGGCCTCGGCCAAGTGCCTCTGATTGTGGGAATCCTCCTGGTCCTGATGGCCGTCGTGCTCGCCTCC

T L V A L V G L F V L L A F L Q Y R R L R K G Y T P L M E T
ACCCCTCGTGGCTCTGGTCGGCCTCTTCGTCCTGCTCGCCTTTCTGCAATACAGAAGGCTCAGGAAGGCTATACCCCTCTGATGGAGACA

L I S P N S V F S Q W R V V C D S L E D Y D T L G T L C N S
CTGATTAGCCCTAACTCCGTGTTTAGCCAATGGAGAGTGGTCTGCGATAGCCTCGAGGATTACGATACCCTCGGCACACTGTGTAACCTCC

L N S T P T A I P Q L G L A A N Q T G A R C L E V S I S D G
CTGAATAGCACACCCACAGCCATTCCCCAACTGGGACTGGCTGCCAATCAGACAGGCGCTAGGTGTCTGGAAGTGTCCATCTCCGACGGA

H R P L Q E V Y P E A N A P I G H N R E S Y M V P F I P L Y
CACAGACCCCTCCAGGAAGTGTATCCCCAAGCCAATGCCCTATCGGACACAATAGGGAAAGCTATATGGTCCCTTTATCCCTCTGTAT

E P S G T T S V Q V P T T E V I S T A P V Q M P T A E S T G
GAGCCTAGCGGAACCACAAGCGTCCAGGTCCCCACAACCGAAGTGATTAGCACAGCCCCCTGTGCAAATGCCTACCGCTGAGTCCACCGGA

K K R V H P D Y V I T T Q H W L G L L G P N G T Q P Q F A N
AAGAAAAGGGTCCACCCTGACTATGTGATTACCACACAGCATTGGCTCGGCCTCCTGGGACCCAATGGCACACAGCCTCAGTTTGCCAAT

L H Q I L K G G S G T Y C L N V S L A D T N S L A V V S T Q
 CTGCATCAGATTCTGAAAGGCGGAAGCGGAACCTATTGCCTCAACGTCAGCCTCGCCGATACCAATAGCCTCGCCGTCGTGTCCACCCAA

P E P E G P D A S S I M S T E S I T G S L G P L L D G T A T
CCCGAACCCGAAGGCCCTGACGCTAGCTCCATCATGAGCACAGAGTCCATCACAGGCTCCCTGGGACCCCTCCTGGATGGCCAGCCACA

S I T G S L G P L L D G T A T L R L V K R Q V P L D C V L Y
AGCATTACCGGAAGCCTCGGCCCTGCTCGACGGAACCGCTACCCCTCAGGCTCGTGAAGGCAAGTCCTCTGGATTGCGTCCTGTAT

D C W R G G Q V S L K V S N D G P T L I G A N A S F S I A L
SACTGTTGGAGAGGCGGACAGGTCAAGCTCAGCAATGACGGACCCACACTGATTGGCGCTAACGCTAGCTTTAGCATTGCCCTC

NRQLYPEWTEAQRRLDCWRGGQVSLVNSMDPFYILRNQDDRELWPRKFHFRCTCKTGNFAGRNGDFFISSKDLGYDYSYSLQSDPDPSQDYAAPAFLTW
HRYHLRLLEKMDQEMLEQPSFGHNRESYMVPIFLYRNGDFFISSKDLGYDLCLLERDLQRLIGNESSPALQYPMNFAFTGRNETTEVVGTPPGQATPE
SGTTSVQVPTTEVSTDYQELQDILSEMFLQYKGGGFLGSNACMETISSPGCAQPLQCPVLSPACQLVDQLGYSYADLPVSVETEGPWPIT
LLVMVGTEGDIRLRNPNAGNVARMVQRLPEPDQVACMTVDGLSVNKECCPRLGAESANVGSQGGQNRQYKTEAASRYNLITSDVSVSDVPFPFSAQA
SMLPWGFLGSLCKGLCKLPGAQQLCPVRADLSYTWDFDGSGLTILSRALVWTHTYIPLBAEMSTPEATGMPFAEVSIVLSGTLTAQVIKFREGSVV
QLTLAFREGTINVHDVETQFGSAATWGDVTSVPVTRPAGDSGLTTPAHADVHLHKRQRPVHQGFLKGAVTTLTILLGIFFLCLALIIICNAIDPLIYAFH
QELRLTLKEVLKFFHRTCTKTNFAGSAGYNGCDKCFKGTGPNCLSLQKFDNPPFFONCTFSFNALSGDKADSKTFFSIPSPHSDDTPTTLASHSTKI
SASAAANRALGSGTAPPHNVNITSAGSAGSNCTNGTYGBGLLRRNRQMGNSMKLPTLKDICTHSSVEPLTSGNHSNTSGTSGVSSFFLFSFIAY

Figure 27 (Cont)

[illegible]

Figure 27 (Cont)

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[illegible]

Figure 27 (Cont)

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[illegible]

Figure 27 (Cont)

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ATATGGTCCCCTTTATCCCTCTGTATGAGCCTAGCGGAACCACAAGCGTCCAGGTCCCCACAACCGAAGTGATTAGCACAGCCCCTGTGCAAATGCCT
ACCGCTGAGTCCACCGAAGAAAAGGGTCCACCCTGACTATGTGATTACACACAGCATTGGCTCGGCCCTCCTGGGACCCAATGGCACACAGCCTCA
GTTTGCCAATCTGCATCAGATTCTGAAAGGCGGAAGCGGAACCTATTGCCTCAACGTCAGCCTCGCCGATACCAATAGCCTCGCCGTGCTGCCACCC
AACCCGAACCCGAAGGCCCTGACGCTAGCTCCATCATGAGCACAGAGTCCATCACAGGCTCCCTGGGACCCCTCCTGGATGGCACAGCCACAAGCATT
ACCGGAAGCCTCGGCCCTCTGCTCGACGGAACCGCTACCCCTCAGGCTCGTGAAAAGGCAAGTGCCCTCTGGATTGCGTCCCTGTATGACTGTTGGAGAGG
CGGACAGGTGAGCCTCAAGGTGACGAATGACGGACCCACACTGATTGGCGCTAACGCTAGCTTTAGCATTGCCCTC

Melanoma cancer Specific Savine Scramble process

Scramble - Output File

Scramble version : 0.1 beta, 08/02/1999

Num. genes : 10

Num. segments : 121

Segment length : 30

Segment overlap : 15

Segments in original order:

Gene : BAGE

Segment# : 1

Offset : 1

1st Codon : 1

A A M A A R A V F L A L S A Q L L Q A R L M K E E S P V V S
GCCGCTATGGCTGCCAGAGCCGTCTTCCTCGCCCTCAGCGCTCAGTCCCTGCAAGCCAGACTGATGAAGGAAGAGTCCCCGTCGTGTCC

Gene : BAGE

Segment# : 2

Offset : 16

1st Codon : 1

L L Q A R L M K E E S P V V S W R L E P E D G T A L C F I F
CTGCTCCAGGCTAGGCTCATGAAAGAGGAAAGCCCTGTGGTCAGCTGGAGGCTCGAGCCTGAGGATGGCACAGCCCTCTGCTTTATCTTT

Gene : BAGE

Segment# : 3

Offset : 31

1st Codon : 1

W R L E P E D G T A L C F I F A A
TGGAGACTGGAAACCGAAGACGGAACCGCTCTGTGTTTCATTTTCGCTGCC

Gene : GAGE-1

Segment# : 1

Offset : 1

1st Codon : 1

A A M S W R G R S T Y R P R P R R Y V E P P E M I G P M R P
GCCGCTATGTCTTGAGAGGCAGAAAGCACATACAGACCCAGACCAGAGGTATGTGGAACCCCTGAGATGATCGGACCCATGAGGCCT

Gene : GAGE-1

Segment# : 2

Offset : 16

1st Codon : 1

R R Y V E P P E M I G P M R P E Q F S D E V E P A T P E E G
AGGAGATACGTCGAGCCTCCCGAAATGATTGGCCCTATGAGACCCGAACAGTTTAGCGATGAGGTCGAGCCTGCCACACCCGAAGAGGGA

Gene : GAGE-1

Segment# : 3

Offset : 31

1st Codon : 1

E Q F S D E V E P A T P E E G E P A T Q R Q D P A A A Q E G
GAGCAATTCTCCGACGAAGTGGAACCCGCTACCCCTGAGGAAGGCGAACCCGCTACCCAAAGGCAAGACCCTGCCGCTGCCCAAGAGGGA

Gene : GAGE-1

Segment# : 4

Offset : 46

1st Codon : 1

E P A T Q R Q D P A A A Q E G E D E G A S A G Q G P K P E A
GAGCCTGCCACACAGAGACAGGATCCCGCTGCCGCTCAGGAAGGCGAAGACGAAGGCGCTAGCGCTGGCCAAGGCCCTAAGCCTGAGGCT

Gene : GAGE-1

Segment# : 5

Offset : 61

1st Codon : 1

Figure 27 (Cont)

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E D E G A S A G Q G P K P E A D S Q E Q G H P Q T G C E C E
GAGGATGAGGGAGCCTCCGCCGACAGGGACCCAAACCCGAAGCCGATAGCCAAGAGCAAGGCCATCCCCAAACCGGATGCGAATGCGAA

Gene : GAGE-1
Segment# : 6
Offset : 76
1st Codon : 1
D S Q E Q G H P Q T G C E C E D G P D G Q E M D P P N P E E
GACTCCAGGAACAGGGACACCTCAGACAGGCTGTGAGTGTGAGGATGGCCCTGACGGACAGGAAATGGATCCCCCTAACCTGAGGAA

Gene : GAGE-1
Segment# : 7
Offset : 91
1st Codon : 1
D G P D G Q E M D P P N P E E V K T P E E E M R S H Y V A Q
GACGGACCCGATGGCCAAGAGATGGACCTCCCAATCCCGAAGAGGTCAAGACACCCGAAGAGGAAATGAGAAGCCATTACGTCGCCCA

Gene : GAGE-1
Segment# : 8
Offset : 106
1st Codon : 1
V K T P E E E M R S H Y V A Q T G I L W L L M N N C F L N L
GTGAAACCCCTGAGGAAGAGATGAGGTCCCACTATGTGGCTCAGACAGGCATTCTGTGGCTGCTCATGAATAACTGTTTCTCAACCTC

Gene : GAGE-1
Segment# : 9
Offset : 121
1st Codon : 1
T G I L W L L M N N C F L N L S P R K P A A
ACCGAATCCTCTGGCTCCTGATGAACAATTGCTTTCTGAATCTGTCCCCAGAAAGCCTGCCGCT

Gene : gp100In4
Segment# : 1
Offset : 1
1st Codon : 1
A A S W S Q K R S F V Y V W K T W G E G L P S Q P I I H T C
GCCGCTAGCTGGAGCCAAAGAGAAGCTTTGTGTATGTGTGGAAGACATGGGGAGAGGACTGCCTAGCCAACCCATTATCCATACCTGT

Gene : gp100In4
Segment# : 2
Offset : 16
1st Codon : 1
T W G E G L P S Q P I I H T C V Y F F L P D H L S F G R P F
ACCTGGGGCGAAGGCCTCCCCTCCAGCCTATCATTACACATGCGTCTACTTTTCTCCTCCCGATCACCTCAGCTTTGGCAGACCCCTT

Gene : gp100In4
Segment# : 3
Offset : 31
1st Codon : 1
V Y F F L P D H L S F G R P F H L N F C D F L A A
GTGTATTTCTTTCTGCTGACCATCTGTCTTCCGAAGGCCTTTCCATCTGAATTTCTGTGACTTTCTGGCTGCC

Gene : MAGE-1
Segment# : 1
Offset : 1
1st Codon : 1
A A M S L E Q R S L H C K P E E A L E A Q Q E A L G L V C V
GCCGCTATGTCCCTGGAACAGAGAAGCCTCCACTGTAAGCCTGAGGAAGCCCTCGAGGCTCAGCAAGAGGCTCTGGGACTGGTCTGCGTC

Gene : MAGE-1
Segment# : 2
Offset : 16
1st Codon : 1
E A L E A Q Q E A L G L V C V Q A A T S S S S P L V L G T L
GAGGCTCTGGAAGCCCAACAGGAAGCCCTCGGCCTCGTGTGTGTGCAAGCGCTACCTCCAGCTCCAGCCCTCTGGTCTGGGAACCCCT

Gene : MAGE-1
Segment# : 3
Offset : 31
1st Codon : 1
Q A A T S S S S P L V L G T L E E V P T A G S T D P P Q S P
CAGGCTGCCACAAGCTCCAGCTCCCCCTCGTGCTCGGCACACTGGAAGAGGTCCCCACAGCCGGAAGCACAGACCCCTCCCCAAGCCCT

Figure 27 (Cont)

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Gene : MAGE-1
Segment# : 4
Offset : 46
1st Codon : 1
E E V P T A G S T D P P Q S P Q G A S A F P T T I N F T R Q
GAGGAAGTGCTACCGCTGGCTCCACCGATCCCCCTCAGTCCCCCAAGGCGCTAGCGCTTTCCTACCACAATCAATTCACAAGGCAA

Gene : MAGE-1
Segment# : 5
Offset : 61
1st Codon : 1
Q G A S A F P T T I N F T R Q R Q P S E G S S S R E E E G P
CAGGGAGCCTCCGCCCTTCCCAACAACCATTAACCTTACCAGACAGAGACAGCCTAGCGAAGGCTCCAGCTCCAGGGAAGAGGAAGGCCCT

Gene : MAGE-1
Segment# : 6
Offset : 76
1st Codon : 1
R Q P S E G S S S R E E E G P S T S C I L E S L F R A V I T
AGGCAACCTCCGAGGGAAGCTCCAGCAGAGAGGAAGAGGGACCTCCACCTCCTGCATTCTGGAAAGCCTCTTCAGAGCCGTCATCACA

Gene : MAGE-1
Segment# : 7
Offset : 91
1st Codon : 1
S T S C I L E S L F R A V I T K K V A D L V G F L L L K Y R
AGCACAAGCTGTATCCTCGAGTCCCTGTTTAGGGCTGTGATTACCAAAAGGTCGCCGATCTGGTCGGCTTTCGTCTCTGAAATACAGA

Gene : MAGE-1
Segment# : 8
Offset : 106
1st Codon : 1
K K V A D L V G F L L L K Y R A R E P V T K A E M L E S V I
AAGAAAGTGGCTGACCTCGTGGGATTCCTCCTGCTCAAGTATAGGGCTAGGGAACCCGTACCAAAGCCGAAATGCTCGAGTCCGTGATT

Gene : MAGE-1
Segment# : 9
Offset : 121
1st Codon : 1
A R E P V T K A E M L E S V I K N Y K H C F P E I F G K A S
GCCAGAGAGCCTGTGACAAAGGCTGAGATGCTGGAAGCGTCATCAAAACTATAAGCATTGCTTTCCCGAAATCTTTGGCAAAGCCCTCC

Gene : MAGE-1
Segment# : 10
Offset : 136
1st Codon : 1
K N Y K H C F P E I F G K A S E S L Q L V F G I D V K E A D
AAGAATTACAAACTGTTCCTGAGATTTTCGGAAGGCTAGCGAAAGCCTCCAGCTCGTGTTCGTCATTGACGTCAAGGAAGCCGAT

Gene : MAGE-1
Segment# : 11
Offset : 151
1st Codon : 1
E S L Q L V F G I D V K E A D P T G H S Y V L V T C L G L S
GAGTCCCTGCAACTGGTCTTCGGAATCGATGTGAAAGAGGCTGACCTACCGGACACTCCTACGTCTGCTGACCTGTCTGGGACTGTCC

Gene : MAGE-1
Segment# : 12
Offset : 166
1st Codon : 1
P T G H S Y V L V T C L G L S Y D G L L G D N Q I M P K T G
CCCACAGGCCATAGCTATGTGCTCGTGACATGCCTCGGCCTCAGCTATGACGGACTGCTCGGCGATAACCAAATCATGCCCCAAACCGGA

Gene : MAGE-1
Segment# : 13
Offset : 181
1st Codon : 1
Y D G L L G D N Q I M P K T G F L I I V L V M I A M E G G H
TACGATGSCCTCCTGGGAGACAATCAGATTATGCCTAAGACAGGCTTCTGATTATCGTCCTGGTCATGATTGCCATGGAGGGAGGCCAT

Gene : MAGE-1

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Segment# : 14
Offset : 196
1st Codon : 1
F L I I V L V M I A M E G G H A P E E E I W E E L S V M E V
TTCTCATCATTGTGCTCGTGATGATCGCTATGGAAGGCGGACACGCTCCCGAAGAGGAAATCTGGGAGGAACCTGCTCGTGATGGAGGTC

Gene : MAGE-1
Segment# : 15
Offset : 211
1st Codon : 1
A P E E E I W E E L S V M E V Y D G R E H S A Y G E P R K L
GCCCTGAGGAAGAGATTGGGAAGAGCTCAGCGTCATGGAAGTGTATGACGGAAGGGAACACTCCGCCTATGGCGAACCAGAAAGCTC

Gene : MAGE-1
Segment# : 16
Offset : 226
1st Codon : 1
Y D G R E H S A Y G E P R K L L T Q D L V Q E K Y L E Y R Q
TACGATGGCAGAGAGCATAGCGCTTACGGAGAGCCTAGGAAACTGCTCACCCAAGACCTCGTGCAAGAGAAATACCTCGAGTATAGGCAA

Gene : MAGE-1
Segment# : 17
Offset : 241
1st Codon : 1
L T Q D L V Q E K Y L E Y R Q V P D S D P A R Y E F L W G P
CTGACACAGGATCTGGTCCAGGAAAAGTATCTGGAATACAGACAGGTCCCCGATAGCGATCCCGCTAGGTATGAGTTTCTGTGGGGCCCT

Gene : MAGE-1
Segment# : 18
Offset : 256
1st Codon : 1
V P D S D P A R Y E F L W G P R A L A E T S Y V K V L E Y V
GTGCTGACTCCGACCTGCGCAGATACGAATTCTCTGGGGACCCAGAGCCCTCGCCGAAACCTCCTACGTCAAGGTCTGGAATACGTC

Gene : MAGE-1
Segment# : 19
Offset : 271
1st Codon : 1
R A L A E T S Y V K V L E Y V I K V S A R V R F F F P S L R
AGGGCTCTGGCTGAGACAAGCTATGTGAAAGTGCTCGAGTATGTGATTAAGGTCAGCGCTAGGGTCAGGTTTTCTTTCCCTCCCTGAGA

Gene : MAGE-1
Segment# : 20
Offset : 286
1st Codon : 1
I K V S A R V R F F F P S L R E A A L R E E E E G V A A
ATCAAAGTGTCGCCAGAGTGAGATTCTTTTCCCTAGCCTCAGGGAAGCCGCTCTGAGAGAGGAAGAGGAAGGCGTCGCCGCT

Gene : MAGE-3
Segment# : 1
Offset : 1
1st Codon : 1
A A M P L E Q R S Q H C K P E E G L E A R G E A L G L V G A
GCCGCTATGCCTCTGGAACAGAGAAGCCAACACTGTAAGCCTGAGGAAGGCTCGAGGCTAGGGGAGAGGCTCTGGGACTGGTCGGCGCT

Gene : MAGE-3
Segment# : 2
Offset : 16
1st Codon : 1
E G L E A R G E A L G L V G A Q A P A T E E Q E A A S S S S
GAGGACTGGAAGCCAGAGGCGAAGCCCTCGGCCTCGTGGGAGCCCAAGCCCTGCCACAGAGGAACAGGAAGCCGCTAGCTCCAGCTCC

Gene : MAGE-3
Segment# : 3
Offset : 31
1st Codon : 1
Q A P A T E E Q E A A S S S S T L V E V T L G E V P A A E S
CAGGCTCCGCTACCGAAGAGCAAGAGGCTGCCCTCCAGCTCCAGCACACTGGTCGAGGTCACCCCTCGGCGAAGTGCTGCCGCTGAGTCC

Gene : MAGE-3
Segment# : 4
Offset : 46

Figure 27 (Cont)

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1st Codon : 1
T L V E V T L G E V P A A E S P D P P Q S P Q G A S S L P T
ACCTCGTGGAAGTGACACTGGGAGAGGTCCCCGCTGCCGAAAGCCCTGACCCTCCCCAAAGCCCTCAGGGAGCCTCCAGCCTCCCCACA

Gene : MAGE-3
Segment# : 5
Offset : 61
1st Codon : 1
P D P P Q S P Q G A S S L P T T M N Y P L W S Q S Y E D S S
CCCGATCCCCCTCAGTCCCCCAAGGCGCTAGCTCCCTGCCTACCACAATGAATTACCCTCTGTGGAGCCAAGCTATGAGGATAGCTCC

Gene : MAGE-3
Segment# : 6
Offset : 76
1st Codon : 1
T M N Y P L W S Q S Y E D S S N Q E E E G P S T F P D L E S
ACCATGAATATCCCCTCTGGTCCCAGTCTTACGAAGACTCCAGCAATCAGGAAGAGGAAGGCCCTAGCACATTCCCTGACCTCGAGTCC

Gene : MAGE-3
Segment# : 7
Offset : 91
1st Codon : 1
N Q E E E G P S T F P D L E S E F Q A A L S R K V A E L V H
AACCAAGAGGAAGAGGGACCCTCCACCTTTCCCGATCTGGAAAGCGAATTCCAGCCGCTCTGTCCAGGAAAGTGGCTGAGCTCGTGCAT

Gene : MAGE-3
Segment# : 8
Offset : 106
1st Codon : 1
E F Q A A L S R K V A E L V H F L L L K Y R A R E P V T K A
GAGTTTCAGGCTGCCCTCAGCAGAAAGGTCCGCCAAGTGGTCCACTTTCTGTCTCTGAAATACAGAGCCAGAGAGCCTGTGACAAAGGCT

Gene : MAGE-3
Segment# : 9
Offset : 121
1st Codon : 1
F L L L K Y R A R E P V T K A E M L G S V V G N W Q Y F F P
TTCTCCTGTCTAAGTATAGGGCTAGGGAACCCGTACCAAGCCGAAATGCTCGGCTCCGTGGTCCGCAATTGGCAATACTTTTCCCT

Gene : MAGE-3
Segment# : 10
Offset : 136
1st Codon : 1
E M L G S V V G N W Q Y F F P V I F S K A S S S L Q L V F G
GAGATGCTGGGAAGCGTCTGGGAAACTGGCAGTATTTCTTCCCGTCTATCTTTAGCAAAGCCTCCAGCTCCCTGCAACTGGTCTTCCGA

Gene : MAGE-3
Segment# : 11
Offset : 151
1st Codon : 1
V I F S K A S S S L Q L V F G I E L M E V D P I G H L Y I F
GTGATTTTCTCAAGGCTAGCTCCAGCCTCCAGCTCGTGTGGCATTGAGCTCATGGAAGTGGATCCCATTTGGCCATCTGTATATCTT

Gene : MAGE-3
Segment# : 12
Offset : 166
1st Codon : 1
I E L M E V D P I G H L Y I F A T C L G L S Y D G L L G D N
ATCGAATGATGGAGGTGACCCCTATCGGACACCTCTACATTTTCGCTACCTGTCTGGGACTGTCTACGATGGCCTCCTGGGAGACAAT

Gene : MAGE-3
Segment# : 13
Offset : 181
1st Codon : 1
A T C L G L S Y D G L L G D N Q I M P K A G L L I I V L A I
GCCACATGCCTCGGCCTCAGCTATGACGGACTGCTCGGCGATAACCAAATCATGCCCAAAGCCGGACTGTCTCATTTGTGCTCGCCATT

Gene : MAGE-3
Segment# : 14
Offset : 196
1st Codon : 1
Q I M P K A G L L I I V L A I I A R E G D C A P E E K I W E

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CAGATTATGCCTAAGGCTGGCCTCCTGATTATCGTCCTGGCTATCATTGCCAGAGAGGGAGACTGTGCCCCCTGAGGAAAAGATTGCGAA

Gene : MAGE-3
 Segment# : 15
 Offset : 211
 1st Codon : 1

I A R E G D C A P E E K I W E E L S V L E V F E G R E D S I
 ATCGCTAGGGAAGGCGATTGCGCTCCCGAAGAGAAAATCTGGGAGGAACGTGTCGCTCGAGGTCTTCAAGGCAGAGAGGATAGCATT

Gene : MAGE-3
 Segment# : 16
 Offset : 226
 1st Codon : 1

E L S V L E V F E G R E D S I L G D P K K L L T Q H F V Q E
 GAGCTCAGCGTCTTGAAGTGTGTTGAGGGAAGGGAAGACTCCATCCTCGGCGATCCCAAAAGCTCCTGACACAGCATTTGCTCCAGGAA

Gene : MAGE-3
 Segment# : 17
 Offset : 241
 1st Codon : 1

L G D P K K L L T Q H F V Q E N Y L E Y R Q V P G S D P A C
 CTGGGAGACCCCTAAGAACTGCTCACCCAACTTTGTGCAAGAGAATTACCTCGAGTATAGGCAAGTGCCTGGCTCCGACCTGCCGTGT

Gene : MAGE-3
 Segment# : 18
 Offset : 256
 1st Codon : 1

N Y L E Y R Q V P G S D P A C Y E F L W G P R A L V E T S Y
 AACTATCTGGAATACAGACAGGTCCCCGGAAGCGATCCCGCTTGCTATGAGTTTCTGTGGGGCCCTAGGGCTCTGGTCGAGACAAGCTAT

Gene : MAGE-3
 Segment# : 19
 Offset : 271
 1st Codon : 1

Y E F L W G P R A L V E T S Y V K V L H H M V K I S G G P H
 TACGAATTCCTCTGGGACCCAGAGCCCTCGTGGAAACCTCCTACGTCAAGGTCCTGCATCACATGGTGAAAATCTCCGCGGACCCCAT

Gene : MAGE-3
 Segment# : 20
 Offset : 286
 1st Codon : 1

V K V L H H M V K I S G G P H I S Y P P L H E W V L R E G E
 GTGAAAGTGCTCCACCATATGGTCAAGATTAGCGGAGGCCCTCACATTAGCTATCCCCCTCTGCATGAGTGGGTGCTCAGGGAAGGCGAA

Gene : MAGE-3
 Segment# : 21
 Offset : 301
 1st Codon : 1

I S Y P P L H E W V L R E G E E A A
 ATCTCTACCTCCCTCCACGAATGGGTCCTGAGAGAGGGAGAGGAAGCCGCT

Gene : PRAME
 Segment# : 1
 Offset : 1
 1st Codon : 1

A A M E R R R L W G S I Q S R Y I S M S V W T S P R R L V E
 GCCGCTATGGAAGGAGAAGGCTCTGGGGAAGCATTAGTCCAGGTATATCTCCATGTCCGTGTGGACCTCCCCCAGAAGGCTCGTGGAA

Gene : PRAME
 Segment# : 2
 Offset : 16
 1st Codon : 1

Y I S M S V W T S P R R L V E L A G Q S L L K D E A L A I A
 TACATTAGCATGAGCGTCTGGACAAGCCCTAGGAGACTGGTCGAGCTCGCCGACAGTCCCTGCTCAAGGATGAGGCTCTGGCTATCGCT

Gene : PRAME
 Segment# : 3
 Offset : 31
 1st Codon : 1

L A G Q S L L K D E A L A I A A L E L L P R E L F P P L F M
 CTGGCTGGCCAAAGCCTCCTGAAAGACGAAGCCCTCGCCATTGCCGCTCTGGAAGTCTCCCCAGAGAGCTTCTCCCTCCCTCTTCATG

Figure 27 (Cont)

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Gene : PRAME
Segment# : 4
Offset : 46
1st Codon : 1
A L E L L P R E L F P P L F M A A F D G R H S Q T L K A M V
GCCCTCGAGCTCCTGCCTAGGGAAGTGTTCCTCCCTCTGTTTATGGCTGCCTTTGACGGAAGGCATAGCCAAACCCTCAAGGCTATGGTC

Gene : PRAME
Segment# : 5
Offset : 61
1st Codon : 1
A A F D G R H S Q T L K A M V Q A W P F T C L P L G V L M K
GCCGCTTTTCGATGGCAGACACTCCAGACACTGAAAGCCATGGTGCAAGCCTGGCCCTTTACCTGTCTGCCTCTGGGAGTGCTCATGAAA

Gene : PRAME
Segment# : 6
Offset : 76
1st Codon : 1
Q A W P F T C L P L G V L M K G Q H L H L E T F K A V L D G
CAGGCTTGGCCTTTTACATGCCTCCCTCGGCGTCTGATGAAGGGACAGCATCTGCATCTGGAAACCTTTAAGGCTGTGCTCGACGGA

Gene : PRAME
Segment# : 7
Offset : 91
1st Codon : 1
G Q H L H L E T F K A V L D G L D V L L A Q E V R P R R W K
GGCCAACACCTCCACCTCGAGACATTCAAAGCCGTCCTGGATGGCCTCGACGTCCTGCTCGCCCAAGAGGTCAGGCCTAGGAGATGGAAA

Gene : PRAME
Segment# : 8
Offset : 106
1st Codon : 1
L D V L L A Q E V R P R R W K L Q V L D L R K N S H Q D F W
CTGGATGTGCTCCTGGCTCAGGAAGTGAGACCCAGAAGGTGGAAGCTCCAGGTCCTGGATCTGAGAAAGAATAGCCATCAGGATTTCTGG

Gene : PRAME
Segment# : 9
Offset : 121
1st Codon : 1
L Q V L D L R K N S H Q D F W T V W S G N R A S L Y S F P E
CTGCAAGTGCTCGACCTCAGGAAAACTCCACCAAGACTTTTGACAGTGTGGAGCGGAAACAGAGCCTCCCTGTATAGCTTTCCCGAA

Gene : PRAME
Segment# : 10
Offset : 136
1st Codon : 1
T V W S G N R A S L Y S F P E P E A A Q P M T K K R K V D G
ACCGTCTGGTCCGGCAATAGGGCTAGCCTCTACTCCTTCCTGAGCCTGAGGCTGCCCAACCCATGACCAAAAAGAGAAAGGTCGACGGA

Gene : PRAME
Segment# : 11
Offset : 151
1st Codon : 1
P E A A Q P M T K K R K V D G L S T E A E Q P F I P V E V L
CCCGAAGCCGCTCAGCCTATGACAAAGAAAAGGAAAGTGATGGCCTCAGCACAGAGGCTGAGCAACCCTTTATCCCTGTGGAAGTGCTC

Gene : PRAME
Segment# : 12
Offset : 166
1st Codon : 1
L S T E A E Q P F I P V E V L V D L F L K E G A C D E L F S
CTGTCCACCGAAGCCGAACAGCCTTTTATTCCTCGAGGTCCTGGTCGACCTCTTCTCCTCAGGAAGGCGCTTGCGATGAGCTCTTCTCC

Gene : PRAME
Segment# : 13
Offset : 181
1st Codon : 1
V D L F L K E G A C D E L F S Y L I E K V K R K K N V L R L
GTGGATCTGTTTCTGAAAGAGGGAGCCTGTGACGAAGTGTGTTAGCTATCTGATTGAGAAAGTGAAAAGGAAAAGAAATGTGCTCAGGCTC

Gene : PRAME
Segment# : 14

Figure 27 (Cont)

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Offset : 196
1st Codon : 1
Y L I E K V K R K K N V L R L C C K K L K I F A M P M Q D I
TACCTCATCGAAAAGGTCAAGAGAAAGAAAACGTCCTGAGACTGTGTGCAAAAAGCTCAAGATTTTCGCTATGCCTATGCAAGACATT

Gene : PRAME
Segment# : 15
Offset : 211
1st Codon : 1
C C K K L K I F A M P M Q D I K M I L K M V Q L D S I E D L
TGCTGTAAGAACTGAAAATCTTTGCCATGCCCATGCAGGATATCAAAATGATTCTGAAAATGGTCCAGCTCGACTCCATCGAAGACCTC

Gene : PRAME
Segment# : 16
Offset : 226
1st Codon : 1
K M I L K M V Q L D S I E D L E V T C T W K L P T L A K F S
AAGATGATCCTCAAGATGGTGCAACTGGATAGCATTGAGGATCTGGAAGTGACATGCACATGGAAGTGCCTACCCCTCGCCAAATCTCC

Gene : PRAME
Segment# : 17
Offset : 241
1st Codon : 1
E V T C T W K L P T L A K F S P Y L G Q M I N L R R L L L S
GAGGTACCTGTACCTGGAAGCTCCCCACTGGCTAAGTTTAGCCCTTACCTCGGCCAAATGATTAACTCAGGAGACTGCTCCTGTCC

Gene : PRAME
Segment# : 18
Offset : 256
1st Codon : 1
P Y L G Q M I N L R R L L L S H I H A S S Y I S P E K E E Q
CCCTATCTGGGACAGATGATCAATCTGAGAAGGCTCCTGCTCAGCCATATCCATGCCTCCAGCTATATCTCCCCGAAAAGGAAGAGCAA

Gene : PRAME
Segment# : 19
Offset : 271
1st Codon : 1
H I H A S S Y I S P E K E E Q Y I A Q F T S Q F L S L Q C L
CACATTACGCTAGCTCCTACATTAGCCCTGAGAAAGAGGAACAGTATATCGCTCAGTTTACCTCCAGTTTCTGTCCCTGCAATGCCTC

Gene : PRAME
Segment# : 20
Offset : 286
1st Codon : 1
Y I A Q F T S Q F L S L Q C L Q A L Y V D S L F F L R G R L
TACATTGCCCAATTACAAAGCCAATTCTCAGCCTCCAGTGTCTGCAAGCCCTCTACGTCGACTCCCTGTTTTCTCAGGGGAAGGCTC

Gene : PRAME
Segment# : 21
Offset : 301
1st Codon : 1
Q A L Y V D S L F F L R G R L D Q L L R H V M N P L E T L S
CAGGCTCTGTATGTGGATAGCCTCTTCTTTCTGAGAGGCAGACTGGATCAGCTCCTGAGACAGTCATGAATCCCTCGAGACACTGTCC

Gene : PRAME
Segment# : 22
Offset : 316
1st Codon : 1
D Q L L R H V M N P L E T L S I T N C R L S E G D V M H L S
GACCAACTGCTCAGGCATGTGATGAACCCTCTGAAAACCTCAGCATTACCAATTGCAGACTGTCCGAGGGAGACGTCATGCATCTGTCC

Gene : PRAME
Segment# : 23
Offset : 331
1st Codon : 1
I T N C R L S E G D V M H L S Q S P S V S Q L S V L S L S G
ATCACAAACTGTAGGCTCAGCGAAGGCGATGTGATGCACCTCAGCCAAAGCCCTAGCGTCAGCCAACTGTCCGTGCTCAGCCTCAGCGGA

Gene : PRAME
Segment# : 24
Offset : 346
1st Codon : 1

Figure 27 (Cont)

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Q S P S V S Q L S V L S L S G V M L T D V S P E P L Q A L L
CAGTCCCCCTCCGTGTCCAGCTCAGCGTCCCTGTCCGCGTCA¹TGCTCACCAGTGTGTCCCCGAACCCCTCCAGGCTCTGTCTC

Gene : PRAME
Segment# : 25
Offset : 361
1st Codon : 1

V M L T D V S P E P L Q A L L E R A S A T L Q D L V F D E C
GTGATGCTGACAGACGTGAGCCCTGAGCCTCTGCAAGCCCTCCTGGAAAGGGCTAGCGCTACCCTCCAGGATCTGGTCTTCGATGAGTGT

Gene : PRAME
Segment# : 26
Offset : 376
1st Codon : 1

E R A S A T L Q D L V F D E C G I T D D Q L L A L L P S L S
GAGAGAGCCTCCGCCACACTGCAAGACCTCGTGT¹TTGACGAATCGGAATCACAGACGATCAGCTCCTGGCTCTGCTCCCCTCCCTGTCC

Gene : PRAME
Segment# : 27
Offset : 391
1st Codon : 1

G I T D D Q L L A L L P S L S H C S Q L T T L S F Y G N S I
GGCATTACCGATGACCAACTGCTCGCCCTCCTGCCTAGCCTCAGCCATTGCTCCCAGCTCACCACACTGTCTCTATGGCAATAGCATT

Gene : PRAME
Segment# : 28
Offset : 406
1st Codon : 1

H C S Q L T T L S F Y G N S I S I S A L Q S L L Q H L I G L
CACTGTAGCCAACTGACAACCTCAGCTTTTACGGAACTCCATCTCCATCTCCGCCCTCCAGTCCCTGCTCCAGCATCTGATTGGCCTC

Gene : PRAME
Segment# : 29
Offset : 421
1st Codon : 1

S I S A L Q S L L Q H L I G L S N L T H V L Y P V P L E S Y
AGCATTAGCGCTCTGCAAAGCCTCCTGCAACACCTCATCGGACTGTCCAACCTCACCATGTGCTCTACCCTGTGCCTCTGGAAAGCTAT

Gene : PRAME
Segment# : 30
Offset : 436
1st Codon : 1

S N L T H V L Y P V P L E S Y E D I H G T L H L E R L A Y L
AGCAATCTGACACACGTCTGTATCCCCTCCCCCTCGAGTCTACGAAGACATTACGGAACCCCTCCACCTCGAGAGACTGGCTTACCTC

Gene : PRAME
Segment# : 31
Offset : 451
1st Codon : 1

E D I H G T L H L E R L A Y L H A R L R E L L C E L G R P S
GAGGATATCCATGGCACACTGCATCTGGAAAGGCTCGCCTATCTGCATGCCAGACTGAGAGAGCTCCTGTGTGAGCTCGGCAGACCCTCC

Gene : PRAME
Segment# : 32
Offset : 466
1st Codon : 1

H A R L R E L L C E L G R P S M V W L S A N P C P H C G D R
CACGCTAGGCTCAGGGAAGTGTCTGCGAACTGGGAAGGCCTAGCATGGTGTGGCTGTCCGCCAATCCCTGTCCCCATTGCGGAGACAGA

Gene : PRAME
Segment# : 33
Offset : 481
1st Codon : 1

M V W L S A N P C P H C G D R T F Y D P E P I L C P C F M P
ATGGTCTGGCTCAGCGCTAACCTTGCCCTCACTGTGGCGATAGGACATTCTATGACCCTGAGCCTATCCTCTGCCCTTGCTTTATGCCT

Gene : PRAME
Segment# : 34
Offset : 496
1st Codon : 1

T F Y D P E P I L C P C F M P N A A
ACCTTTTACGATCCCCGAACCATTTCTGTGTCCCTGTTTCATGCCCAATGCGCT

Figure 27 (Cont)

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Gene : TRP2IN2
Segment# : 1
Offset : 1
1st Codon : 1
A A L M E T H L S S K R Y T E E A G G F F P W L K V Y Y Y R
GCCGCTCTGATGGAGACACACCTCAGCTCCAAGAGATACACAGAGGAAGCCGAGGCTTTTCCCTTGGCTCAAGGTCTACTATTACAGA

Gene : TRP2IN2
Segment# : 2
Offset : 16
1st Codon : 1
E A G G F F P W L K V Y Y Y R F V I G L R V W Q W E V I S C
GAGGCTGGCGATTCTTCCCTGGCTGAAAGTGATTACTATAGTTTGTGATTGGCCTCAGGGTCTGGCAATGGGAAGTGATTAGCTGT

Gene : TRP2IN2
Segment# : 3
Offset : 31
1st Codon : 1
F V I G L R V W Q W E V I S C K L I K R A T T R Q P A A
TTCGTATCGGACTGAGAGTGTGGCAGTGGGAGGTATCTCTGCAAACGATTAAGAGAGCCACAACCAGACAGCCTGCCGCT

Gene : NYNSO1a
Segment# : 1
Offset : 1
1st Codon : 1
A A M Q A E G R G T G G S T G D A D G P G G P G I P D G P G
GCCGCTATGCAAGCCGAAGGCAGAGGCACAGGCGGAAGCACAGGCGATGCCGATGGCCCTGGCGGACCCGGAATCCCTGACGGACCCGGA

Gene : NYNSO1a
Segment# : 2
Offset : 16
1st Codon : 1
D A D G P G G P G I P D G P G G N A G G P G E A G A T G G R
GACGCTGACGGACCCGGAGGCCCTGGCATTCCCGATGGCCCTGGCGGAAACGCTGGCGGACCCGAGAGGCTGGCGCTACCGGAGGCAGA

Gene : NYNSO1a
Segment# : 3
Offset : 31
1st Codon : 1
G N A G G P G E A G A T G G R G P R G A G A A R A S G P G G
GGCAATGCCGAGGCCCTGGCGAAGCCGAGCCACAGGCGGAAGGGGACCCAGAGGCGCTGGCGCTGCCAGAGCCTCCGGCCCTGGCGGA

Gene : NYNSO1a
Segment# : 4
Offset : 46
1st Codon : 1
G P R G A G A A R A S G P G G G A P R G P H G G A A S G L N
GGCCCTAGGGGAGCCGAGCCGCTAGGGCTAGCGGACCCGAGGCGAGCCCTAGGGGACCCCATGGCGGAGCCGCTAGCGGACTGAAT

Gene : NYNSO1a
Segment# : 5
Offset : 61
1st Codon : 1
G A P R G P H G G A A S G L N G C C R C G A R G P E S R L L
GGCGCTCCAGAGGCCCTCAGGAGGCGCTGCCTCCGGCCTCAACGGATGCTGTAGGTGTGGCGCTAGGGGACCCGAAAGCAGACTGCTC

Gene : NYNSO1a
Segment# : 6
Offset : 76
1st Codon : 1
G C C R C G A R G P E S R L L E F Y L A M P F A T P M E A E
GGCTTTGCAGATGCGGAGCCAGAGGCCCTGAGTCCAGGCTCCTGGAATTCTATCTGGCTATGCCTTTTCGCTACCCCTATGGAAGCCGAA

Gene : NYNSO1a
Segment# : 7
Offset : 91
1st Codon : 1
E F Y L A M P F A T P M E A E L A R R S L A Q D A P P L P V
GAGTTTACCTCGCCATGCCCTTTGCCACCCCATGGAGGCTGAGCTCGCCAGAAGGTCCCTGGCTCAGGATGCCCTCCCTCCCTCCCGTC

Gene : NYNSO1a

Figure 27 (Cont)

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Segment# : 8
Offset : 106
1st Codon : 1
L A R R S L A Q D A P P L P V P G V L L K E F T V S G N I L
CTGGCTAGGAGAAGCCTCGCCCAAGACGCTCCCCCTCTGCCTGTGCCTGGCGTCTGCTCAAGGAATTCACAGTGTCCGGCAATATCCTC

Gene : NYNSO1a
Segment# : 9
Offset : 121
1st Codon : 1
P G V L L K E F T V S G N I L T I R L T A A D H R Q L Q L S
CCCGAGTGTCTTGAAAGAGTTTACCGTCAGCGGAAACATTCTGACAATCAGACTGACAGCCGCTGACCATAGGCAACTGCAACTGTCC

Gene : NYNSO1a
Segment# : 10
Offset : 136
1st Codon : 1
T I R L T A A D H R Q L Q L S I S S C L Q Q L S L L M W I T
ACCATTAGGCTCACCGCTGCCGATCACAGACAGCTCCAGCTCAGCATTAGCTCCTGCCTCCAGCAACTGTCCCTGCTCATGTGGATCACA

Gene : NYNSO1a
Segment# : 11
Offset : 151
1st Codon : 1
I S S C L Q Q L S L L M W I T Q C F L P V F L A Q P P S G Q
ATCTCCAGCTGTCTGCAACAGCTCAGCCTCCTGATGTGGATTACCCAATGCTTTCTGCCTGTGTTTCTGGCTCAGCCTCCCTCCGGCCAA

Gene : NYNSO1a
Segment# : 12
Offset : 166
1st Codon : 1
Q C F L P V F L A Q P P S G Q R R A A
CAGTGTTCCTCCCGTCTTCTCGCCCAACCCCTAGCGGACAGAGAAGGGCTGCC

Gene : NYNSO1b
Segment# : 1
Offset : 1
1st Codon : 1
A A M L M A Q E A L A F L M A Q G A M L A A Q E R R V P R A
GCCGCTATGCTCATGGCTCAGGAAGCCCTCGCCTTTCTGATGGCCCAAGGCGCTATGCTCGCCGCTCAGGAAAGGAGAGTGCTTAGGGCT

Gene : NYNSO1b
Segment# : 2
Offset : 16
1st Codon : 1
Q G A M L A A Q E R R V P R A A E V P G A Q G Q Q G P R G R
CAGGGAGCCATGCTGGCTGCCCAAGAGAGAAGGGTCCCCAGAGCCGCTGAGGTCCCCGGAGCCCAAGGCCAACAGGGACCCAGAGGCAGA

Gene : NYNSO1b
Segment# : 3
Offset : 31
1st Codon : 1
A E V P G A Q G Q Q G P R G R E E A P R G V R M A A R L Q G
GCCGAAGTGCCTGGCGCTCAGGGACAGCAAGGCCCTAGGGGAAGGGAAGAGGCTCCAGAGGCGTCAGGATGGCCGCTAGGCTCCAGGGA

Gene : NYNSO1b
Segment# : 4
Offset : 46
1st Codon : 1
E E A P R G V R M A A R L Q G A A
GAGGAAGCCCTAGGGGAGTGAGAATGGCTGCCAGACTGCAAGGCGCTGCC

Gene : LAGE1
Segment# : 1
Offset : 1
1st Codon : 1
A A M Q A E G Q G T G G S T G D A D G P G G P G I P D G P G
CCGCTATGCAAGCCGAAGGCCAAGGCACAGGCGAAGCACAGGCGATGCCGATGGCCCTGGCGGACCCGGAATCCCTGACGGACCCGGA

Gene : LAGE1
Segment# : 2
Offset : 16

Figure 27 (Cont)

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1st Codon : 1
D A D G P G G P G I P D G P G G N A G G P G E A G A T G G R
GACGCTGACGGACCCGGAGGCCCTGGCATTCCCGATGGCCCTGGCGGAAACGCTGGCGGACCCGGAGAGGCTGGCGCTACCGGAGGCAGA

Gene : LAGE1
Segment# : 3
Offset : 31
1st Codon : 1
G N A G G P G E A G A T G G R G P R G A G A A R A S G P R G
GGCAATGCCGAGGCCCTGGCGAAGCCGGAGCCACAGGCGAAGGGGACCCAGAGGCGCTGGCGCTGCCAGAGCCTCCGGCCCTAGGGGA

Gene : LAGE1
Segment# : 4
Offset : 46
1st Codon : 1
G P R G A G A A R A S G P R G G A P R G P H G G A A S A Q D
GGCCCTAGGGGAGCCGGAGCCGCTAGGGCTAGCGGACCCAGAGGCGGAGCCCTAGGGGACCCATGGCGGAGCCGCTAGCGCTCAGGAT

Gene : LAGE1
Segment# : 5
Offset : 61
1st Codon : 1
G A P R G P H G G A A S A Q D G R C P C G A R R P D S R L L
GGCGCTCCAGAGGCCCTACGGAGGCGCTGCCTCCGCCCAAGACGGAAGGTGTCCCTGTGGCGCTAGGAGACCCGATAGCAGACTGCTC

Gene : LAGE1
Segment# : 6
Offset : 76
1st Codon : 1
G R C P C G A R R P D S R L L Q L H I T M P F S S P M E A E
GGCAGATGCCCTTCCGGAGCCAGAAGGCTGACTCCAGGCTCCTGCAACTGCATATCACATGCCTTTCTCCAGCCCTATGGAAGCCGAA

Gene : LAGE1
Segment# : 7
Offset : 91
1st Codon : 1
Q L H I T M P F S S P M E A E L V R R I L S R D A A P L P R
CAGCTCCACATTACCATGCCCTTTAGCTCCCCCATGGAGGCTGAGCTCGTGAGAAGGATTCTGTCCAGGGATGCCGCTCCCTTCCCCAGA

Gene : LAGE1
Segment# : 8
Offset : 106
1st Codon : 1
L V R R I L S R D A A P L P R P G A V L K D F T V S G N L L
CTGGTCAGGAGAATCCTCAGCAGAGACGCTGCCCCCTGCGCTAGGCGCTGGCGCTGTGTCAAGGATTTACAGTGTCCGGCAATCTGCTC

Gene : LAGE1
Segment# : 9
Offset : 121
1st Codon : 1
P G A V L K D F T V S G N L L F I R L T A A D H R Q L Q L S
CCCGGAGCCGCTCTGAAAGACTTTACCGTCAGCGGAAACCTCCTGTTTATCAGACTGACAGCCGCTGACCATAGGCAACTGCAACTGTCC

Gene : LAGE1
Segment# : 10
Offset : 136
1st Codon : 1
F I R L T A A D H R Q L Q L S I S S C L Q Q L S L L M W I T
TTCATTAGGCTCACCCTGCGGATCACAGACAGCTCCAGCTCAGCATTAGCTCCTGCCTCCAGCAACTGTCCCTGCTCATGTGGATCACA

Gene : LAGE1
Segment# : 11
Offset : 151
1st Codon : 1
I S S C L Q Q L S L L M W I T Q C F L P V F L A Q A P S G Q
ATCTCCAGCTGTCTGCAACAGCTCAGCCTCCTGATGTGGATTACCCAATGCTTTCTGCCTGTGTTTCTGGCTCAGGCTCCCTCCGGCCAA

Gene : LAGE1
Segment# : 12
Offset : 166
1st Codon : 1
Q C F L P V F L A Q A P S G Q R R A A

Figure 27 (Cont)

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CAGTGTTCCTCCCGTCTTCCTCGCCCAAGCCCCTAGCGGACAGAGAAGGGCTGCC

Segments in scrambled order:

MAGE-1 #15

A P E E E I W E E L S V M E V Y D G R E H S A Y G E P R K L
 GCCCTGAGGAAGAGATTGGGAAGAGCTCAGCGTCATGGAAGTGTATGACGGAAGGGAACACTCCGCTATGGCGAACCCAGAAAGCTC

MAGE-1 #4

E E V P T A G S T D P P Q S P Q G A S A F P T T I N F T R Q
 GAGGAAGTGCTACCGCTGGCTCCACCGATCCCCCTCAGTCCCCCAAGGCGCTAGCGCTTCCCTACCACAATCAATTTACAAGGCAA

PRAME #10

T V W S G N R A S L Y S F P E P E A A Q P M T K K R K V D G
 ACCGTCTGGTCCGGCAATAGGGCTAGCCTCTACTCCTTCCTGAGCCTGAGGCTGCCCAACCCATGACCAAAAAGAGAAAGGTCGACGGA

MAGE-3 #14

Q I M P K A G L L I I V L A I I A R E G D C A P E E K I W E
 CAGATTATGCCTAAGGCTGGCCTCCTGATTATCGTCCTGGCTATCATTGCCAGAGAGGGAGACTGTGCCCCTGAGGAAAAGATTGGGAA

PRAME #9

L Q V L D L R K N S H Q D F W T V W S G N R A S L Y S F P E
 CTGCAAGTGCTCGACCTCAGGAAAACTCCCACCAAGACTTTTGGACAGTGTGGAGCGGAAACAGAGCCTCCCTGTATAGCTTTCCCGAA

PRAME #8

L D V L L A Q E V R P R R W K L Q V L D L R K N S H Q D F W
 CTGGATGTGCTCCTGGCTCAGGAAGTGAGACCCAGAAGGTGGAAGCTCCAGGTCTGGATCTGAGAAAGAATAGCCATCAGGATTTCTGG

NYNS01b #2

Q G A M L A A Q E R R V P R A A E V P G A Q G Q Q G P R G R
 CAGGGAGCCATGTCTGGCTGCCCAAGAGAGAAGGGTCCCCAGAGCCGCTGAGGTCCCCGAGCCCAAGGCCAACAGGGACCCAGAGGCAGA

PRAME #24

Q S P S V S Q L S V L S L S G V M L T D V S P E P L Q A L L
 CAGTCCCCCTCCGTGTCCAGCTCAGCGTCTGTCTCCTGTCCGGCGTCATGCTCACCAGTGTGTCCCCGAACCCCTCCAGGCTCTGCTC

MAGE-1 #17

L T Q D L V Q E K Y L E Y R Q V P D S D P A R Y E F L W G P
 CTGACACAGGATCTGGTCCAGGAAAAGTATCTGGAATACAGACAGGTCCCCGATAGCGATCCCGCTAGGTATGAGTTTCTGTGGGGCCCT

MAGE-1 #6

R Q P S E G S S S R E E E G P S T S C I L E S L F R A V I T
 AGGCAACCCCTCCGAGGGAAGCTCCAGCAGAGAGGAAGAGGGACCCCTCCACCTCCTGCATTCTGGAAAGCCTCTTCAGAGCCGTCATCACA

BAGE #1

A A M A A R A V F L A L S A Q L L Q A R L M K E E S P V V S
 GCCGCTATGGCTGCCAGAGCCGTCTTCCTCGCCCTCAGCGCTCAGCTCCTGCAAGCCAGACTGATGAAGGAAGAGTCCCCCGTCGTGTCC

PRAME #34

T F Y D P E P I L C P C F M P N A A
 ACCTTTACGATCCCGAACCCATTCTGTGTCCCTGTTTCATGCCCAATGCCGCT

MAGE-3 #12

I E L M E V D P I G H L Y I F A T C L G L S Y D G L L G D N
 ATCGAACTGATGGAGGTGCACCCCTATCGGACACCTCTACATTTTCGTACCTGTCTGGGACTGTCTACGATGGCTCCTGGGAGACAAT

GAGE-1 #2

R R Y V E P P E M I G P M R P E Q F S D E V E P A T P E E G
 AGGAGATACGTCGAGCCTCCCGAAATGATTGGCCCTATGAGACCCGAACAGTTTAGCGATGAGGTGAGCCTGCCACACCCGAAGAGGGA

TRP2IN2 #2

E A G G F F P W L K V Y Y Y R F V I G L R V W Q W E V I S C
 GAGGCTGGCGATTCTTCCCTGGCTGAAAGTGTATTACTATAGGTTTGTGATTGGCCTCAGGGTCTGGCAATGGGAAGTGATTAGCTGT

PRAME #1

A A M E R R R L W G S I Q S R Y I S M S V W T S P R R L V E
 GCCGCTATGGAAGGAGAAGGCTCTGGGGAAGCATTAGTCCAGGTATATCTCCATGTCCGTGTGGACCTCCCCAGAAGGCTCCTGGAA

TRP2IN2 #1

A A L M E T H L S S K R Y T E E A G G F F P W L K V Y Y Y R
 GCCGCTCTGATGGAGACACCTCAGCTCCAAGAGATACACAGAGGAAGCCGGAGGCTTTTTCCCTGGCTCAAGGTCTACTATTACAGA

Figure 27 (Cont)

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MAGE-1 #1
A A M S L E Q R S L H C K P E E A L E A Q Q E A L G L V C V
GCCGCTATGTCCCTGGAACAGAGAAGCCTCCACTGTAAGCCTGAGGAAGCCCTCGAGGCTCAGCAAGAGGCTCTGGGACTGGTCTGCGTC

MAGE-1 #3
Q A A T S S S S P L V L G T L E E V P T A G S T D P P Q S P
CAGGCTGCCACAAGCTCCAGCTCCCCCTCGTGCTCGGCACACTGGAAGAGGTCCCCACAGCCGGAAGCACAGACCCTCCCCAAAGCCCT

PRAME #4
A L E L L P R E L F P P L F M A A F D G R H S Q T L K A M V
GCCCTCGAGCTCCTGCCTAGGGAAGTGTTCCTCTGTTTATGGCTGCCTTTGACGGAAGGCATAGCCAAACCCTCAAGGCTATGGTC

MAGE-3 #16
E L S V L E V F E G R E D S I L G D P K K L L T Q H F V Q E
GAGCTCAGCTCCTGGAAGTGTTCGAGGGAAGGGAAGACTCCATCCTCGGCGATCCCAAAAGCTCCTGACACAGCATTTCGTCCAGGAA

MAGE-1 #11
E S L Q L V F G I D V K E A D P T G H S Y V L V T C L G L S
GAGTCCCTGCAACTGGTCTTCGGAATCGATGTGAAGAGGCTGACCCTACCGGACACTCCTACGTCCTGGTCACCTGTCTGGGACTGTCC

MAGE-3 #5
P D P P Q S P Q G A S S L P T T M N Y P L W S Q S Y E D S S
CCCGATCCCCCTCAGTCCCCCAAGGCGTAGCTCCCTGCCTACCACAATGAATTACCTCTGTGGAGCCAAAGCTATGAGGATAGCTCC

LAGE1 #1
A A M Q A E G Q G T G G S T G D A D G P G G P G I P D G P G
GCCGCTATGCAAGCCGAAGGCCAAGGCACAGGCGGAAGCACAGGCGATGCCGATGGCCCTGGCGGACCCGGAATCCCTGACGGACCCGGA

NYNSO1a #12
Q C F L P V F L A Q P P S G Q R R A A
CAGTGTTCCTCCCCGTCTTCCTCGCCCAACCCCTAGCGGACAGAGAAGGGCTGCC

gp100In4 #2
T W G E G L P S Q P I I H T C V Y F F L P D H L S F G R P F
ACCTGGGGCGAAGGCCTCCCTCCAGCCTATCATTACACATGCGTCTACTTTTCCTCCCGATCACCTCAGCTTTGGCAGACCCTTT

MAGE-1 #7
S T S C I L E S L F R A V I T K K V A D L V G F L L L K Y R
AGCACAGCTGTATCCTCGAGTCCCTGTTTAGGGCTGTGATTACCAAAAGGTGCGCGATCTGGTGGCTTTCTGCTCCTGAAATACAGA

NYNSO1a #1
A A M Q A E G R G T G G S T G D A D G P G G P G I P D G P G
GCCGCTATGCAAGCCGAAGGCAGAGGCACAGGCGGAAGCACAGGCGATGCCGATGGCCCTGGCGGACCCGGAATCCCTGACGGACCCGGA

GAGE-1 #7
D G P D G Q E M D P P N P E E V K T P E E E M R S H Y V A Q
GACGGACCCGATGGCCAAGAGATGGACCCTCCCAATCCCGAAGAGGTCAAGACACCCGAAGAGGAAATGAGAAGCCATTACGTGCGCCAA

NYNSO1a #11
I S S C L Q Q L S L L M W I T Q C F L P V F L A Q P P S G Q
ATCTCCAGCTGTCTGCAACAGCTCAGCCTCCTGATGTGGATTACCAATGCTTTCTGCCTGTGTTCTGGCTCAGCCTCCCTCCGGCCAA

PRAME #26
E R A S A T L Q D L V F D E C G I T D D Q L L A L L P S L S
GAGAGAGCCTCCGCCACTGCAAGACCTCGTGTTTGACGAATGCGGAATCACAGACGATCAGCTCCTGGCTCTGCTCCCTCCCTGTCC

MAGE-3 #17
L G D P K K L L T Q H F V Q E N Y L E Y R Q V P G S D P A C
CTGGGAGACCCTAAGAACTGCTCACCCAACTTTGTGCAAGAGAATTACCTCGAGTATAGGCAAGTGCCCTGGCTCCGACCCTGCCTGT

MAGE-1 #2
E A L E A Q Q E A L G L V C V Q A A T S S S S P L V L G T L
GAGGCTCTGGAAGCCCAACAGGAAGCCCTCGGCCTCGTGTTGTGCAAGCCGCTACCTCCAGCTCCAGCCCTCTGGTCTGGGAACCCCTC

NYNSO1a #7
E F Y L A M P F A T P M E A E L A R R S L A Q D A P P L P V
GAGTTCCTACCTCGCCATGCCCTTTGCCACACCCATGGAGGCTGAGCTCGCCAGAAGGTCCCTGGCTCAGGATGCCCTCCCTCCCTCCCGTC

NYNSO1b #4
E E A P R G V R M A A R L Q G A A
GAGGAAGCCCTAGGGGAGTGAGAATGGCTGCCAGACTGCAAGGCGCTGCC

Figure 27 (Cont)

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BAGE #3
W R L E P E D G T A L C F I F A A
TGGAGACTGGAACCCGAAGACGGAACCGCTCTGTGTTTCATTTTCGCTGCC

GAGE-1 #3
E Q F S D E V E P A T P E E G E P A T Q R Q D P A A A Q E G
GAGCAATTCTCCGACGAAGTGGAACCCGCTACCCCTGAGGAAGGCGAACCCGCTACCCAAAGGCAAGACCCCTGCCGCTGCCCAAGAGGGA

MAGE-3 #6
T M N Y P L W S Q S Y E D S S N Q E E E G P S T F P D L E S
ACCATGAACATATCCCCTCTGGTCCCAGTCTACGAAGACTCCAGCAATCAGGAAGAGGAAGGCCCTAGCACATTCCCTGACCTCGAGTCC

MAGE-3 #7
N Q E E E G P S T F P D L E S E F Q A A L S R K V A E L V H
AACCAAGAGGAAGAGGACCCCTCCACCTTTCCCGATCTGGAAGCGAATTCCAAGCCGCTCTGTCCAGGAAAGTGGCTGAGCTCGTGCAT

PRAME #13
V D L F L K E G A C D E L F S Y L I E K V K R K K N V L R L
GTGGATCTGTTTCTGAAAGAGGGAGCCTGTGACGAACGTCTTAGCTATCTGATTGAGAAAGTGAAAGGAAAAAGAATGTGCTCAGGCTC

NYNSO1a #10
T I R L T A A D H R Q L Q L S I S S C L Q Q L S L L M W I T
ACCATTAGGCTCACCGCTGCCGATCACAGACAGCTCCAGCTCAGCATTAGCTCCTGCCTCCAGCAACTGTCCCTGCTCATGTGGATCACA

MAGE-3 #1
A A M P L E Q R S Q H C K P E E G L E A R G E A L G L V G A
GCCGCTATGCCTCTGGAACAGAGAAGCCAACACTGTAAGCCTGAGGAAGGCCTCGAGGCTAGGGGAGAGGCTCTGGGACTGGTCGGCGCT

NYNSO1a #2
D A D G P G G P G I P D G P G G N A G G P G E A G A T G G R
GACGCTGACGGACCCGGAGGCCCTGGCATTCCCGATGGCCCTGGCGGAAACGCTGGCGGACCCGGAGAGGCTGGCGCTACCGGAGGCAGA

MAGE-3 #19
Y E F L W G P R A L V E T S Y V K V L H H M V K I S G G P H
TACGAATTCCTCTGGGGACCCAGAGCCCTCGTGGAAACCTCCTACGTCAAGGTCTGTCATCATGGTGAAATCTCCGGCGGACCCCAT

PRAME #23
I T N C R L S E G D V M H L S Q S P S V S Q L S V L S L S G
ATCACAAACTGTAGGCTCAGCGAAGGCGATGTGATGCACCTCAGCCAAAGCCCTAGCGTCAGCCAACTGTCCGTGCTCAGCCTCAGCGGA

MAGE-3 #18
N Y L E Y R Q V P G S D P A C Y E F L W G P R A L V E T S Y
AACTATCTGGAATACAGACAGGTCCCCGGAAGCGATCCCGCTTGCTATGAGTTTCTGTGGGGCCCTAGGGCTCTGGTCCGAGACAAGCTAT

MAGE-3 #11
V I F S K A S S S L Q L V F G I E L M E V D P I G H L Y I F
GTGATTTTCTCCAAGGCTAGCTCCAGCCTCCAGCTCGTGTGTTGGCATTGAGCTCATGGAAGTGGATCCCATGGCCATCTGTATATCTTT

PRAME #21
Q A L Y V D S L F F L R G R L D Q L L R H V M N P L E T L S
CAGGCTCTGTATGTGGATAGCCTCTTCTTCTGAGAGGCAGACTGGATCAGCTCCTGAGACAGTTCATGAATCCCTCGAGACACTGTCC

PRAME #20
Y I A Q F T S Q F L S L Q C L Q A L Y V D S L F F L R G R L
TACATTGCCCAATTACAAGCCAATTCCTCAGCCTCCAGTGTCTGCAAGCCCTCTACGTGACTCCCTGTTTTTCTCAGGGGAAGGCTC

PRAME #7
G Q H L H L E T F K A V L D G L D V L L A Q E V R P R R W K
GGCCACACCTCCACCTCGAGACATTCAAAGCCGCTCTGGATGGCCTCGACGTCTGCTCGCCCAAGAGGTGAGGCTAGGAGATGGAAA

LAGE1 #10
F I R L T A A D H R Q L Q L S I S S C L Q Q L S L L M W I T
TTCATTAGGCTCACCGCTGCCGATCACAGACAGCTCCAGCTCAGCATTAGCTCCTGCCTCCAGCAACTGTCCCTGCTCATGTGGATCACA

PRAME #15
C C K K L K I F A M P M Q D I K M I L K M V Q L D S I E D L
TGCTGTAAGAACTGAAAATCTTTGCCATGCCCATGCAGGATATCAAATGATTCTGAAAATGGTCCAGCTCGACTCCATCGAAGACCTC

NYNSO1a #5
G A P R G P H G G A A S G L N G C C R C G A R G P E S R L L
GGCGCTCCCAGAGGCCCTCACGGAGGCGCTGCCCTCCGGCCTCAACGGATGCTGTAGGTGTGGCGCTAGGGGACCCGAAAGCAGACTGCTC

Figure 27 (Cont)

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MAGE-1 #8

K K V A D L V G F L L L K Y R A R E P V T K A E M L E S V I
AAGAAAGTGGCTGACCTCGTGGGATTCTCTGCTCAAGTATAGGGCTAGGGAACCCGTCACCAAAGCCGAAATGCTCGAGTCCGTGATT

MAGE-1 #13

Y D G L L G D N Q I M P K T G F L I I V L V M I A M E G G H
TACGATGGCTCTGGGAGACAATCAGATTATGCCTAAGACAGGCTTTCTGATTATCGTCTGGTCATGATTGCCATGGAGGGAGGCCAT

PRAME #29

S I S A L Q S L L Q H L I G L S N L T H V L Y P V P L E S Y
AGCATTAGCGCTCTGCAAAGCCTCTGCAACACCTCATCGGACTGTCCAACCTCACCCATGTGCTCTACCCGTGTCCTCTGGAAGCTAT

MAGE-3 #15

I A R E G D C A P E E K I W E E L S V L E V F E G R E D S I
ATCGCTAGGGAAGCGATTGCGCTCCCGAAGAGAAAATCTGGGAGGAACCTGTCCGTGCTCGAGGTCTTCGAAGGCAGAGAGGATAGCATT

PRAME #22

D Q L L R H V M N P L E T L S I T N C R L S E G D V M H L S
GACCAACTGCTCAGGCATGTGATGAACCTCTGGAACCCCTCAGCATTACCAATGCAGACTGTCCGAGGGAGACGTCATGCATCTGTCC

MAGE-1 #19

R A L A E T S Y V K V L E Y V I K V S A R V R F F F P S L R
AGGGCTCTGGCTGAGACAAGCTATGTGAAAGTGTCTGAGTATGTGATTAAGGTGAGCGCTAGGGTCAGGTTTTCTTTCCCTCCCTGAGA

PRAME #30

S N L T H V L Y P V P L E S Y E D I H G T L H L E R L A Y L
AGCAATCTGACACACGTCCTGTATCCCGTCCCCCTCGAGTCTACGAAGACATTACGGAACCCCTCCACCTCGAGAGACTGGCTTACCTC

NYN501b #1

A A M L M A Q E A L A F L M A Q G A M L A A Q E R R V P R A
GCCGCTATGCTCATGGCTCAGGAAGCCCTCGCCTTTCTGATGGCCCAAGGCGCTATGCTCGCGCTCAGGAAAGGAGAGTGCTTAGGGCT

MAGE-1 #10

K N Y K H C F P E I F G K A S E S L Q L V F G I D V K E A D
AAGAATTACAAACACTGTTTCCCTGAGATTTTCGGAAGGCTAGCGAAAGCCTCCAGCTCGTGTGTTGGCATTGACGTCAAGGAAGCCGAT

MAGE-3 #4

T L V E V T L G E V P A A E S P D P P Q S P Q G A S S L P T
ACCCTCGTGGAAGTGACACTGGGAGAGGTCCCCGCTGCCGAAAGCCCTGACCCTCCCCAAAGCCCTCAGGGAGCCTCCAGCCTCCCCACA

PRAME #32

H A R L R E L L C E L G R P S M V W L S A N P C P H C G D R
CACGCTAGGCTCAGGGAAGTCTCTGCGAACTGGGAAGGCCTAGCATGGTGTGGCTGTCCGCCAATCCCTGTCCCATTGCGGAGACAGA

PRAME #25

V M L T D V S P E P L Q A L L E R A S A T L Q D L V F D E C
GTGATGCTGACAGACGTGAGCCCTGAGCCTCTGCAAGCCCTCCTGGAAGGGCTAGCGCTACCCTCCAGGATCTGGTCTTCGATGAGTGT

GAGE-1 #5

E D E G A S A G Q G P K P E A D S Q E Q G H P Q T G C E C E
GAGGATGAGGGAGCCTCCGCCGACAGGGACCCAAACCCGAAGCCGATAGCCAAGAGCAAGGCCATCCCCAAACCGGATGCGAATGCGAA

MAGE-3 #10

E M L G S V V G N W Q Y F F P V I F S K A S S S L Q L V F G
GAGATGCTGGGAAGCGTCGTGGGAACTGGCAGTATTTCTTTCCCGTCATCTTAGCAAAGCCTCCAGCTCCCTGCAACTGGTCTTCGGA

GAGE-1 #1

A A M S W R G R S T Y R P R P R R Y V E P P E M I G P M R P
GCCGCTATGTCCTGGAGAGGCAGAAGCACATACAGACCCAGACCCAGAAGGTATGTGGAACCCCTGAGATGATCGGACCCATGAGGCCT

PRAME #2

Y I S M S V W T S P R R L V E L A G Q S L L K D E A L A I A
TACATTAGCATGAGCGTCTGGACAAGCCCTAGGAGACTGGTTCGAGCTCGCCGACAGTCCCTGCTCAAGGATGAGGCTCTGGCTATCGCT

MAGE-1 #16

Y D G R E H S A Y G E P R K L L T Q D L V Q E K Y L E Y R Q
TACGATGGCAGAGAGCATAGCGCTTACGGAGAGCCTAGGAAACTGCTCACCCAAGACCTCGTGAAGAGAAATACCTCGAGTATAGGCAA

LAGE1 #12

Q C F L P V F L A Q A P S G Q R R A A
CAGTGTTCCTCCCGTCTTCTCGCCCAAGCCCTAGCGGACAGAGAAGGGCTGCC

Figure 27 (Cont)

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MAGE-3 #20

V K V L H H M V K I S G G P H I S Y P P L H E W V L R E G E
GTGAAAGTGCTCCACCATATGGTCAAGATTAGCGGAGGCCCTCACATTAGCTATCCCCCTGTCATGAGTGGGTGCTCAGGGAAGGCGAA

LAGE1 #7

Q L H I T M P F S S P M E A E L V R R I L S R D A A P L P R
CAGCTCCACATTACCATGCCCTTTAGCTCCCCCATGGAGGCTGAGCTCGTGAGAAGGATTCTGTCCAGGGATGCCGCTCCCCCTCCCCAGA

NYNSO1a #9

P G V L L K E F T V S G N I L T I R L T A A D H R Q L Q L S
CCCGAGTGCTCCTGAAAGAGTTTACCGTCAGCGGAAACATTCTGACAACTGACAGCCGCTGACCATAGGCAACTGCAACTGTCC

PRAME #16

K M I L K M V Q L D S I E D L E V T C T W K L P T L A K F S
AAGATGATCCTCAAGATGGTGCAACTGGATAGCATTGAGGATCTGGAAGTGACATGCACATGGAAGCTGCTTACCTCGCCAAATTCTCC

MAGE-1 #14

F L I I V L V M I A M E G G H A P E E E I W E E L S V M E V
TTCCTCATCATTTGTGCTCGTGATGATCGTATGGAAGGCGGACACGCTCCCGAAGAGGAAATCTGGGAGGAACTGTCCGTGATGGAGGTC

PRAME #17

E V T C T W K L P T L A K F S P Y L G Q M I N L R R L L L S
GAGGTACCTGTACCTGGAAGCTCCCCACACTGGCTAAGTTTAGCCCTTACCTCGGCCAAATGATTAACCTCAGGAGACTGCTCCTGTCC

MAGE-3 #2

E G L E A R G E A L G L V G A Q A P A T E E Q E A A S S S S
GAGGGACTGGAAGCCAGAGGCGAAGCCCTCGGCCCTCGTGGGAGCCCAAGCCCTGCCACAGAGGAACAGGAAGCCGCTAGCTCCAGCTCC

MAGE-3 #21

I S Y P P L H E W V L R E G E E A A
ATCTCTACCTCCCCCTCCACGAATGGGTCTGAGAGAGGGAGAGGAAGCCGCT

PRAME #19

H I H A S S Y I S P E K E E Q Y I A Q F T S Q F L S L Q C L
CACATTCACGCTAGCTCCTACATTAGCCCTGAGAAAGAGGAACAGTATATCGCTCAGTTTACCTCCCAGTTTCTGTCCCTGCAATGCCTC

NYNSO1a #3

G N A G G P G E A G A T G G R G P R G A G A A R A S G P G G
GGCAATGCCGAGGCCCTGGCGAAGCCGAGCCACAGGCCGAAGGGGACCCAGAGGCGCTGGCGCTGCCAGAGCCTCCGGCCCTGGCGGA

NYNSO1a #4

G P R G A G A A R A S G P G G G A P R G P H G G A A S G L N
GGCCCTAGGGGAGCCGAGCCGCTAGGGCTAGCGGACCCGGAGGCGGAGCCCTAGGGGACCCATGGCGGAGCCGCTAGCGGACTGAAT

MAGE-1 #5

Q G A S A F P T T I N F T R Q R Q P S E G S S S R E E E G P
CAGGGAGCCTCCGCTTTCCCAACCATTAACCTTTACCAGACAGAGACAGCCTAGCGAAGGCTCCAGCTCCAGGGAAGAGGAAGGCCCT

NYNSO1a #8

L A R R S L A Q D A P P L P V P G V L L K E F T V S G N I L
CTGGCTAGGAGAAGCCTCGCCCAAGACGCTCCCCCTCTGCCTGTGCCTGGCGTCTGCTCAAGGAATTCACAGTGTCCGGCAATATCCTC

PRAME #5

A A F D G R H S Q T L K A M V Q A W P F T C L P L G V L M K
GCCGCTTTTCGATGGCAGACACTCCCAGACACTGAAAGCCATGGTGCAAGCTGGCCCTTTACCTGTCTGCCTCTGGGAGTGCTCATGAAA

MAGE-1 #20

I K V S A R V R F F F P S L R E A A L R E E E E G V A A
ATCAAAGTGTCGCCAGAGTGAGATTCTTTTCCCTAGCCTCAGGGAAGCCGCTCTGAGAGAGGAAGAGGAAGGCGTCGCCGCT

PRAME #27

G I T D D Q L L A L L P S L S H C S Q L T T L S F Y G N S I
GGCATTACCATGACCAACTGCTCGCCCTCCTGCCTAGCCTCAGCCATTGCTCCAGCTCACCACACTGTCTTCTATGGCAATAGCATT

GAGE-1 #8

V K T P E E E M R S H Y V A Q T G I L W L L M N N C F L N L
GTGAAAACCCCTGAGGAAGAGATGAGGTCCCACTATGTGGCTCAGACAGGCATTCTGTGGCTGCTCATGAATAACTGTTTCTCTCAACCTC

LAGE1 #11

I S S C L Q Q L S L L M W I T Q C F L P V F L A Q A P S G Q
ATCTCCAGCTGTCTGCAACAGCTCAGCCTCCTGATGTGGATTACCCAATGCTTTCTGCCTGTGTTTCTGGCTCAGGCTCCCTCCGGCCAA

Figure 27 (Cont)

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PRAME #14

Y L I E K V K R K K N V L R L C C K K L K I F A M P M Q D I
TACCTCATCGAAAAGGTCAAGAGAAAAGAAAACGTCCTGAGACTGTGTTGCAAAAAGCTCAAGATTTTCGCTATGCCTATGCAAGACATT

MAGE-1 #9

A R E P V T K A E M L E S V I K N Y K H C F P E I F G K A S
GCCAGAGAGCCTGTGACAAAGGCTGAGATGCTGGAAAGCGTCATCAAAAACCTATAAGCATTGCTTTCCCGAAATCTTTGGCAAAGCCTCC

LAGE1 #8

L V R R I L S R D A A P L P R P G A V L K D F T V S G N L L
CTGGTCAGGAGAATCCTCAGCAGAGACGCTGCCCTCTGCCTAGGCCTGGCGCTGTGCTCAAGGATTTACAGTGTCCGGCAATCTGCTC

PRAME #28

H C S Q L T T L S F Y G N S I S I S A L Q S L L Q H L I G L
CACTGTAGCCAAGTACCAACCTCAGCTTTTACGGAACCTCCATCTCCATCTCCGCCCTCCAGTCCCTGCTCCAGCATCTGATTGGCCTC

PRAME #33

M V W L S A N P C P H C G D R T F Y D P E P I L C P C F M P
ATGGTCTGGCTCAGCGCTAACCTTGCCCTCACTGTGGCGATAGGACATTCTATGACCCTGAGCCTATCCTCTGCCCTTGCTTTATGCCT

gp100In4 #1

A A S W S Q K R S F V Y V W K T W G E G L P S Q P I I H T C
GCCGCTAGCTGGAGCCAAAAGAGAAGCTTTGTGTATGTGTGGAAGACATGGGGAGAGGGACTGCCCTAGCCAACCCATTATCCATACCTGT

BAGE #2

L L Q A R L M K E E S P V V S W R L E P E D G T A L C F I F
CTGCTCCAGGCTAGGCTCATGAAAGAGGAAAGCCCTGTGGTCAGCTGGAGGCTCGAGCCTGAGGATGGCACAGCCCTCTGCTTTATCTTT

gp100In4 #3

V Y F F L P D H L S F G R P F H L N F C D F L A A
GTGTATTCTTTCTGCTGACCATCTGTCTTCGGAAGGCCCTTCCATCTGAATTTCTGTGACTTTCTGGCTGCC

PRAME #18

P Y L G Q M I N L R R L L L S H I H A S S Y I S P E K E E Q
CCCTATCTGGGACAGATGATCAATCTGAGAAGGCTCCTGCTCAGCCATATCCATGCCTCCAGCTATATCTCCCCGAAAAGGAAGAGCAA

MAGE-3 #3

Q A P A T E E Q E A A S S S S T L V E V T L G E V P A A E S
CAGGCTCCCGCTACCGAAGAGCAAGAGGCTGCCCTCCAGCTCCAGCACACTGGTCGAGGTCACCCCTCGGCGAAGTGCTGCCGCTGAGTCC

PRAME #6

Q A W P F T C L P L G V L M K G Q H L H L E T F K A V L D G
CAGGCTTGCCCTTTACATGCCTCCCCCTCGGCGCTCTGATGAAGGACAGCATCTGCATCTGGAAACCTTTAAGGCTGTGCTCGACGGA

PRAME #12

L S T E A E Q P F I P V E V L V D L F L K E G A C D E L F S
CTGTCCACCGAAGCCGAACAGCCTTTTCATTCCCGTCGAGGTCTGTGTCGACCTCTTCCTCAAGGAAGGCGCTTGCGATGAGCTCTTCTCC

NYNS01b #3

A E V P G A Q G Q Q G P R G R E E A P R G V R M A A R L Q G
GCCGAAGTGCTGGCGCTCAGGGACAGCAAGGCCCTAGGGGAAGGGAAGAGGCTCCAGAGGCGTCAGGATGGCCGCTAGGCTCCAGGGA

LAGE1 #5

G A P R G P H G G A A S A Q D G R C P C G A R R P D S R L L
GGCGCTCCAGAGGCCCTCACGGAGGCGCTGCCTCCGCCCAAGACGGAAGGTGTCCCTGTGGCGCTAGGAGACCCGATAGCAGACTGTCT

LAGE1 #4

G P R G A G A A R A S G P R G G A P R G P H G G A A S A Q D
GGCCCTAGGGGAGCCGAGCCGCTAGGGCTAGCGGACCCAGAGGCGGAGCCCTAGGGGACCCCATGGCGGAGCCGCTAGCGCTCAGGAT

PRAME #3

L A G Q S L L K D E A L A I A A L E L L P R E L F P P L F M
CTGGCTGGCCAAAGCCTCCTGAAAGACGAAGCCCTCGCCATTGCCGCTCTGGAACCTGCTCCCCAGAGAGCTCTTCCCTCCCCTCTTCATG

GAGE-1 #4

E P A T Q R Q D P A A A Q E G E D E G A S A G Q G P K P E A
GAGCCTGCCACACAGAGACAGGATCCCGCTGCCGCTCAGGAAGGCGAAGACGAAGGCGCTAGCGCTGGCCAAGGCCCTAAGCCTGAGGCT

PRAME #11

P E A A Q P M T K K R K V D G L S T E A E Q P F I P V E V L
CCCGAAGCCGCTCAGCCTATGACAAAGAAAAGGAAAGTGATGGCCTCAGCACAGAGGCTGAGCAACCCCTTTATCCCTGTGGAAGTGCTC

Figure 27 (Cont)

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LAGE1 #6

G R C P C G A R R P D S R L L Q L H I T M P F S S P M E A E
GGCAGATGCCCTTGGGAGCCAGAAGGCTGACTCCAGGCTCCTGCAACTGCATATCACAAATGCCCTTCTCCAGCCCTATGGAAGCCGAA

LAGE1 #9

P G A V L K D F T V S G N L L F I R L T A A D H R Q L Q L S
CCCGGAGCCGTCTGAAAGACTTTACCGTCAGCGGAAACCTCCTGTTTATCAGACTGACAGCCGCTGACCATAGGCAACTGCAACTGTCC

PRAME #31

E D I H G T L H L E R L A Y L H A R L R E L L C E L G R P S
GAGGATATCCATGGCACACTGCATCTGAAAGGCTCGCCTATCTGCATGCCAGACTGAGAGAGCTCCTGTGTGAGCTCGGCAGACCCCTCC

GAGE-1 #6

D S Q E Q G H P Q T G C E C E D G P D G Q E M D P P N P E E
GACTCCAGGAACAGGGACACCCTCAGACAGGCTGTGAGTGTGAGGATGGCCCTGACGGACAGGAAATGGATCCCCCTAACCTGAGGAA

TRP2IN2 #3

F V I G L R V W Q W E V I S C K L I K R A T T R Q P A A
TTCGTATCGGACTGAGAGTGTGGCAGTGGGAGGTCATCTCTGCAAACTGATTAAGAGAGCCACAACCAGACAGCCTGCCGCT

LAGE1 #2

D A D G P G G P G I P D G P G G N A G G P G E A G A T G G R
GACGCTGACGGACCCGGAGGCCCTGGCATTCCCGATGGCCCTGGCGGAAACGCTGGCGGACCCGGAGAGGCTGGCGCTACCGGAGGCAGA

MAGE-1 #12

P T G H S Y V L V T C L G L S Y D G L L G D N Q I M P K T G
CCCACAGGCCATAGCTATGTGCTCGTGACATGCCCTCGGCCTCAGCTATGACGGACTGCTCGGCGATAACCAAATCATGCCCAAACCGGA

MAGE-3 #9

F L L L K Y R A R E P V T K A E M L G S V V G N W Q Y F F P
TTCCTCTGCTCAAGTATAGGGCTAGGGAACCCGTACCAAGCCGAAATGCTCGGCTCCGTGGTGGCAATTGGCAATACTTTTTCCTT

GAGE-1 #9

T G I L W L L M N N C F L N L S P R K P A A
ACCGGAATCCTCTGGCTCCTGATGAACAATTGCTTTCTGAATCTGTCCCCAGAAAGCCTGCCGCT

MAGE-3 #8

E F Q A A L S R K V A E L V H F L L L K Y R A R E P V T K A
GAGTTTCAGGCTGCCCTCAGCAGAAAGGTGCGCGAACTGGTCCACTTTCTGCTCCTGAAATACAGAGCCAGAGAGCCTGTGACAAAGGCT

MAGE-1 #18

V P D S D P A R Y E F L W G P R A L A E T S Y V K V L E Y V
GTGCTGACTCCGACCCTGCCAGATACGAATTCCTCTGGGGACCCAGAGCCCTCGCGGAAACCTCCTACGTCAAGGTCTTGGAATACGTC

NYNSO1a #6

G C C R C G A R G P E S R L L E F Y L A M P F A T P M E A E
GGCTGTTGCAGATGCGGAGCCAGAGGCCCTGAGTCCAGGCTCCTGGAATTCTATCTGGCTATGCCTTTTCGTACCCCTATGGAAGCCGAA

MAGE-3 #13

A T C L G L S Y D G L L G D N Q I M P K A G L L I I V L A I
GCCACATGCCCTCGGCCTCAGCTATGACGGACTGCTCGGCGATAACCAAATCATGCCCAAAGCCGGACTGCTCATCATTGTGCTCGCCATT

LAGE1 #3

G N A G G P G E A G A T G G R G P R G A G A A R A S G P R G
GGCAATGCCGAGGCCCTGGCGAAGCCGGAGCCACAGGCGGAAGGGGACCCAGAGGCGCTGGCGCTGCCAGAGCCTCCGGCCCTAGGGGA

Artificial Protein:

APEEEIWEELSVMEVYDGREHSAYGEPRKLEEVPATAGSTDPQPSPQASAFPTTINFTRQTVWSGNRASLYSFPEPEAAQPMTKKRKVDGQIMPKAGL
LIIVLAI IAREGDCAPEEKIWELOVLDLRKNHQDFWTVWSGNRASLYSFPELDVLLAQEVPRPRWKLQVLDLRKNHQDFWQGAMLAQERRVPRAA
EVPGAQQGQGRGRQSPSVSLSVLSLGVMLTDVSPPEPLQALLLTQDLVQEKYLEYRQVPDSDPARYEFLWGPQRPSEGGSSSREEEGPSTSCILESL
FRAVITAAMAAARAVFLALSQALLQARLMKEESFVVSTFYDPEPILPCFCFMPNAAIELMEVDPIGHLYIFATCLGLSYDGLLGDNRNRYVEPPMIGFMR
PEQFSDEVEPATPEEGEAGGFFPWLKVVYRFVIGLRVWQWEVISCAAMERRRLWGSIQSRYISMSVWTSPPRLVEAALMETHLSKRYTEEGAGFFP
WLKVVYRAAMSLEQSRSLHCKPEEALQAEALGLVVCQAATSSSSPLVLGTLLEVPATAGSTDPQPSPALELLPRELFPPLFMAAFDGRHSQTLKAMV
ELSVLEVFEGRSDILGDPKLLTQHVFQESLQLVFGIDVKEADPTGHSYVLVTCGLGLSPDPQPSPQGASSLPTTMNYPLWSQSSEDSSAAMQAEQG
GTGGSTGDADGPGGPGIPDGPQCFLPVFLAQPPSGQRRRAATWGEGLPSQPIIHTCVYFFLPDHLDFGRPFSTSCILESLFRAVITKKVADLVGFLL
KYRAAMQAEGRGTGGSTGDADGPGGPGIPDGPQDGPQEMDPPNPEEVKTPEEEMRSHYVAQISSCLQQLSLLMWITQCFLPVFLAQPPSGQERASA
TLQDLVFDCEGITDDQLLALLPSLSLGDPKLLTQHVFQENYLEYRQVPQSDPACEALQAEALGLVVCQAATSSSSPLVLGTLFYLAMPFATPME
AELARRSLAQDAPPLPVEEAPRGVMAARLQGAARLEPEDGTALCFIFAAEQFSDEVEPATPEEGEPATQRQDPAAAEQGTMMNYPLWSQSSEDSSNQ
EEEGPSTFPDLESNQEEEGPSTFPDLESEFQAALSRKVAELVHVDLFLKEGACDELFSYLIEKVKRKNVLRILTIRLTAADHRQLQLSISCLQQLSL
LWVITAMPLEQRSQHCKPEEGLEARGEALGLVGADADGPGGPGIPDGPQGNAGGPGEAGATGGRYEFLWGPRLVETSYVKVLHMHVMKISGGPHITN
CRLSEGDVMMHLSQSPSVSLSVLSLSGNYLEYRQVPQSDPACYEFLWGPRLVETSYVIFSKASSSLQLVFGIELMEVDPIGHLYIFQALYVDSLFFL

Figure 27 (Cont)

RGRLDQLLRHVMNPLETLSYIAQFTSQFSLQCLQALYVDSLFFRGRGLGQHLHLETFKAVLDGLDVLILAQEVPRRRWKFIRLTAADHRQLQLSISSC
LQQLSLMLMWTTCCKKLKIFAMPMPQDKIMILKMWQLDSEIDLGAAPRGPHGGAASGLNGCCRCGARGPESRLLKKVADLVGFLLLKYRAREPVTKAEMLE
SVIYDGLLGDNQIMPTGFLIIVLVMIAEBGGHSISALQSLQLHLGLSNLTHVLPVPLESYIAREGDCAPEKIEWEELSVLVEFEGREDSIDQLLR
HVMNPLETSLTINCRLSEGDVMHLSRALAETSIVYKVEYVIKVSARVRFFFPSPSLRNLTHVLPVPLESYEDIHGTLHLERLAYLAAMLMAQEALAF
MAQGAMLAQAQERRVPRAKNYKCHFPEIFGKASESLQLVFGIDGKADTLVEVTLGEBVPAAESDPDPQSPQGAGSSLPATHARLELCELGRPSMVWL
NCPCHCGDRVMLTDSVPEPLQALLERASATQLDLVFDECEDEGASAGQPKPEADSEQGHQPQCECEEMLSGSPVGNWQYFFPIVSKASSSLQV
GAAMSWGRRSTYRPRRYVEPEMIGMPRIYSMSVWTSPPRLVELAGQSLDKBALAIAYDGREHSAYGEPRKLLTQDLVQEKYLEYRQCCFLPVF
LAQAPSQRRRAAVKVLHMHMKISGGPHISYPPPLEHEWVLREGEQLHITMPFSSPMEAELVRRILSRDAAPLPRPGVLLKEFTVSGNILTIRLTAADHRQ
LQLSKMILKMWQLDSEIDLEVTCTWKLPTLAKFSLIIVLVMIAEBGGHAPEEEIWEELSVMVEVETCTWKLPTLAKFSPYLGQMINLRLLLSGLE
ARGEALGLVGAQAPATEEQEAASSSSISYPPLEHEWVLREGEAAHIHASSYISPEKEQYIAQFTSQFSLQCLNGAGGPEGAGATGGRGPRGAGAAR
ASGPGGGPRGAGAARASGPGGAPRGPHGGAASGLNQGASAPFTINFTRQRPQSPBGSSSREEGPIARRSLAQDAPLPVPGVLLKEFTVSGNITLAA
FDGRHSQTLKAMVQAWPFTCLPLGVLMKIKVSARVRFFFPSPSLREAALREEEGVAAGITDDQLLALLPSLSHCSQLTTLFSYGNISVKTPEEMRSHY
VAQTGILWLLMNNCFNLNLSCLQQLSLMLWDTQCFLPVFLAQAPSQGYLLEKVKRKNVLRLLCKKLKIFAMPMDIAREPVTKAEMLESVINKYK
CFPEIFGKASLVRILSRDAAPLPRPGAAMVKTQFVSGNLLHCSQLTTLFSYGNISISALQSLQLHLGLMVLNSANPCPHCGDRTFYDPEPILCPK
MPAASVWSQKRSFVYVWITWGEGLSPQIHTCLLQARLMBKESPVVSWRLEPEDGTALCFIVFYVFLPDHLSFGRPHLNFCDFLAAPPVGLQMINLR
LLLSHIHASSYISPEKEEQQAPATEEQEAASSSSSTLVEVTLGEBVPAAESQAWPFTCLPLGVLMKGQHLHLETFKAVLDGLSTEAEQFPPIPVEVLVDLF
LKEGASQDLFSAEVPGAQQGQPPRGREAREPRGVRMAARLQGGAPRGPHGGAASAGDGRPCGARRPDMTLPRGAGAAASGPRGAPRGPHGGAAS
AQDLAGQSLDKDEALAIALLLELPREFLPFMFATQRQDPAAGQEGEDGASAGQPKPEAPEAAQPMTKRKVDLSTEAEQFPPIPVEVLGRCP
GARRPDSRLQLHLTHMPFSSPMEAEPGAVLKDFTVSGNLLFIRLTAADHRQLQSLSEDIHGTLHLERLAYLHARLELCELGRPSDSQEGHPQTGCE
CEDGPDGQEMDPNPEEFVIGLRVWQWEVISCKLIKRAATTRQPAADADGPGGPGIPDGPNGNAGGPEGAGATGGRPTGHSYVLTCLGLSYDGLLGD
QIMPTGFLLLKYRAREPVTKAEMLSVGNWQYFFPTGILWLLMNNCFNLNLSPRKPAAEFQAALSARKVAELVHFLLLKYRAREPVTKAVPDSDPARY
BFLWGPRLAETSIVYKVEYVGCRCRGARGPESRLLFYLAMPFATPMEABATCLGLSYDGLLGDNQIMPKAGLLIIVLAIGNAGGPEGAGATGGRGP
RGAGAARASGPRG

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Figure 27 (Cont)

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CCAGCTCGACTCCATCGAAGACCTCGGCGCTCCAGAGGCCCTCACGGAGGCGCTGCCCTCCGGCCTCAACGGATGCTGTAGGTGTGGCGCTAGGGGAC
CCGAAAGCAGACTGCTCAAGAAAGTGGCTGACCTCGTGGGATTCTCTCTGCTCAAGTATAGGGCTAGGGAAACCGGTACCAAAGCCGAAATGCTCGAG
TCCGTGATTTACGATGGCCTCCTGGGAGACAATCAGATTATGCCTAAGACAGGCTTTCTGATTATCGTCTGGTCATGATTGCCATGGAGGGAGGCCA
TAGCATTAGCGCTCTGCAAGCCTCCTGCAACACCTCATCGGACTGTCCACCTACCCCATGTGCTCTACCCGTGCTGCTGGAAGCTATATCGCTA
GGGAGGGCGATTGCGCTCCCGAAGAGAAAATCTGGGAGGAATGTCCGTGCTCGAGGTCTTGAAGGCAGAGAGGATAGCATTTGACCAACTGCTCAGG
CATGTGATGAACCTCTGGAAACCTCAGCATTACCAATTGACAGTCTCCGAGGGAGACGTCTATGCATCTGTCCAGGGCTCTGGCTGAGACAAGCTA
TGTGAAAGTGTCTCGAGTATGTGATTAAGGTACGCGCTAGGGTCAAGTTTTCTTCCCTCCCTGAGAAGCAATCTGACACACGTCTGTATCCCGTCC
CCCTCGAGTCTACGAGACATTACGGAACCTCCACCTCGAGAGACTGGCTTACCTCGCGCTATGCTCATGGCTCAGGAAGCCCTCGCCTTTCTG
ATGGCCCAAGGGCTATGCTCGCGCTCAGGAAGGAGAGTGCCTAGGGCTAAGAATTACAAACACTGTTTCCCTGAGATTTTCGGAAGGCTAGCGA
AAGCCTCCAGCTCGTGTGTTGGCATTGACGTCAAGGAAGCCGATACCCCTCGTGAAGTGACACTGGGAGAGGTCCCGCTGCCGAAAGCCCTGACCCCTC
CCCAAGCCCTCAGGGAGCCTCCAGCCTCCCAACACACGCTAGGCTCAGGGAACGTCTCTGCGAAGTGGGAAGGCTAGCATGTTGTGCTGTCCGCT
AATCCCTGTCCCATGCGGAGACAGAGTGTGCTGACAGCGTCAGCCCTGAGCCTCTGCAAGCCCTCTCTGGAAGGGCTAGCCTACCCCTCCAGGA
TCTGGTCTTCGATGAGTGTGAGGATGAGGAGCCTCCCGGACAGGACCTCCGAGCCGATAGCCAAAGAGCAGGCCATCCCAAAACCGGAT
GCGAATGCGAAGAGATGCTGGGAAGCGTCTGGGAAACTGGCAGTATTTCTTCCCGTCTATTTAGCAAAGCCTCCAGCTCCCTGCAACTGGTCTTC
GGAGCCGCTATGTCTCGGAGAGGACAGACATACAGACCCAGACCCAGAAGGTATGTGGAACCCCTGAGATGATCGGACCCATGAGGCTTACAT
TAGCATGAGCGTCTGGAACAAGCCCTAGGAGACTGCTGAGCTCGCGGACAGTCTGAGGATGAGGCTCTGGCTATCGCTTACGATGGCAGAG
AGCATAGCGCTTACGAGAGGCTTAGGAACTGTCTACCCAAGACCTCGTGAAGAGAAATACCTCGAGTATAGGCAACAGTGTTCCTCCCGTCTTC
CTCGCCCAAGCCCTTAGCGGACAGAGAAGGGCTGCCGTGAAAGTGTCTCCACCATATGTTCAAGATAGCGGAGGCCCTCACATTAGCTATCCCTCT
GCATGAGTGGGTGCTCAGGGAAGGCGAACAGCTCCACATTACCATGCCCCCTTAGCTCCCCATGGAGGCTGAGCTCTGAGAGGATTCCTGTCAGGG
ATGCCGCTCCCTCCCGAGGAGTGTCTGCTGAAAGAGTTCCTCGTACCGGAACATTTCTGACAATCAGACTGACAGCCGTGACCATAGGCAA
CTGCAACTGTCCAAGATGATCTCAAGATGGTGAACCTGGATAGCATTGAGGATCTGGAAGTGACATGCACATGGAAGTGCCTACCCCTCCGCAAT
CTCCTTCTCATCATTTGTGCTCGTGTATGCTATGGAAGGCGGACACGCTCCCGAAGAGGAAATCTGGGAGGAAGTGTCCGTGATGGAGGTGAGG
TCACCTGTACCTGGAAGCTCCCAACACATGGCTAAGTTTAGCCCTTACCTCGCCCAAATGATTAACCTCAGGAGACTGCTCTGCTCAGGATGAG
GCCAGAGGCGAAGCCCTCGGCTCTGTTGGGAGCCCAAGCCCTGCCACAGAGGAACAGGAAGCCGCTAGCTCCAGCTCCATCTCTACCCCTCCCTCCA
CGAATGGGTCTCTGAGAGAGGAGAGGAAGCCGCTCACATTACGCTAGCTTCTACATTAGCCCTGAGAAAGAGGAAACAGTATATCGCTCAGTTTACCT
CCCAGTTTCTGTCCCTGCAATGCTCGGCAATGCCGAGGCCCTGGCGAAGCCGAGGCCACAGGCGGAGCCCTAGGGGACCCCATGGCGGAGCCGCTAG
GCCCTCCGGCCTGGCGGAGGCCCTAGGGGAGCCGAGCCGCTAGGGCTAGCGGACCCGAGGCGGAGCCCTAGGGGACCCCATGGCGGAGCCGCTAG
CGGACTGAATCAGGGAGCCTCCGCTTTCCCAACCATTAACCTTACAGACAGAGACAGCCTAGCGAAGGCTCCAGCTCCAGGGAAGGGAAGGCC
CTCTGGCTAGGAGAAGCCTCGCCCAAGAGCCTCCCTCTGCTGTGCTGCGCTCTGCTCAAGGAATTACAGTGTCCGGCAATATCTCTGCGCT
TTCTGATGAGACATCCCAAGACATGAAAGCCATGGTGTGCAAGCCTGGCCCTTACCTGTCTGCTCTGAGGATGAGGATGAGGATGAGGATGAG
CAGATGAGATTCTTTTCCCTAGCCTCAGGGAAGCCGCTCTGAGAGAGGAAGAGGAAGGCGTCCGCGTGGCATACCGATGACCAACTGCTCGCC
TCCTGCTAGCCTCAGCATTGCTCCAGCTCACCACACTGTCTCTTATGGAATAGCATTTGTGAAACCCCTGAGGAAGAGATGAGGTCCCACTAT
GTGGCTCAGACAGGCATTCTGTGGCTGCTCATGAATACTGTTTCTCAACCTCATCTCCAGCTGTCTGCAACAGCTCAGCCTGATGAGGATTAC
CCAATGCTTTCTGCTGTGTTTCTGGCTCAGGCTCCCTCCGGCCAACTCCTCATCGAAAAGGTCAAGAGAAGAAAAACGTCTGAGACTGTGTTGCA
AAAAGCTCAAGATTTTCTGCTATGCTATGCAAGACATTGCCAGAGAGCCTGTGACAAGGCTGAGATGCTGGAAGCGTCAAAAACTATAAGCAT
TGCTTTCCCGAAATCTTTGGCAAGCCTCCCTGGTCAAGAGAACTCCTCAGCAGAGACGCTGCCCTCTGCTCAGGCTGCTGCTCAAGGATTT
CACAGTGTCCGGCAATCTGCTCCACTGTAGCCCACTGACAAACCTCAGCTTTTACGGAACCTCCATCTCCGCTCCGCTCCAGTCCCTGCTCCAGC
ATCTGATTGGCCTCATGGTCTGGCTCAGCGCTAACCCCTGCCCCTCACTGTGGCGATAGGACATTCTATGACCCCTGAGCCTATCTCTGCCCTGTCTT
ATGCTGCGCTAGCTGGAGCAAAAAGAGAAGCTTTGTGTATGTGTGGAAGACATGGGGAGAGGGACTGCCTAGCCAACCCATTATCCATACCTGTCT
GCTCCAGGCTAGGCTCATGAAGAGGAAGCCCTGTGGTATGCTGATGAGGCTGAGCAACCTTTATCCCTGTGGAAGTGTCTCGGCAGATGCCCTTGC
TTCTGCTGACCATCTGTCTTCTCGGAAGGCCCTTTCCATCTGAATTTCTGTGACTTTCTGGCTGCCCTTATCTGGGACAGATGATCAATCTGAGAAGG
CTCTGCTCAGCCATATCCATGCTCCAGCTATATCTCCCCGAAAAGGAGAGCAACAGGCTCCCGCTACCGAAGAGCAAGAGGCTGCCCTCAGCTC
CAGCACACTGGTCAAGGTACCCCTCGCGAAGTGCCTGCGCTGAGTCCAGGCTTGCCCTTTCACATGCTCTCCCTCGGCGTCTGATGAAGGGAC
AGCATCTGCATCTGGAACCTTTAAGGCTGTGCTCGACGGAAGTGTCCACCGAAGCCGAACAGCCTTTTATTCCCGTCAAGGTCTGCTGACCTCTTC
CTCAAGGAAGGCGCTTGCATGAGCTCTTCTCCGCGAAGTGCCTGGCGCTCAGGGACAGCAAGGCCCTAGGGGAAGGGAAGAGGCTCCAGAGGCGT
CAGGATGGCCGCTAGGCTCCAGGGAGGCGCTCCAGAGGCCCTCAGGAGGCGCTGCCCTCCGCCAAGACGGAAGGTGTCCTGTGGCGCTAGGAGAC
CCGATAGCAGACTGCTCGGCCCTAGGGGAGCCGAGCCGCTAGGGCTAGCGGACCCAGAGGCGGAGCCCTAGGGGACCCCATGGCGGAGCCGCTAGC
GCTCAGGATCTGGCTGGCCAAAGCCTCTGAAAGACGAAGCCCTCGCCATTGCGCTCTGGAAGTGTCTCCCAAGAGAGCTTCTCCCTCCCTCTTCTAT
GGAGCCTGCCACACAGAGACAGGATCCCGCTGCCGCTCAGGAAGGCGAAGGACGAAGGCGCTAGCGCTGGCCAAGGCCCTAAGCCTGAGGCTCCCGAAG
CCGCTCAGCCTATGACAAAAGAAAGGAAGTGGATGGCTCAGCAGAGGCTGAGCAACCTTTATCCCTGTGGAAGTGTCTCGGCAGATGCCCTTGC
GGAGCCAGAAGGCCCTGACTCAGGCTCTGCAACTGCATATACCAATGCCCTTTCTCCAGCCCTATGGAAGCCGAACCCGAGCCGCTCTGAAAGACTT
TACCGTCAAGGAAACCTCCTGTTTATCAGACTGACAGCGCTGACCATAGGCAACTGCAACTGTCCGAGGATATCCATGGCACACTGCATCTGGAAG
GGCTCGCCTATCTGCATGCCAGACTGAGAGAGCTCTGTGTGAGCTCGGCAGACCCCTCCGACTCCAGGAACAGGACACCCCTCAGAGGCTGAGT
TGTGAGGATGGCCCTGACGGACAGGAATGGATCCCTTAACCTGAGGAATTCGTATCGGACTGAGAGTGTGGCAGTGGGAGGTGATCTCTCTGCAA
ACTGATTAAGAGAGCCACAACAGACAGCCTGCCGCTGACGCTGACGGACCCGAGGCCCTGGCATTCGGATGGCCCTGGCGGAACCGTGGCGGAC
CCGAGAGGCTGGCGCTACCGGAGGACAGCCACAGGCCATAGGTATGTGCTCGTGACATGCCCTGGCCTCAGCTATGACGGACTGCTCGGCGATAAC
CAAATCATGCCCAAAACCGGATTCCTCTGCTCAAGTATAGGGCTAGGGAACCGTACCAAAGCCGAATGCTCGGCTCCGTGGTGGCGAATTTGGCA
ATACTTTTTCCCTACCGAATCCTCTGGCTCTGATGAACAATTGCTTTCTGAATCTGTCCCCAGAAAGCCTGCCGCTGAGTTTCAAGCTGCCCCCA
GCAGAAAGGTGCGCGAAGTGGTCCACTTCTGCTCCTGAAATACAGAGCCAGAGAGCCTGTGACAAAGGCTGTGCTGACTCCGACCTGCCAGATAC
GAATTCCTCTGGGACCCAGAGCCCTCGCGAAACCTCTCATGCTCAAGTCTGGAATACGTCGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT
CAGGTCCTGGAATCTATCTGGCTATGCCCTTTCGCTACCCCTAGGAGCCGGAAGCCATGCTCCGCTCAGCTATGACGGACTGCTCGGCGATA
ACCAATCATGCCCAAGCCGAGTGTCTCATATTGTGCTCGCCATTGGCAATGCCGAGGCCCTGGCGAAGCCGAGCCACAGGCGGAAGGGGACCC
AGAGGCGCTGGCGCTGCCAGAGCCTCCGCGCCTAGGGGA

Figure 27 (Cont)

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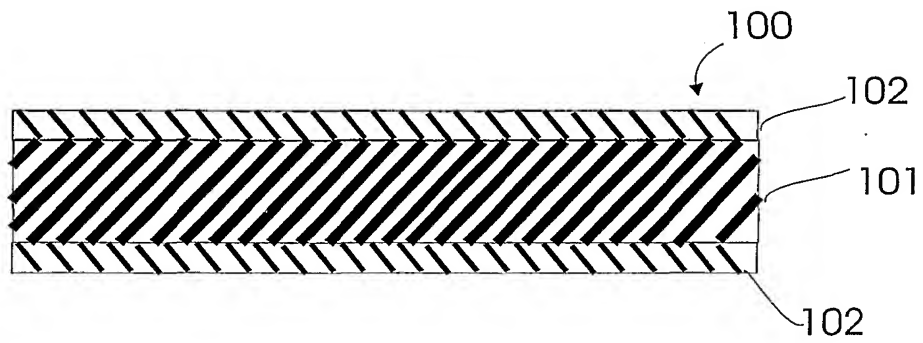


FIGURE 28

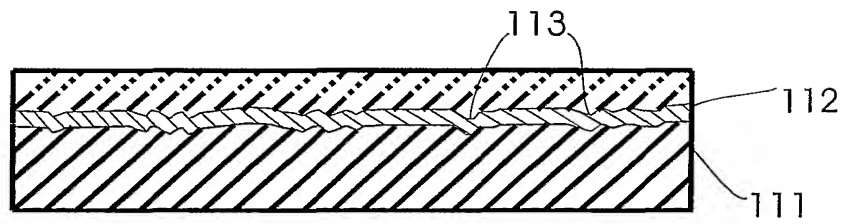


FIGURE 29

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Cassettes for construction of a full-length HIV Savine

Cassette A1

ggatccaccATGACAGGCCCTTGCACAAACGTCAGCACCGTGCAATGCACACACGGAATCAGACCCGTCGTGTCCA
CCCAACTGCTCCTGAATGGCTCCCTGAGAAGCCTCTACAATACCGTCGCCACACTGTGGTGCGTCCACCAAAGGAT
TGACGTCAGGGACACAAAGGAAGCCCTCGACAAAATCGAACTCGGCGATGGCGGAGGCGCTGAAAGGCAAGGCACC
TCCAGCTCCTTCAACTTTCCACAAATCACACTGTGGCAAAGGCCTCTGGTCACCGAACCCCTTCAGAAAAAAGAATC
CCGATATGGTGATTTACCAGTACATGGACGATCTGTATGTGGGAAGCGATCTGGAAATCGGACAGCATTTTACCAC
ACCCGATAAGAAAACACCAAAGGAACCACCATTCTCTGGATGGGATACGAACTGCATCCCGATAGGTGGACCGTC
CAGCCTCTTAATTTCCCTCAGATTACCCTCTGGCAGCGTCCCCCTCGTGACAATCAAAATCGGCGGACAGCTCATAG
AGGCTCTGCTCGACACAGGCTCCTATGGCAGAAAGAAACGTAGGCAACGTAGACGCGCTCCTCAGAGCAGCAAGGA
TCACCAATACCCTATCTCTGAGCAACCCCTCTCCTTCTTTAGGGAAAACCTGGCTTTCCAGCAAGGTAAAGCCAGA
GAGTTTTCCAGCGAACAGACAAGAGCCAATAGCTCCGCCCTCCAGGAAGAGCCCCCAAATCTCCGGCGAAAGCTCCG
TCATTCTGGGATCTGGCACCAAAAACGCCGCTACTAGAAGAATCGAAGTGAAAGATACCAAAGAGGCTTTGGATAA
GATTGAGGAGGTGCAAAAGAAAAGCGAGCAAAAGACACAACAGGCTGCCGCTAAAGCCGGATACGTCACCGATAGG
GGAAGGCAAAAGATTATCTCCCTGACAGAGACAACCAATCAGAAAACCGAACTGCATGCCATTCAAGAAGCCACTA
CCACACTGTTTTGCGCCAGCGATGCCAAAGCCTATGAGACAGAGGTCCACAATGTGTGGGCCACACACGCTTGCGT
CCCCGCTGACGATACAGTGCTGGAGGAGATGAACCTCCCCGGAAAATGGAAGCCTAAGATGATTGGCGGAATCGGC
GGATTCTATTAAGGTGAGAAAAATCGGACCCGAAAACCCCTTACAATACCCCAATCTTCGCTATCAAGAAAAAGGACT
CCACCAAATGGAGAAAGCTCGTGATTTTCTAGAGTTAGGATTATCAATATCCTCTACCAAAGCAATCCCTATCCTAG
CTCCGAAGGCTCCAGGCAAACCAGAAAGAATAGGAGAAGGAGATGGGGAGGCGAACGGGGTAGGGATAGGTCCGTG
AGACTGGTCAACGGATTCTTAGCCCTCGCCTGGGACGATCTGAGAAACCTCTGCCTCTTCGAAAACCTCTGGGTCA
CCGTCTACTATGGCGTCCCCGTCTGGAGAGAGGCTGCCACAACCCCTCTTCTGTGCCTCCGACGCTAAGGCTTACGC
TGCCATGGCTGGCAGAAGCGGCGGCACAGACGAAGAGCTCCTGAGGGCTATCAGAATCATTAACATTCTGTATCAG
TCCAACCCCTTACCCTTCCGCTAGTATGAGAATCAGAACCTGGAACAGCCTGGTCAAGCATCACATGCACATCTCCA
AGAAAGCCAAAGGCTGGTTCTATAGGCATCACTTTGAGGAGTCCGAGCTCGTGAATCAGATTATCGAAAAGCTCAT
CAAAAAGGAAAAGGTCTACCTATCATGGGTACCAGCCACAAGGGAATCGGACAAACCAAAGAGCTCCAGAAACAG
ATTATCAAAATCCAAACTTTAGGGTCTACTATAGGGATAGCAGAGACCCTATCTGGAAGGGACCCAAAAGCTTTG
AGGAAATCTGGAACAATATGACATGGATTGAGTGGGAGAGAGAGATTAGCAATTACACAAGCCAAATCTATAAGAT
TCTGAAACCCGAACCCACAGCCCCCTCCGCTGAGAATTTTCAAGATTTCGGTGAGGAACTACACCCTCCCAAAAGCAA
GAGCAAAAGGATAAGGAGCAATACGATCAGATTCTTATTGAGATTTGCGGCAAGAAAGCTATTGGTACGGTGTCTCG
TGGGACCTACCCCTGTGAATATCATTTGGCAGAATTTACGAAACCTATGGCGATACCTGGGAGGGCGTCGAGGCTCT
GATCAGAATCCTCCAGCAACTGATGTTTATCCATTTTCAAGATTCGGATGTTTTCATTGCCAAGTGTGTTTTCTCACC
AAAGGTCCTCGGCATTAGCCACGGAAGGAAAAAGAGAAAAACAGAGAAGGGGAGCTCCCCAAGCTGCCATGGACCCCG
TGGACCCCAAGCTGGAGCCTTGGAACACCCCTGGCTCCCGAGCCTAAGACAGCCTGTTACAAATGCTATTGCAAAAA
GTGCCCTAGCGAAGAGACAACCCCTAGCCAGAAACAGGAACAGAAAGACAAAGAACTCTACCCCCCTTTAGCCAGC
CTCAAGTCCCTGTTTTGGCAATGACAATTTCAATATGTGGAAGAATGACATGGTGGAAACAGATGCAAGAAGACATTA
TCTTACTATGGGACCAAAGCCTCAAGCCTTGCGTCAAGCTCGACGTCGGCGATGCCTATTTCTCCGTGCCTCTGGA
TAAAACTTCAGAAAGTATACCGCTTTCACAATCCCTAGCACAAACAATGAGCAACTGAAAGGCGAAGCCATCCAT
GGCCAAGTGAATTGCTCACCAGGCATTTGGCAACTGGAATTGCACACACCTGGAGGGAAAGATTATCCCTAAGGTCA
AGCAATGGCCTCTGACAGAGGAAAAGATTAAGGCTCTGACTGAGATTTGCAAAGAGATGGAGGAAGAGGGAAAGAT
TAGCATGGATGACCTCTACGTCGGCTCCGACCTGG

FIGURE 30

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AGATTGGCCAACATAGGACCAAAATCGAAGAGCTCAGGGAACACCTCCTGAAATGGGGACTCACCGAAACCACAAA
CCAAAAGACTGAGCTCCAAGCTATCCATCTGGCTCTGCAAGACTCCGGCTTAGAGGTCAACATTGTGACAGACATT
CCCGCTGAGACTGGTCAAGAGACCGCCTTTTTTCATTCTGAAACTGGCTGGCAGATGGCCTGTGAAAGTCATTCACA
CAGACAAATGGCAGGACAAAGATTGAGGAACTGAGACCGCATCTGCTCAAATGGGGCTTCACAACCCCTGACAAAAA
GCATCAGAAAAGAGCCTCCCTTTCTGTCTAGTGTCAAGAACTGACAGAGGATAAGTGGAACGAACCCAGAAAAATC
AAGAGACGCAGAGAAAAATCACACAATGAATGGCCATACTGCCACAGAGTCCCAGAATCAGCAAGACAGAAACGAAA
AGGAACTGCTGGAGCTCGACAAATGGGCAAGCCTCTGGAATTGGTTTAACATTACCGACACCCGAAATAGCTCCAA
AGTGTCCCGAATTACCCTATCGTCCAGAATGTCCAAGGCCAAATGGTCCACCAACCCCTCTCCCCAGACTCATC
GGACTGAGAATCGTTTTTCGCTGTGCTCAGCATTATCAATAGGGTCAGGCAAGGCTATAGCCCTCTGTCCTTCCAAA
CCCTCCCCCTCATCCATCTGCAATACTTTGACTGTTTTCGCTGACTCCACCATTAGGAGAGCCATCTTGGGACACAT
AGTGAGAAGGAGATGCGAATACGCTGTGGGACTCGGAGCCATGTTCCCTTGGCTTTCTGGGTGCCGCTGGCTCCACC
ATGGGCGCTGCCTCCATGACACTGACAGTGAAGCCTATGACCCTAGCAAAGACCTCATGTGCTGAGATTGAGAAAC
AGGGCCAGGGTCAGTGGACATTTTCAAGAGCCTTTCAAAAACGGAACCGTCTCGGTGGGCCCTACACC
CGTCAACATCATCGGAAGGAACATGCTGACACAGCTTGGCCGCACCTCTCAACTTTCCCATTAGCAAAGGCAGCCCT
GCTATCTTTTCACTCCAGCATGCCACAGATTCTGGAGCCTTTTAGGATAAAAAACCCCTGAGATGGTCATCTATCAGT
ATCCTAGCCCTCTGACATTTCGGATGGTGTTCAAACTGGTCCCCGTGGACCCAGCGAAGTGGAAGAGATCAACAA
GGGCGAAAAACAATTGCCCCCTGTTTAGGAAATACACAGCCTTTACCATTCCCTCCATCAATAACGAAACCCCTGGC
ATTAGGTATCAGTATAACGTCCTGCCTCAGGGATGGGGAAGCACAATGGGAGCCGCCAGCATGACCCTCACCGTCC
AGGCTAGGCTACTGCTCAGCGGAATCGTCCAGCAACAGAGCAATCTGCTGGAGGAGAATAGGGAAATCCTCAGAGA
GCCTGTGCATGGCGTCTACTACGATCCCTCCAAGGATCTGGTCTGCTGAAATCCAAAAGCAAGGCAGAGAGGAACTG
TCCACCATGGTGGATATGGGAAACTACGACCTCGGAGTGGACAATAACCTCGCCGCTATTAGAATCCTGCAACAGC
TCATGTTTCATTCACTTTAGGATTGGCTGCCAGCACTCCAGGATTGGCATCATCCGTGAGAGAAGGGCCAGAGCTCC
CAGGAAAAAGGGATGCTGGAAGTGTGGCAGAGAGGGACACCAGATGAAGGATTGCACTGAGAGACAGGCTAACTTT
CTGGGAAAGGATGCCAGACTGGTTATCAAAACCTATTGGGGACTGCATACCGGTGAGAGAGACTGGCACCTCGGCC
ATGGCGTCAGCATTGAGTGGAGGATAAGGGAAAGGGCTGAGGATAGCGCAACGAAAGCGAAGGCGACACAGAAGA
GCTCAGCACATTGGTGGACATGGGCAATTACGATCTGTCTAGCCCTGCCCCAGGGGACCCGATAGGCTGGAGAGA
ATCGAAGAGGAAGGCGGAGAGCAAGGCAGAGGCAGAAGCGTCAGGCTCGTGAATGGCAGAGAGGTGAGGAAGTCA
ATGAGGGAGAGAATAACTGTCTGCTTACCCTATCAGTCAACATGGCATGGAAGACGAAGAGAGAGAGGTCAATAG
CGATATCAAAGTGGTCCCAGAAGGAAAGCCAAAATCATTAGGGATTACGGAAAGCAAATGGCTGGCGATGACTGT
GTGGCCAGCTTCTCTTCCGAGCAAACAGGGGCTAACTCCTCTACAAGCAGAAAGCTGGGAGACGGAGGCGGAGCCG
ACAGACAGGGAACAAGCTCCAGCTGTTTCAATTGCGGCAAAGAGGGACACATTGCCAAAAACTGTAGGGCCCCCTCG
CAAGAAAGGTTGTTGGAAATGCGGAAAGGAAGGCCATCAAATGAAAGACTGTACCGAAAGGCAAGCCAATTTCTC
GGCAAAATCTGGCCCTCCAACAAAGGCAGACCCGAAACTTTCTCCAAAGCAAATGGCTCTGGTATATCAAAATCT
TTATCATGATCGTCCGTGGACTGATTGGCCTCAGGATTATCTTTGCCGTCTGTCCATCGTTAACGGAGCCGTGAG
CCGAGACCTCGATAAACATGGCGCTATTACAAGCTCCAATACCGCTGCCAATAACGCTGACTGTGTCTGGCTGAAG
GCTGCTGCCATGACACCCCTGGAGATCATCGCTATCGTCCGCTTTATCGTCCGCTCATCATAGCCATTGTGGTCT
GGACAATCGTCTACATTGAGTATGTCGACTgaagatctgaattc

Figure 30 (Cont)

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A2 fragment

ggatccaccATGACAGGCCCTTGACAAAACGTCAGCTCCGTGCAATGCACACACGGAATCAAACCCGTCGTGTCCA
CCCAACTGCTCCTGAATGGCTCCCTGAAAAGCCTCTACAATACCGTCGCCACACTGTGGTGTGTCCACCAAAGGAT
TGAGGTCAAGGACACAAAGGAAGCCCTCGACAAAATCGAACTCGGCGATGGCGGAGGCGCTGAAAGGCAAGGCACC
TCCAGCTCCATCAACTTTCCACAAATCACACTGTGGCAAAGGCCTCTGGTCACCGAACCCCTTCAGAAAAGAGAATC
CCGAAATGGTGATTTACCAGTACATGGACGATCTGTATGTGGGAAGCGATCTGGAAATCGGACAGCATTTTACCAC
ACCCGATAAGAAACACCAAAAGGAACCACCATTCTCTGGATGGGATACGAACTGCATCCCGATAGGTGGACCGTC
CAGCCTTTTAAATTTCCCTCAGATTACCCTCTGGCAGCGTCCCTCGTGACAATCAAATCGGCGGACAGCTCATAG
AGGCTCTGCTCGACACAGGCTCCTATGGCAGAAAGAAACGTAGGCAACGTAGACGCGCTCCTCAGAGCAGAAAGGA
TCACCAATACCCTATCTCTGAGCAACCCCTCTCCTTTTAGGGAAAACCTGGCTTTCCAGCAAGGTAAAGCCAGA
GAGTTTTCAGCGAACAGACAGGAGCCAATAGCTCCGCTCCAGGAAGAGCCCCCAAATCTCCGGCGAAAGCTCCG
TCATTCTGGGATCTGGCACCAAAAACGCCGCTACTAGAAGAATCGATGTGAGAGATACCAAAGAGGCTCTGGATAA
GATTGAGGAGGAGCAAAAACAAAGCAAGCAAAAGACACAACAGGCTGCCGCTAAAGCCGGATACGTCACCGATAGG
GGAAGGCAAAAAGATTATCTCCCTGACAGAGACAACCAATCAGAAAACCGAACTGCATGCCATTCAAGAAGCCGATA
CCACACTGTTTTGCGCCAGCGATGCCAAAGCCTATGACACAGAGGTCCACAATGTGTGGGCCACACACGCTTGCGT
CCCCGCTGACGATACAGTGCTGGAGGAGATGAACCTCCCCGAAAATGGAAGCCTAAGATGATTGGCGGAATCGGC
GGATTCAATTAAGGTGAGAAAGATCGGACCCGAAAACCCCTTACAATACCCCAATCTTCGCTATCAAGAAAAAGAACT
CCACCAAATGGAGAAAGCTCGTGGATTTTCAAAATTAGGATTATCAAAATCCTCTACCAAAGCAATCCCTATCCTAG
CTCCGAAGGCACCAGGCAAAACCAGAAAGAATAGGAGAAGGGGATGGGGAGGCGAACAGGGTAGGGATAGGTCCGTG
AGACTGGTCAACGGATTCTTAGCCCTCGCCTGGGACGATCTGAGAAGCCTCTGCCTCTTCGACAACCTCTGGGTCA
CCGTCTACTATGGCGTCCCCGTCTGGAGAGAGGCTAACACAACCCTCTTCTGTGCCTCCGACGCTAAGGCTTACGC
TGCCATGGCTGGCAGCAGCGGCAGCACAGACGAAGAGCTCCTGAAGGCTGTCAGAATCATTAAGATTCTGTATCAG
TCCAACCCCTTACCCTTCCGCTAGTATGAAAATCAGAACCCTGGAAGAGCCTGGTCAAGCATCACATGTACATCTCCA
AGAAAGCCAATGGCTGGTTCTATAGGCATCACTTTGAGGAGTCCGAGGTCTGTAATCAGATTATCGAAAAGCTTAT
CAAAAAGGAAAAGGTCTACCTATCATGGGTACCAGCCACAAGGGAATCGGACGAACCAAGAGCTCCAGAAACAG
ATTATCAAAATCCAAAACCTTTAGGGTCTACTATAGGGATAGCAGAGACCTATCTGGAAGGGACCCAAAAGCCTTG
AGGAAATCTGGAACAATATGACATGGATTCACTGGGAGAGAGAGATTAGCAATTACACAAACCTAATCTATAAGAT
TCTGAGACCCGAACCCACAGCCCCCTCCCGCTGAGAATTCGGATTCCGGTGAGGAAACTACACCCCTCCCAAAAGCAA
GAGCCAAAGGATAAGGAGCAATACGATCAGATTATTATTGAGATTTGCGGCAAGAAAGCTATTGGTACAGTGCTCG
TGGGACCTACCCCTGTGAATATCATTGGCAGAATTTACGAAACCTATGGCGATACCTGGGAGGGCGTCGAGGCTCT
GATCAGAATCCTCCAGCAACTGATGTTTATCCATTTCAAGATCGGATGTTTTTATTGCCAAGTGIGTTTTCTCACC
AAAGGTCTCGGCATTAGCCACGGAAGGAAAAAGAGAAAACAGAGAAGGCGAGCTCCCCAAGCTGCCATGGACCCCG
TGGACCCCAACCTGGAGCCTTGGAACACCCCTGGCTCCGAGCCTAAGACAGCCTGTAACAAATGCTATTGCAAAAA
GTGCCCTAGCGAAGAGACAACCCCTAGCCAGAAACAGGAACGAAAGACAAAGAACTCTACCCCCCTTTAGCCAGC
CTCAAGTCCCTGTTTGGCAATGACAATTTCAATATGTGGAAGAATAACATGGTGGAACAGATGCAAGAAGACATTA
TCTCACTATGGGACCAAAGCCTCAAGCCTTGCGTCAAGCTCGACGTCGGCGATGCCTATTTCTCCGTGCCCTTGGA
TAAAAACTTCAGAAAGTATACCGCTTTTACAATCCCTAGCACAAACAATGAGCAACTGAAAGGCGAAGCCATGCAT
GGCCAAGTGAATTGCTCACCAGGCATTTGGCAACTGGATTGCACACACCTGGAGGGAAAGATTATCCCTAAGGTCA
AGCAATGGCCTCAGACAGAGGAAAAGATTAAGGCTCTGACTGAGATTTGCACAGAGATGGAGCAAGAGGGAAAGAT
TAGCATGGATGACCTCTACGTCGGCTCCGACCTGGAGATTGGCCAACATAGGACCAAAATCGAAGAGCTCAGGGCA

Figure 30 (Cont)

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CACCTCCTGAGATGGGGACTCACCGACACCACAAACCAAAGACTGAGCTCCACGCTATCCATCTGGCTCTGCAAG
ACTCCGGCTTAGAGGTCAACATTGTGACAGACATTCCCGCTGAGACTGGTCAAGAGACCACCTATTTTCATTCTGAA
ACTGGCTGGCAGATGGCCTGTGAGAATCATTACACAGACAATGGCAGGACAAAGATTGAGGAACTGAGACCGCAT
CTGCTCAAATGGGGCTTCACAACCCCTGACAAAAAGCGTCAGAAAGAGCCTCCCTTTCTGTCTAGTGTCAAGAAAC
TGACAGAGGATAAGTGGAACAAACCCAGAAAATCAAGGGACACAGAGAAAATCACACAATGAATGGCCATGCTGC
CACAGAGTCCCAGAATCAGCAAGACAGAAACGAAAAGGAACTGCTGGAGCTCGACAAATGGGCAAGCCTCTGGAAT
TGGTTTAACATTACCGACACCGGAAGTAGCTCCCAAGTGTCCAGAATTACCTATCGTCCAGAATCTCCAAGGCC
AAATGGTCCACCAACCCATCTCCCCAGACTCGTCGGACTGAGAATCATTTCGCTGTGCTCAGCATTATCAATAG
GGTCAGGCAAGGCTATAGCCCTCTGTCTTCCAAACCCCTCACCTCATCCATCTGTATTACTTTGACTGTTTCGCT
GACTCCACCATTAGGAGAGCCATCCTTGGACACAGAGTGAGCAGGAGATGCGAATACGCTGTGGGAATCGGAGCCA
TGTTCCCTTGGCTTTCTGGGTGCCGCTGGCTCCACCATGGGCGCTGCCTCCATCACACTGACAGTGCAAGCCTATGA
CCCTAGCAAAGACCTCATTGCTGAGATTAGAAAACAGGGTCAGGATCAGTGGACATATCAGATTTTCCAAGAGCCT
TTCAAAAACGGAACCGTCTCTGGTCGGCCCTACACCCGTCAACATCATCGGAAGGAACCTGCTGACACAGATAGGCT
GCACCTCAACTTTTCCCATTAGCAAAGGCAGCCCTGCTATCTTTTCACTCCAGCATGACACAGATTCTGGAGCCTTT
TAGGAAACAAAACCCCTGACATGGTCATCTATCAGTATCCTAGCCCTCTGACATTCGGATGGTGTTCAAACTGGTC
CCCGTGGACCCAGCGAAGTGGAAGAGACCAACAAGGGCGAAAACAATTGCTCCTGTTTTAGGAAATACACAGCCT
TTACCATTCCCTCCACCAATAACGAAACCCCTGGCATTAGGTATCAGTATAACGTCCTGCCTCAGGGATGGGGAAG
CACAATGGGAGCCGCCAGCATGACCTCACCGTCCAGGCTAGGCAACTGCTCAGCGGAATCGTCCAGCAACAGAAC
AATCTGCTGGAGGAGAATAGGGAAATCCTCAAAGAGCCTGTGCATGGCGTCTACTACGATCCCTCCAAGGATCTGA
TCGCTGAAATCCAAAAGCAAGGCACAGAGGAACGTCCGCTTGGTGGATATGGGAACTACCACCTCGGAGTGGA
CAATAACCTCGCCGCTATTAGAATCTGCAACAGCTCATGTTCACTTTAGGATTGGCTGCCAGCACTCCAGG
ATTGGCATCATCCGTGAGAGAAGGGCCAGAGCTCCAGGAAAAAGGGATGCTGGAAGTGTGGCAAAGAGGGACACC
AGATGAAGGATTGCACTGAGAGACAGGCTAACTTTCTGGGAAAGGATGCCAGACTGGTTATCAAAACCTATTGGGG
ACTGCATACCGGTGAGAGAGACTGGCACCTCGGCCATGGCGTCAGCATTGAGTGGAGGACAAGGGAAAGGGCTGAG
GATAGCGGCAACGAAAGCGAAGGCGACAGAGAAGAGCTCAGCACAATGGTGGACATGGGCAATTACGATCTGTCTA
GCCCTGCCCCCAGGGGACCCGATAGGCTGGAGAGAATCGAAGAGGAAGGCGGAGAGCAAGACAGAGACAGAAGCGT
CAGGCTCGTGAATGGCAGTGAGGGCGAGGAAGTCAATAAGGGAGAGAATAACTGTCTGCTCCACCTATGAGTCAA
CATGGCATGGAAGACGAAGACAGAGAGGTCAATAGCGATATCAAAGTGGTCCCAGAAAGGAAAGCCAAAATCATTA
GGGATTACGGAAGCAAATGGCTGACGATGACTGTGTGGCCGGCTTCTCTTCCGAGCAAACAAGGGCTAACTCCCC
TGCAAGCAGAAAGCTGGGAGACGGAGGCGGAGCCGACAGACAGGGAAACAAGCTCCAGCTGTTTCAATTGCGGCAAA
GAGGGACACATTGCCAAAAGCTGTAGGGCCCCCTCGCAAGAAAGGTTGTTGGAAATGCGGAAGGGAAGGCCATCAAA
TGAAAGACTGTACCGAAAGGCAAGCCAATTTCTCGGCAAAATCTGGCCCTCCAAAAAGGCAGACCCGGAAACTT
TCTCCAAAGCAAATGGCTCTGGTATATCAAAATCTTTATCATGATCGTGGTGGACTGATTGGCCTCAGGATTATC
TTTGCCGTCCTGTCCATCATTAACGGGGCCGTGAGCCGAGACCTCGATAAACATGGCGCTATTACAAGCTCCAATA
CCGCTGCCAATAACCCCTGACTGTGTCTGGCTGGAGGCTGCTGCCATGACACCCCTGGAGATCATCGCTATCGTCGC
CCTTATCGTCGCCCTCATCATAGCCATTGTGGTCTGGACAATCGTCTACATTGAGTATGTCGActgaagatctgaa
ttc

Figure 30 (Cont)

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B1 fragment

ggatccaccATGCTCGAGAATATGCTCACCCAAATCGGATGCACACTGAATTTCCCTATCTCCCCCATTTGAGACAG
TGCCCTGTGAAACTGAAACCCGGAATGGATGGCGCCGCCACCTTTAGGCCTGGCGGAGGCAATATCAAAGACAATTG
GAGAAGCGAACTGTATAAGTATAAGGTCGTGAAGATTAAGCCTCTGGGAATCACATGGATTCCCGAATGGGAGTTCT
GTCAACACACCCCCCACTGGTCAAGCTATGGTATCAGCTGGAGAAAGACCCCTATCGTTGGCGTTGAGCCTCAGGATC
TCAACACGATGCTGAATCTTGTAGGAGGCCATCAGGCCGCTATGCAAATGCTGAAAGAGACAATCAATGAGGAAGC
CTCTGTCTCTGTTTCTGGATGGCATTGACAAAGCTCAAGAGGAACATGAAAAGTATCACTCCAACCTGGAGGACAATG
GCCAACGACTTTAATCTGATGAAGCATCTCGTCTGGGCCTCTAGGGAGCTGGAGAGATTTCGCTCTGAATCCCAGCC
TGCTGGAGACATCCGAAGGCTGTCAGCAAATTGCTGAGGAAGAGATTATCATTAGGTCCGAGAATTTACAAAACAA
TGTCAAAACCATTTATCGTCCAACCTCAACGAAAGCGTCGAGATTAACATGGGCGCTAGGGCTAGTGTCTCAGAGGC
GGCAAGCTGGACGCTGGGAAAAGATTAGGCTCAGGCCTGGCGGAAAGAAAAGTATAGGCTCAAGGAGAAGGGAG
GCCTGGAGGGACTGGTTTACTCCAAAAGAGGCAAGACATTCTGGATCTGTGGGTGTATAACACACAGGGATTAC
TAGATGGGGAACCATGATCCTCGGCTTGTTGATTATCTGTAGCGCCAGCGAGAATCTGTGGGTGACAGTGTATTAC
GGAGTGCCTGTGTGGAGGAGACAGCTCCTGTCCGGCATTGTGCAACAACAAAATAACCTCCTGAGGGCTATCGAAG
CCCAACAGCATCTGCTCCAGCTCACCGTCTGGGTGAGGCATTTCCCAGGCCTTGGCTCCACGGCCTGGGACAGTA
CATCTATGAGACATACGGAGACACATGGGCGGGAGTGGAAGCCCTCACAGCCCTCATCACACCCAAAAAGATTAGG
CCTCCCCCTCCCATCCGTGAAAAAGCTCACCGAAGACAGATGGAATGAGCCTCAAAGACATATAGCGCTGGCGAAA
GGATTATCGATATCATTGCATCCGACATTTCAGACTAAGGAAC TGCAAAGCAAATCCTAAAGATT CAGAATTTTCGC
TGTGTTTATCCATAACTTTAAGAGGAAGGGAGGCATTGGCGGCTACTCCGCCGAGAGAGAATCATTGACATTATC
GCCACCGATATCATTCCCGTGGGCGAAATCTATAAGAGATGGATCATTTCTGGGACTCAACAAAATCGTGAGAATGT
ATCTACCCGTCAGCATTCTGGATATCAGAGTGAGACAGGGATACTCCCCCTCAGCTTTCAGACACTGCTGCCCCG
TCCCAGAGGCCCTGACAGACTCGGAGGCATTGAGGAAGAGTCCAGCCAGGACCATCAGTATCCCATTCCCGAACAG
CCTCTGCCTCAGACAAGGGGAGACAATCCCAAGACCCCTAAGGAAAGCAAAAAGGCTAGTGGAGGGGTGAGTCCA
TGAATAAGGAACTGAAAAAGATTATCGGACAGGTGAGGGACCAGGCTGAGCACCTGAAAACCGCTGTGCAAATGGC
TGCCATGCAGATGCTCAAGGATACCATTAAACGAAGAGGCTGCCGAGTGGGACAGAGTCCATCCCGTCCATGCCGGG
CCCGTTCCCCCTCTCACCGAGATTTGTAAAGAAATGGAAAAAGAAGGCAAAATCTCCAAGATTGGCCCTGAGAATC
CCTATAACACACCCATCTTTGCCATTCAAGTGAGAGAGCAAGCCGAACACCTCAAGACAGCCGTCCAGATGGCAGT
CTTCATTCACAATTTCAAAGGAGAGGCGGAATCGGAGGCAAAAAGAAAGATAGCACAAAGTGGAGGAAACTGGTA
GACTTTAGGGAGCTCAACAAACGTACACAGGATTTCTGGGAGGTCCAGCTCGGCTTTTTGGCTCTGGCTTGGGATG
ACCTCAGGAGCCTGTGTCTGTTTCAGCTATCACAGACTGAGAGACTTTATCCTCATCGTTGCCAGAATCTGCCGACA
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GACCCCATTTCCATTCACTATTGCGCTCCCGCTGGCTTCGCTATCCTCAAGTGTAACGATAAGAACTTCAATGGCG
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CCTCGCCGATCAGCCTAGCCTCTATCCTCCCTTAGCTTCCCTGAAAAGCCTCTTCGGAAACGATCCCTTATCCCAA
GCCGCTAGAAGGGCTATCCTCGGCCATATAGTCAGGAGAAGGTGTGAGTATCAGTCCGGACACAATAAGGTGGCT
CCCTGCAATACCTCGCACTCAGTCAACCCACAACCGCTTGCTACAAGTGTTACTGTAAAGAAATGTTGCTTCCACTG
TCAGGTCTGCTTCTGAAGAAGGGACTGGGAATCAGGGATTACGGAAAGCAAATGGCTGGCGATGACTGTGTGGCC
AGCAGGCAAGACGAAGACGCAGCCAAGTACCATAGCAATTGGAGAACCATTGGCAATGAGTTTAACCTCCCCCTA
TCGTCCCTAAGGAAATCGTCGCAAATTGCAATAAGTGTAACGAATGGACACTGGAACCTGCTGGAGGAACTGAAACA
TGAAGCCGTGAGACACTTTCCAGACCTGGCTGCATGGCCTCGGTCAACACGATATCATTAGCCTCTGGGATCAG

Figure 30 (Cont)

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TCCCTGAAACCCTGTGTGAAACTGACACCCCTCTGCGTCACCCCTCAACTGTACCAATGCCAATCTGATGAAGAGAT
ACTCCACCCCAAGTGGACCCCGATCTGGCTGACCAACTGATTACCTCCACTATTTTCGATTGCTTTGCCGATAGCGC
AATCCATCCCATCGGCCAACACGGAATGGAGGATGAGGATAGGGAAGTGCTGAAATGGAAATTCGATAGCCATCTG
GCTCTCAGGCATATCGCTTCTAGTCCTATCGATACCGTCCCCGTCAAGCTCAAGCCTGGCATGGACGGACCCAAAG
TGAAACACTGGCCCCTCACCGAAGAGAAAAATCAAAGCCATTTGGCCTAGCAACAAGGGAAGGCCTGGCAATTTCCC
GCAGTCCAGGCCTGAGCCTACCGCACCCCCAGCCGAGAGCTTTAGATTTCGGCATTAGCAAAAAGGCTAAGGGATGG
TTTTACAGACACCATTACGATAGCCGACACCCTAAGGTGAGCTCCGAGGTCCACATTTCCCTCGGCATGATGACCG
CTTGCCAAGGCGTCGGCGGACCCAGTCACAAAGCCAGGGTACTGGCAGAGGCTATATCCCAGGTGAACAACGCTAA
CATTCCTCCCATTGTGGCCAAAGAGATTGTGGCAAACCTGTGACAAATGCCAGCTCAAGAGTGAGGCTATTACGGA
CAGGTGAACGTAGCCCTTCCGAGGGAACAAGACAGACTAGGAAGAACAGACGTAGAAGGTGGCGTGCGAGGCAAA
GGCAAATCCACTCCATCTCCGAGAGGATTCTGGGACAGATGAGGGAACCCAGAGGCTCCGACATTGCCGGTACTAC
AAGCACACTGCAAGAGCAAATCGCATGGATGACAAGCAATCCCCCTAGCATTCAACAAGAGTTTGGCATTCCCTAT
AACCCTCAGTCCCAGGGCGTCGTGGAAAGCATGAACAAAGAGCTAAAGAAAAATCATTTGGCAGACAGGAGATCCTCG
ATCTCTGGGTCTACCATAACCAAGGCTATTTCCCTGACTGGCAGAATTACACACCCGGACCCGGAGTCAGATACCC
TAGCAGAGAAAGACAGAGACAGATTCTATTCTATTAACGAATGGATTCTCAGCAACTGCCTCGGCAGATCCGCTGAG
CCTGTGCCTCTGCAACTGTATAAGACACTGAGAGCCGAACAGGCTACCCAAGAGGTCAAGAATTGGATGACCGAGA
CACTGCTCGTGCAAAACGCTAACCCTGACTGTGAGAGAGTGTATCTGGCTTGGGTCCCCGCTCATAAAGGCATTGG
CGGAAACGAACAGGTGGACAAACTGGTCAGCGCTGGCATTAGGAAAAACAGACCCCTAACCCTCAGGAAATCCATCTG
GAAACGTCACCGAGAACTTTAACATGTGGAAAAACGATATGGTGGAGCAAATGCATGAGGCTGGCTATGCCATTCT
TGAAATGCAATAACAAAAGGTTCAACGGAACCTGGACCCAGTAAGAATGTGTCCACCGTCCAGTGTACCCATGGCCT
AGAGCTCAAGAATAGCGCTATCTCCCTGCTCAACGCTACCGCTATCGCTGTGGCTGGGTGGACCGATAGGGTTATC
GAAGTGGTTTCAGTCCCGGCATCCCAAAGTGTCCAGCGAAGTGCATATCCCTCTGGGAGACGCTAGGCTCATCATTA
GGACATACTGGGGCCTCCACACAGGCGCTGCTATGGGCGGTAAATGGTCCAAGTGCTCCCTCGTCGGATGGCCCCG
AGTGAGAGAGAGAATCAGACAGACACCCCTGCCGCTGAGGGAGTGCTCAAGACCGGCAAGTACTCTAGGAAGAGG
GGTGCCCATACCAATGACGTCAAGCAACTGACAGAGGCTGTGCAAAAGATTGCCACAGAGTCTAGCTGGGAGGGTC
TGAAATACTGGGGGAATCTGCTCCAGTACTGGGGCCAGGAACTGAAATCTCCGCCGTCAGCCTCCTGAATGCCAC
AGCCATTGAGCTGCCGTGAGAAAGAAAGCTGGACCGTCAACGATATCCAAAAGCTCGTGGGAAAGCTCAACTGGGCA
TCCCAGATTTACCCCGGAAGAGCCATTGAGGCTCAGCAACACATGCTGCAACTGACAGTGTGGGGCATTAAGCAAC
TGCAAGCCAGAGTGCTCGCCATTGAGAGATACCTCGCCCTCCAGGATAGCGGATTGGAAGTGAATATCGTCACCGA
TAGCCAATACGCTCTAGGCATCATTCAGGCTCAGCCTGACAAAAGCGAAAGGGAAATCTCCAACATATACCAATCAG
ATTTACAAGATCCTCACCGAATCTCAAAATCAACAGGATAGGAATGAGAAAGACCTCCTGGCTCCACAAAAGGCTA
AGAGAAGGGTCGTGCAAAGGGAAAAGCGTGCCGTCGGCATTGGCGCTATGTTTCTCGGATTCTCGGCGCTGCCAA
ACCCAAAATGATCGGAGGCATTGGAGGCTTTATCAAAGTCAGGCAGTATGACCAAATCCTTATCGAAATCTGTGGA
AACAAGGCTATCTCTACCATAGGCTCAGGGATTTCATTCTGATCGTCGCTAGGATTGTGGAACCTGCTCGGCCGTA
GCTCCCTGAAAGGCCTCCAGAGAGGCACACTGAATGCCTGGGTGAAAGTGATTGAGGAAAAGGGATTGAGTCCCGA
AGTGATTCCCATGTTTTCCGCTCTGTCCGAGGGAGCCACACTCGAGTgaagatctgaattc

Figure 30 (Cont)

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B2 fragment

ggatccaccATGCTCGAGAATATGCTCACCCAAATCGGATGCACACTGAATTTCCCTATCTCCCCATTGACACAG
TGCCCTGTGAAACTGAAACCCGGAATGGATGGCGCCGCCATCTTTAGGCCCTGGCGGAGGCAATATGAAAGACAATTG
GAGAAGCGAACTGTATAAGTATAAGGTCGTGAAGATTAAGCCTCTGGGAATCACATGGATTCCCGAATGGGAGTTC
GTCAACACACCCCCACTGGTCAAGCTATGGTATCAGCTGGAGAAAGAGCC'TATCGTTGGCGCTGAGCCTCAGGATC
TCAACACGATGCCGAATACTGTAGGAGGCCATCAGGCTGCTATGCAAATGCTGAAAGACACAATCAATGAGGAAGC
CGCTGTCTCTGTTTCTGGATGGCATTAACAAAGCTCAAGAGGAACATGAGAAGTATCACTCCAACCTGGAGGACAATG
GCCAACGACTTTAATCTGATGAAGCATCTCGTCTGGGCCTCTAGGGAGCTGGAGAGATTCTGCTCTGAATCCCGGCC
TTGGAGACATCCGAAGGCTGTAAGCAAATTGCTGAGGAAGAGATTATCAT'TAGGTCCGAGAATTTCAAAACAA
TGTCAAAACCATTATCGTCCACCTCAACGAAAGCGTCGAGATTAACATGGGCGCTAGGGCAAGTGTCTCAGCGGC
GGCAAGCTGGACGCCTGGGAAAAGATTAGGCTCAGGCCTGGCGGCAAGAAAAAGTATAGGCTCAAGGAGAAGGGAG
GCCTGGACGGACTGATTTACTCCCAAAGAGGCAAGACATTCTGGATCTGTGGGTGTATAACACACAGGGATTAC
TAGATGGGGAACCTTGATCCTCGGCTTGTTGATTATCTGTAGCGCCAGCGAGAATCTGTGGGTGACAGTGTATTAC
GGAGTGCCTGTGTGGAGGAGACAGCTCCTGTCCGGCATTGTGCAACAGCAAAATAACCTCCTGAGGGCTATCGAAG
CCCAACAGCATCTGCTCCAGCTCACCGTCTGGGTGAGGCATTTCCCCAGGCCTTGGCTCCACAGCCTGGGACAGTA
CATCTATGAGACATACGGAGACACATGGTCGGGAGTGGAAAGCCCTCAAAGCCCTCATCAAAACCCAAAAAGATTAAAG
CCTCCCTCCCATCCGTGAAAAAGCTCACCGAAGACAAATGGAATAAGCCTCAAAGACATATAGCGCTGGCGAAA
GGATTGTGATATCATTGCAACCGACATTCAGACTAAGGAACTGCAAAACCAAATCATAAAGATTGAGAATTTTCGC
TGTGTTTATCCATAACTTTAAGAGGAAGGGAGGCATTGGCGGCTACTCCGCCGGAGAGAGAATCATTGACATTATC
GCCAGCGATATCGTTCCCGTGGGCGATATCTATAAGAGATGGATCATCTCTGGGACTCAACAAAATCGTGAGAATGT
ATTCACCCGTCAGCATTCTGGATATCAGAGTGAGACAGGGATACTCCCCCTCAGCTTTCAGACACTGATGCCCGC
TCCAGAGGCCCTGACAGACTCGAACGCATTGAGGAAGAGTCCAGGCAGGACCATCAGTATCCCATTTCCGAACAG
CCTCTGTCTCAGACAAGGGGAGACAATCCACAGACCTTAAGGAAAGCAAAAAGGCTAGTGGAGTGGTCGAGTCCA
TGAATAAGGAACTGAAAAAGATTATCGGACAGGTGAGGGACCAGGCTGAGCACCTGAAAACCGCTGTGCAATGGC
TGCCATGCGATGCTCAAGGATACCATTAACGAAGAGGCTGCCGAGTGGGACAGAATCCATCCCGTCCATGCCGGA
CCCATTGCCCCCTCTACCGAGATTTGTAAAGAAATGGAAAAAGAAGGCCAAAATCTCCAGGATTGGCCCTGAGAATC
CCTATAACACACCCGTCTTTGCCATTCAAGTGAGAGACCAAGCCGAACACCTCAAGACAGCCGTCCAGATGGCAGT
CTTCATTCACAATTTCAAAGGAAAGGCGGAATCGGAGGCAAAAAGAAAGATAGCACAAAGTGGAGGAAACTGGTT
GACTTTAGGGAGCTCAACAAACGTACACAGGATTTCTGGGAGGTCCAGCTCGGCTTTTCGGCTCTGGCTTGGGATG
ACCTCAGGAGCCTGTGTCTGTTCAGCTATCACAGACTGAGAGACTTTATCCTCATCGTTGCCAGAACCTGCCGACA
TAGCAGAATCGGCATCACTAGGCAACGTAGAGGTAGGAACGGCTCCTCCAGGTCCGCTGCCCCCAAATCTCCTTC
GACCCCATTCCTTCACTATTGCGCTCCCGCTGGCTTCGCTATCCTCAAGTGTAACAATAAGACATTCAATGGCG
AAAAGGATTGGCATCTGGGACAGGGAGTGTCCATCGAATGGAGAAAGAAAAGCTATAGCACACAGGTGGACCTGA
CCTCGCCGATCAGCCTAGCCTCTATCCTCCCTTAGCTTCCCTGAAAAGCCTCTTCGGAACGATCCCTCATCCCAA
GCCGCTAGAAGGGCTATCCTCGGCCAAATAGTCAGGAGAAGGTGTGAGTATCAGTCCGGACACAATAAGGTCCGCT
CCCTGCAATACCTTGACCTCAGCCAACCCAAAACCGCTTGCTACAAGTGTACTGTAAGAAATGTTGCTACCACTG
TCAGGTCTGCTTCTGAAAGAGGGACTGGGAATCAGGGATTACGGAAGCAAATCGCTGGCGCTGACTGTGTGGCC
AGCAGGCAAGACGAAGACGCAGCCAAGTACCATAGCAATTGGAGAACCATGGCCAGTGAGTTAACCTCCCCCTA
TCGTGCTAAGGAAATCGTCGCAAGTTGTGATAAGTGTAACGAATGGACACTGGAAGTCTGGAGGAACTGAAACA
TGAAGCCGTGAGACACTTTCCAGACCTGGCTGCATGGCCTCGGTCAACACGATATCATTAGCCTCTGGGATCAG

Figure 30 (Cont)

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TCCCTGAAACCCTGTGTGAACTGACACCCCTCTGCGTCACCCTCAACTGTACCAATGCCAATCTGCTGAAGAGCT
ACTCCACCCCAAGTGGACCCCGATCTGGCTGACCATCTGATTACCTCCACTATTTTCGATTGCTTTTCCGATAGCGC
AATCCATCCCATGGGCCCTACACGGAATGGAGGATGAGGAAAGGGAAGTGCTGAAATGGAAATTCGATAGCCATCTG
GCTCTCAGGCATATCGCTTCTAGTCCTATCGATAACCGTCCCCGTCAAGCTCAAGCCTGGCATGGACGGACCCAAAG
TGAAACAGTGGCCCCCTCACCGAAGAGAAAATCAAAGCCATTTGGCCTAGCAACAAGGGAGGGCCTGGCAATTTCCCT
GCAGTCCAGGCCTGAGCCTACCGCACCCCCAGCCGAGAACTTTAGATTTCGGCATTAGCAAAAAGGCTAAGGGATGG
TTTTACAGACACCATTACGAAAGCCAACACCCTAAGGTGAGCTCCGAGGTCCACATTTCCCTCAGCATGATGACCG
CTTGCCAAGGCGTCGGCGGACCCAGTCACAAAGCCAGGGTACTGGCAGAGGCTATGTCCCAGGTGAACAACGCTAA
CATTCCTCCCATTGTGCCCCAAAGAGATTGTGGCAAACCTGTGACAAATGCCAGCTCAAGGGTGAGGCTATGCACGGA
CAGGTGGACTGTAGCCCTTCCGAGGGATCAAGACAGGCTAGGAAGAACAGACGTAGAAGGTGGCGTGAGAGGCAAA
GGCAAATCCGCGCCATCTCCGAGTGGATTCTGGGACAGATAAGGGAACCCAGAGGCTCCGACATTGCCGGTACCAC
AAGCACACTGCAAGAGCAAATCGCATGGATGACAAACAATCCCCCTGGCATTAAAGCAAGAGTTTGGCATTCCCTAT
AACCCTCAGTCCCAGGGCGTCGTGGAAAGCATGAACAAAGAGCTCAAGAAAATCATTGGCAGACAGGAGATCCTCG
ATCTCTGGGTCTACAATACCCAAGGCTTTTTCCCTGACTGGCAGAATTACACACCCGGACCCGGAATCAGATACCC
TAGCAGAGCAAGACAGAGACAGATTCTATGCTATTAGCGAAAGGATTCTCAGCAACTTCCTCGGCAGACCCGCTGAG
CCTGTGCCTCTGCAACTGTATAAGACACTGAGAGCCGAACAGGCTACCCAAAGAGGTCAAGAATTGGATGACCGACA
CACTGCTCGTGCAAAACGCAAACCCTGACTGTGAGAAAGTGATCTGGCTTGGGTCCCCGCTCATAAAGGCATTGG
CGGAAACGAACAGGTGGACAAACTGGTCAGCGCTGGCATTAGGAAAAACAGACCCTAACCCCTCAGGAAATCGATCTG
GAAAACGTCACCGAGAACTTTAACATGTGGAAAAACAATATGGTGGAGCAAATGCAAGAGGCTGGCTATGCCATTCT
TGAAATGCAATAACAAAAAGTTCAACGGAACCTGGACCCTGTAAGAATGTGTCCACCGTCCAGTGTACCCATGGCCT
AGAGCTCAAGAATAGCGCTGTCTCCCTGCTCAACGCTACCGCTATCGCTGTGGCTGAGTGGACCGATAGGGTTATC
GAAGTGGTTTCAGTCCCAGCATCCCAAAGTGTCCAGCGAAGTGCAATATCCCTCTGGGAGACGCTAGGCTCGTCATTA
AGACATACTGGGGCCTCCACACAGGCGCTGCTATGGGCGGTAAATGGTCCAAGTGCTCCCTCGTCGGATGGCCCCGC
AGTGAGAGAGAGAATCAGACAGACACCCCTGCCGCTGAGGGAGTGCTCAAGACCGGCAAGTACTCCAGGATGAGG
AGTGCCCATACCAATGACGTCAAGCAACTGACAGAGGTTGTGCAAAAGATTGCCACAGAGTCTAGCTGGGAGGGTC
TGAAATACTTGTGGAATCTGCTCCTGTACTGGGGCCTGGAAC TGAAAACTCCGCCGTGAGCCTCCTGAATGCCAC
AGCCATTGTGCTGCTGAGAAAGAAGGCTGGACCGTCAACGATATCCAAAAGCTCGTGGGAAAGCTCAACTGGGCA
TCCCAGATTTACGCCGGAAGAGCCATTGAGGCTCAGCAACACTTGCTGCAACTGACAGTGTGGGGCATTAAAGCAAC
TGCAAGCCAGAGTGCTCGCCATTGAGAGATACCTCGCCCTCCAGGATAGCGGATCGGAAGTGAATATCGTCACCGA
TAGCCAATACGCTCTAGGCATCATTGAGGCTCAGCCTGACAAAAGCGAAAGGGAAATCTCCAACATATACCAATCAG
ATTTACAAGATCCTCACCGAATCTCAAATCAACAGGATAGGAATGAGCAAGAATCCTGGCTCCCAAAAGGCTA
AGAGAAGGGTCGTGCAAAGGGAAAAGCGTGCCGTGGCATTGGCGCTATGTTTTTCGGATTCTCGGCGCTGCCAA
ACCCAAAATGATCGGAGGCATTGGAGGCTTTATCAAAGTCAGGCAGTATGACCAAATCCTTATCGAAATCTGTGGA
CAGAAGGCTATCTCCTACCATAGGCTCAGGGATTTCATTCTGATCGTCGCTAGGATTGTGGAAC TGCTCGGCCATA
GCTCCCTGAGAGGCCTCCGGAGAGGCACACTGAATGCCTGGGTGAAAGTGGTTGAGGAAAAGGGATTCAATCCCGA
AGTGATTCCCATGTTTACCGCTCTGTCCGAGGGAGCCACACTCGAGTgaagatctgaattc

Figure 30 (Cont)

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C1 fragment

ggatccaccATGCTCGAGAGCAACACACCCGCTAATAATGCCGATTGCGCGTGGCTGAAAGCCCAGGAAGAGGAAG
AAGTGGGATTTTCCTGTGAGACCCCAAGTGCCTAGAGCTTGGAGGGCTATCCTCAACATTTCCAGGAGGATTAGGCA
AGGCTTTGAGAGAGCCCTCCTAGCCGCCGAATGGGACAGGGTTACCCCTGTGCACGCTGGCCCTGTCTGCTCCCGGC
CAAATGAGAGAGCCCAGAGGAAGCGATATCGCTGGCACAACCCCTCAGGCCCATGACATATAAGGCCGCTATTGACC
TCAGCTTGTTCCTGAAAGAGAAAGGCGGACTGGAAGGCCTCATCTATAGCAAGAAAGCTGCTATGGAACAGGCTCC
CGAAGACCAAAGCCCTCAGAGAGAGCCTTACAATGAGTGGACCCCTGGAGCTCCTGGAAGAGCTCAAGAAAAGAGGCT
CAAGGCCAATGGACCTACCAAATCTTTAGGAACCCCTTTAAGAATCTGAAAACCGGAAAGTATTCCAGAATGAGAA
GCGCTCACACAAACTGGATGACAGAAACCCCTCCTGGTCCAGAATGCCAATCCCGATTGCAAGTCCATCCTCAGGGC
TCTGGGAACCGGAGCCACACTGGAAGAGCCTGAGGTATCCCTATGTTCTCAGCCCTCAGCGAAGGCGCTACCCCC
CAAGACCTGAATACGATGCTCAACATCGTCAGCGGACACCAATCCACCCCTCCAGGAACAGATTGGCTGGATGACAA
ATAACCCCTCCCATCCCTGTCTGGAGAGATTTACAAAAGGTGGATTATCCTCGGCCCTGACTAGAATCCCCCATCCCGC
CGGCCTCAAGAAAAAGAAAAGCGTCACCGTCTGGATGTGGGAGACGCTTACTTCAGCGTCCCCCTCGACGAAGAC
CAAAAGGAAACCTGGGAGGCTTGGTGGACGGAATAC'TGGCAGGCTACCTGGATTCTCTGAGTGGGAGTTTGTGAATA
CCCCCTCCCCCTCGTGTTCCTCGATTGGCATAACTATACCCCTGGCCCTGGCATAAGGTATCCCCCTACCTTTGGATG
GTGCTTTAAGCTCGTGCCTGTGGACCCCAAAC'TGTGTTACCAACTGGAAAAGGAACCCATTGTCTGGAGCCGAAACC
TTTTACGTGGACGGAGCCGCCAACAGAGAGACAAAGCTCGGCCAAAACGTCCAGGGACAGATGGTGCATCAGGCTA
TTAGCCCCAGGACCCCTCAACGCTTGGGTCAAGGTCTGTCGAAGAGAAAAGCCTTTAACGAAACCGAAGTGCATAACGT
CTGGGCTACCCATGCCTGTGTGCGTACCGATCCCAATCCCCAAGAGATTCTCCTGGAGAATGTGACAGAGCTCAAG
GATCAGAAACTCCTCGGCATTTGGGGATGCTCCGGCAAAATCATTTGCACAACCACTGTGCCTTGGAACAGCTCCT
GGTCCAACCAAGCTGGCCATAACAAAGTGGGAAGCCTCCAGTATCTGGCTCTGACGGCTCTGATTAAGCCTAAGAA
AATCAAACCCCCCTCTGCCTAGCGTTAAGACAATCATTTGTGCATCTGAATGAGTCCGTGGAAATCAATTGCACAAGG
CCTAACAATAACACAAGGAAAGCCGCCGCTAGTGAAGTACGGAATAAGTCCAAACAGAAAACCCAGCAAGCTGCCG
CCGATACAGGCGACTCCAGCCAGGTACGCCAAAACCTATCCCATTTGTGTCCAACCTTTACCTCCACCAC'TGTGAAAGC
CGCTTGT'TGGTGGGCCAATATCAAACAGGAGTTTGGAAATCCCTTACAATCCCCAAAGCCAAACATTC'TATGTGGAT
GGCGCTGCCAATAGGGAAACCCAACTGGGAAAGGCGGGCTATGTGACAGACAAAGGCAGACAGAAAGTCATTAGCG
GAATCTGGCAGCTCGACTGTACCCATCTGGAAGGCAAAAGTCATTCTGGTAGCCGTCCACGTCGCCTCCGGCTACAT
TGAGGCTGAGGTCTGGCAATGAGCAAGTGGATAAGCTCGTGAGTTCGGGAATCAGAAAGGTGCTATTCTCTCGACGGA
ATCAATAAGGCTCAGGAAGAGCACGAAGTCAGGGAAAGGATTAGGCGAACCCTCCCGCTGCTGAAGGCGTCGGCG
CTGTCTCCCAGGATCTGGATAAGTACGGAGCCCTCACCTCCACAAGCGGAACCCAACAGTCCCAGGGAACTGAAAC
TGGCGTCTGGCAACCCCTCAGATTTTGGGAGAGTCCAGCGTTGTCTCTGGCTCCGGCTCCATCGTCATCTGGGGTAAA
ACCCCTAAGTTTAAGTTCCCCATTCAGAAAGAGACATGGGAAGCCTGGTGGACGGAGTATTGGCAAGCCGCTGCTT
ACAGACTGATCAGCTGTAAACACAAGCGTTATCAAACAGGCTTGCCCTAAGATTACCTTTGACCCTATCCCTATCCA
TTACTGTGCCCTCCTAGCTGGATGGGCTATGAGCTCCACCCTGACAGATGGACAGTGAACCCATCGTGCTCCCC
GAAAAGGACTCCTGGACAGTGAATGACATTCAGAAATCAATTCTGAGAGCCCTCGGCCCAGGCGCTTCCCTGGAGG
AAATGATGACAGCATGTCTAGGGAGTGGGAGGCCCTGGCCATAAGGCTAGAGTGTATTACAGAGACTCCAGGGACCC
CATTTGGAAAGGCCCTGCCAAACTGCTCTGGAAAGGCGAAGGCGCTGTGGTCATCCAAGACATTAAGATTGGAGGC
CAACTGATAGAAGCCCTCCTGGATACAGGAGCCGATGACACCGTCTGGAAGATATGAATCTGCCTGGCAAGTGGG
GAATCAAACAGCTCCAGGCTAGGGTCTGGCTATCGAGAGGTATCTGAAAGATCAACAGTTTCTGGGACTCTGGGG
CTGTAGCGGAAAGGCTGCTATGGAAAACAGATGGCAAGTGATGATCGTCTGGCAAGTGGACAGGATGAAGATTAGG

Figure 30 (Cont)

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ACATGGAATAGCCTCGTGAAACACCATATGTATATTATCTGTACCACAACCGTCCCCTGGAACCTCCACCTGGAGCA
 ATAAGTCCTTCGAAGAGATTTGGAATAACATGACCTGGATTCAATGGCTGATTCTCGCTATCGTTCGTGTGGACCAT
 TGTGTATATCGAATACAAGAACTGCTCAGGCAAAGGAGAATCGATAGGCTCATCAAAGGCTCAACCTTGGCCTC
 CTGGAACCCGCTGAGGGATGTAAACAGATCCTGGAACAGCTCCAGCCCGCCCTCCAGACAGGCACCGAAGAGCTCT
 CTAGTAGAAAGCTCCTGAAACAGAGAAAGATTGACAGACTGATTGAGAGAATCAGAGAGAGAGCCGAAGACTCCCG
 CAATGAGTCCGAGGGAGACACACCCCGAATCAGATACCAATACAATGTGCTCCCCAAGGCTGGAAGGGCTCCCCA
 CCCATTTTCCAAAGCTCCATGACCCAAATCCTCATGATGCAAAGGGGAACTTTAAGGGACAGAAAAGGATTATCA
 AGTGCTTCAACTGTGGAAGGAAGGCCATCTCGCTAGGAATTGCAGACCTCCCCCTAGAGAGACTGAACCTGGATTG
 CTCCGAGGATAGCGACACCTCCGGCACACAGCAAAGCCAAGGCACAGAGACAGAAGTGGGACTCGTGGCTGTGCAT
 GTGGCCAGCGATATATCGAAGCCGAAGTGATCCCTGCCGAACTGGACAGGAAACCGCTTACTTTATCCTCAAGA
 TTAAGCCTGTGGTTCAGCACACAGCTCCTGCTCAACGGTAGCCTCGCTGAAGAGGAAATCATTTATCAGAAGCGAAAA
 CTTTACCGATAACAACTGGTCCGCAAACCTGAATTGGGCTTCCCAAATCTACGCTGGCATCAAAGTGAAGCAACTG
 TGTAAGCTCCTGAGAGGCACCAAAGCCCTCACTCCTCTGTGTGTGACACTGAATTGCACAAACGCTAACCTCATCA
 ATGTGAATGCTGCTCAAACCAGAGGCGATAACCTACCGGTCCCGAAGAGTCCAAGAAAGAGGTTCGCGTCCAAGAC
 AGAGACAGACCCCTTGTGACGCCGCCCTAGCTCCAACCTTTCTGGGAAGGTCTGCCGAACCCGTCCCCCTCCAGCCC
 CCCCCCTCTGGAAGGCTCCACCTCGACTGTAGCGAAGACTGTGGCGAACTGGATAAGTGGGCCTCCCTGTGGAACCT
 GGTTCATATACCAACTGGCTGTGGTACATTAAGATTTTCATTATGATTGTGGGAGGCAATAAGATTGTGAGGAT
 GTACTCACCTGTCTCCATCCTCGACATTAAGCAAGGCCCTAAGGAACCTTCAGGGATTACGTGGACAGATTGCT
 AAGCTCCTGTGGAAGGGAGAGGGAGCCGTGCTGATTTCAGGACAACTCCGACATTAAGGTGCTGCCAGGAGAAAGG
 CTAAGATTATCGAACTGAATAAGAGAACCAGACTTTTGTGAAGTGCAACTGGGAATCCCTCACCTGTGGAAGT
 GAAGAAGAAAAAGTCAGTGACAGTGGCCGCTATGAGAGTGAAAGAGACACAGATGAAGTGGCCCAATCTGTGGAAG
 TGGGGCACAATGATTCTGGGACTGGTCATCATTTGCTCCGCCCTCCATTAAGGTGAGACAGCTCTGCAAACCTGCTCA
 GGGGTACAAAGGCTCTGACAGAGATTGTGACACTGACAGAGGAAGCCGAACCTGGAAGTGTCTATATGGAAGTTTGA
 CTCCCGCCTCGCCCTGAGACATATCGCCAGGGAACTGCATCCCGAGTTCTACAAAGACTGCGTGTGTGAGCTC
 CTGGGACGCTCCAGCCTCAAGGGACTGCAAAGGGGATGGGAAGGCCCTCAAGTATTTGTGGAACCTCCTGCAGTATT
 GGGGCTCTAGCCTGGGGCAACTGCAACCTGCTCTGAAAACCGGATCAGAGGAAGTGAAGTCCCTGTATAACACAAT
 CGCTACCTCTGCTGTGTGCATCAGGAGCTCTACAAATACAAAGTGGTCAAATCAAACCCCTCGGCATTGCCCTT
 ACCAGAGCCAAAAGGAGAGTGGTTCGAGAGAGAGAAAAAGGCTCACCGAAATCGTCCCCTCACCGAAGAGGCTGAGC
 TGGAGCTGGAGGAAAACAGAGAGATTCTGAGGGAACCCGTCCACGGAGTGATAGAGTGCTCGCCGAAGCCATGAG
 CCAAGTCAACAATGCCAACATCATGATGCAGAGAGGCAATTTCAAAGGCCCTAAAGAGAATCATCAAACAAGAGGAA
 GAGGAGGTGCGCTTCCCCGTCAGGCCCCAGGTCCCACTGAGACCTATGACCTACAAAGGAGCCGTCGATCTGTCTT
 TCTTCAGACAGGGACCCAAAGAGCCTTTTCAGAGACTATGTGGATAGGTTTTTCAAACCCCTCAGGGCTGAGCAAGC
 CTCACAGGAAGTGAAAACTGGGAGAAAAATCAGACTGAGACCTGGTGGCAAAAAGAAATACAAAATGAAACACATT
 GTGTGGGCCTCCAGGGAAGTGGAAAGGTTTGCCTCCAGTATGCCCTCGGCATCATCGTAGCCCAACCCGATAAGT
 CCGAGTCCGAGCTCGTGAATCAGATTATCGAAGAGCTCATCAAGAAGATTGCCGTGCCCGGATGGACAGACAGAAT
 CATTGAGGTGACCAAAGGGCTTGGAGAGCCATTCTGAATATCCCAGGAGAATCAGACAGACTAGACTCGCCGGA
 AGGTGGCCCGTCAAGACAATCTATACCGATAACGGAAGCAATTTACAAGCGCTACCGTCAAGGCTGCCTGCTGGT
 GGGCTGATGTGAAACAGCTCACCGCAGTCGTCCAGAAAATCGCTACCGAAAGCATTTGTGATATGGGGAAAGACGCC
 CAAGTTCAGACTGCCTATCGCTGCCGCCAGCAACGAGAATGAGACCATGGCTGCTtgaagatctgaattc

Figure 30 (Cont)

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C2 fragment

ggatccaccATGCTCGAGAGCAACACAGCCGCTAACAATACCGATTGCGTGTGGCTGAAAGCCCAGGAAGAGGAAG
AAGTGGGATTTTCCTGTGAGACCCCAAGTGCTAGAGCCGGGAGGGCTATCCTCAACATTCCCACGAGGATTAGGCA
AGGCCTTGAGAGAGCCCTCCTAGCCGCCGAATGGGATAGGATTACCCCTGTGCACGCTGGCCCTATCGCTCCCGGC
CAAATGAGAGAGCCCAGGGGAAGCGATATCGCTGGCACAACCCCTCAGGCCCATGACATATAAGGCCGCTATTGACC
TCAGCTTGT'TTCTGAAAGAGAAAGGCGGACTGGATGGCCTCATCTATAGCAAGAAAGCTGCTATGGAACAGGCTCC
CGAAGACCAAAGCTCTCAGAGAGAGCCTTACAATGAGTGGACCCTGGAGCTCCTGGAAGAGCTCAAGCACGAGGCT
CAAGGCCAATGGACCTTCCAAATCTTTTCAGGAACCCCTTTAAGAATCTGAAAACCGGAAAGTATGCCAGAATGAGAG
GCGCTCACACAAACTGGATGACAGATACCCCTCCTGGTCCAGAATGCCAATCCCGATTGCAAGTCCATCCTCAAGGC
TCTGGGACCCGGAGCCTCACTGGAAGAGCCTGAGGTATCCCTATGTTCTCAGCCCTCAGCGAAGGCGCTACCCCC
CAAGACCTGAATATGATGCTCAACACCGTTCGGCGGACACCAATCCACCCCTCCAGGAACAGATTGGCTGGATGACAA
ATAACCCCTCCCATCCCTGTTCGGAGAGATTTACAAAAGGTGGATTATCCTCGGCCTGACTAGAATCCCCATCCCGC
CGGCCTCAAGAAAAAGAAAGCGTCACCGTCTGGATGTGGGAGACGCTTACTTCAGCGTCCCCCTCGACGAAGGC
CAAAGGGAAACCTGGGAGGCTTGGTGGATGGAATACTGGCAGGCTACCTGGATTCTGAGGGGGAGTTTGTGAATA
CCCCTCCCCCTCGTGT'TTCCCGATTGGCAAAACTATACCCCTGGCCCTGGCACAAGGTATCCCTCACCTTTGGATG
GTGCTTTAAGCTCGTGCCTGTGGACCCCAAACCTGTGGTACCAACTGGAAGGAGCCCCATTGTCGGAGTGGAAACC
TTTACGCGGACGGAGCCGCCAACAGAGAGACAAAGCTCGGCCAAAACGTCCAGGGACAGATGGTGCATCAGCCTA
TTAGCCCCAGGACCCCTCAACGCTTGGGTCAAGGTATCGAAGAGAAAGGCTTTAGCGACACCGAAGTGCATAACGT
CTGGGCTACCCATGCCTGTGTGCCTACCGATCCCAATCCCAAGAGATTCTCCTGGAGAATGTGACAGAGCTCAAG
GATCAGAAAACCTCCTCGGCATTTGGGGATGCTCCGGCAAACCTCATTTGCACAACCACTGTGCCTTGGAACAGCTCCT
GGTCCAACCCAGCTGGCCATAACAAAGTGGGAAGCCTCCAGTATCTGGCTCTGAAGGCTCTGATTACGCCTAAGAA
AATCAAACCCCTCTGCCTAGCGTTAAGACAATCATTTGTGCATCTGAATGAGTCCGTGGAAATCAATTGCACAAGG
CCTAACAATAACACAAGGACAGCCGCCGCTAGTGAAGTACAGAATAAGTCCAGACAGAAAACCCAGCAAGCCGCCG
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CGCTTGT'TGGTGGGCCAATATCAAACAGGAGTTTGGGAATCCCTTACAATCCCCAAAGCCGAACATTCTATGTGGAT
GGCGCTGCCAATAGGGAAACCAAACCTGGGAAAGGCTGGCTATGTGACAGACAGAGGCAGACAGAAAGTCGTTAGCG
GAATCTGGCAGCTCGACTGTACCCATCTGAAAGGCAAAGTCATTTCTGGTAGCCGTCCACGTGCCTCCGGCTACAT
TGAGGCTGAGGTGGCAATGAGCAAGTGGATAAGCTCGTGATTTCCGGAATCAGAAAGGTGCTATTCTCAGCGGA
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CTGTCTCCAGGATCTGGATAAGTACGGAGCCATCACCTCCACAAGCGGAACCCAACAGTCCAGGGAACCTGAAAC
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ACCCCTAAGTTTAAGCTCCCATTCAGAAAAGAGACATGGGAAACCTGGTGGATGGACTATTGGCAAGCCGCTGCTT
ACAGACTGATCAGCTGTAACACAAGCGTTATCACACAGGCTTGCCCTAAGATTAGCTTTGAGCCTATCCCTATCCA
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GAAAAGGAGTCTTGGACAGTGAATGACATTCAGAAAACAATTCTGAAAGCCCTCGGCCCAGGCGCTACCCCTGGAGG
AAAATATGACAGCATGTCTAGGGAGTGGGAGGCCCTGGCCATAAGGCTAGAGTGTATTACAGAGACTCCAGGGACCC
CATTTGGAAAGGCCCTGCCAAACTGCTCTGGAAAGGCGAAGGCGCTGTGGTTCATCCAAGACATTAAGATTGGAGGC
CAACTGAAAGAAGCCCTCCTGGATACAGGAGCCGATGACACCGTCTGGAAGATATCAATCTGCCTGGCAAGTGGG
GAATCAAACAGCTCCAGGCTAGGGTCTGGCTATCGAGAGGTATCTGAAAGATCAACAGCTTCTGGGAATCTGGAG
CTGTAGCGGAAAGGCTGCTATGGAACACAGATGGCAAGTGATGATCGTCTGGCAAGTGGACAGGATGAAGATTAGG

Figure 30 (Cont)

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ACATGGAATAGCCTCGTGAAACACCATATGTATCTTATCTGTACCACAGCCGTCCCCTGGAACCTCCACCTGGAGCA
ATAAGTCCCTTCGAAGAGATTGGAATAACATGACCTGGATTGAATGGCTGATTATCGCTATCGTCGTGTGGACCAT
TGTGTTTATCGAATACAAAGAACTGCTCAGGCAAAAGGAAAATCGATAGGCTCATCGAAAGGCTCAACCCTGGCCTC
CTGGAACCGCTGAGGGATGTAAACAGATCCTGGAACAGCTCCAGCCCGCCCTCAAGGCAGGCACCGAAGAGCTCT
CTAGTAGAAAGCTCCTGAGACAGAGAAAGATTGACAGACTGATTGAGAGAATCAGAGAGAGAGCCGAAGACTCCGG
CAATGAGTCCGAGGGAGACACACCCGGAATCAGATACCAATACAATGTGCTCCCCAAGGCTGGAAGGGCTCCCCA
GCCATTTTCCAAAGCTCCATGACCAAAATCCTCATGATGCAAAGGGGAACTTTAAGGGACAGAAAAGGATTATCA
AGTGCTTCAACTGTGGAAAGGAAGGCCATCTCGCTAGGAATTGCAGACCTCCCCTGGAGAGACTGAACCTGGATTG
CTCCGAGGATAGCGACACCTCCGGCACACAGCAAAGCCAAGGCACAGAGACAGGAGTGGGACTCGTGGCTGTGCAT
GTGGCCAGCGATATATCGAAGCCGAAGTGATCCCTGCCGAACTGGACAGGAAACCGCTTACTTTCTCCTCAAGA
TTAAGCCTGTGGTCAGCACACAGCTCCTGCTCAACGGTAGCCTCGCTGAAGAGGAAATCATTATCAGAAGCGAAAA
CTTTACCAATAACAACTGGTCGGCAAACCTGAATTGGGCTTCCCAAATCTACCCCTGGCATCAAAGTGAGGCAACTG
TGTAAGCTCCTGAGAGGCACCAAAGCCCTCACCCCTCTGTGTGTGACACTGAATTGCACAAACGCTAACCTCATCA
ATGTGAATGCTGCTCAACCCAGAGGCGATAACCCCTACCGATCCCAAAGAGTCTAAGAAAGAGGTGCGCTCCAAGGC
AGAGACAGACCCTTTTGACGCGCCCTAGCTCCACCTTTCTGGGAAGGTCTGTGCAACCCGTCCCCCTCCAGCTC
CCCCCTCTGGAAAGGCTCCACCTCGACTGTAGCGAAGACAGTGACGAACTGGATAAGTGGGCCTCCCTGTGGAAC
GGTTCAATATCACCAACTGGCTGTGGTACATTAAGATTTTCATTATGATTGTGGGAGGCAATAAGATTGTGAGGAT
GTACCAACCTGTCTCCATCCTCGACATTAAGCAAGGCCCTAAGGAACCCCTCAGGGATTACGTGGACAGATTGCT
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CTAAGATTATCGAACTGAATAAGAGAACCCAAAGACTTTTGGGAAGCGCAACTGGGAATCCCTCACCATGCTGGACT
GAAAAAGAAAAAGTCCGTGACAGTGGCCGCTATGAGAGTGAAAGAGACACAGATGAACTGGCCCAATCTGTGGAAG
TGGGGCACAATGATTCTGGGACTGGTCATCATTTGCTCCGCCCTCCATTAAGGTCAAACAGCTCTGCAAACCTGCTCA
GGGGTGCAAAGGCTCTGATAGACATTGTGCCACTGACAGAGGAAGCCGAACCTGGAACTGCTCATATGGAAGTTTGA
CTCCCACCTCGCCCTGAGACATATCGCCAGGGAACTGCATCCCGAGTACTACAAAGACTGCGCTGCTGTGAGCTC
CTGGGACGCTCCAGCCTCAAGGAAC TGCGAAGGGGATGGGAAGCCCTCAAGTATTTGTGGAACCTCCTGCAGTATT
GGGGCTCTAGCCTGGAGCAACTGCAATCTGCTCTGAAAACCGGATCAGAGGAACTGAGGTCCCTGTTTAACACAGT
CGCTACCCTCTGGTGTGTGCATCAGGAGCTCTACAAATACAAAGTGGTCAAATCGAACCCCTCGGCATTGCCCT
ACCAAAGCCAAAAGGAGAGTGGTCCAGAGAGAGAAAAGGCTCACCGATATCGTCACTCACCAGAGAGGCTGAGC
TGGAGCTGGAGGAAAACAGAGAGATTCTGAAGGAACCCGTCCACGGAGTGTATAGAGTGCTCGCCGAAGCCATGAG
CCAAGCCAACAATGCCAACATCATGATGCAGAGAGGCAATTTAGAGGCCCAAAGAGAATCATCAAACAAGAGGAA
GAGGGGTGCGCTTCCCCGTCAGGCCTCAGGTCCCACTGAGACCTATGACCTACAAAGCAGCCATCGATCTGTCT
TCTTCAAACAGGGACCCAAAGAGCCTTTAGAGACTATGTGGATAGGTTTTTCAAACCCCTCAGGGCTGAGCAAGC
CTCACAGGAAGTGAAAACTGGGAGAAAATCAGACTGAGATCTGGTGGCAAAGAAATACAACTGAAACACATT
GTGTGGGCCTCCAGGGAAC TGGAAGGTTTGCCTCCAGTATGCCCTCGGCATCATCTAGCCCAACCCGATAAGT
CCGAGTCCGAGCTCGTGAGTCAGATTATCGAAGAGCTCATCAAGAAGATTGCCGTGCGCGGATGGACAGACAGAGT
CATTTAGGTCGTCCAAAGGGCTTGAGAGGCCATTCTGAATATCCCAGGAGAATCAGACAGACTAGACTCGCCGGA
AGGTGGCCCCGTCAAGATAATCCATACCGATAACGGAAGCAATTTACAAGCACTGCCGTCAAGGCTGCCTGTGGT
GGGCTGATGTGAAACAGCTCACCGAAGTCGTTAGAAAATCGCTACCGAAAGCATTGTGATATGGGGAAAGACACC
CAAGTTCAGACAGCCTATCGCTGCCGCCAGCAACGAGAACATGGACGCCATGGCTGCTtgaagatctgaattc

Figure 30 (Cont)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/AU01/00622

A. CLASSIFICATION OF SUBJECT MATTER		
Int. Cl. ⁷ : C07K 19/00; C12Q 1/68; C07K 2/00, 14/005, 14/15, 14/20, 14/435; C12N 15/09		
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED		
Minimum documentation searched (classification system followed by classification symbols) SEE ELECTRONIC DATABASES BELOW		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched SEE ELECTRONIC DATABASES BELOW		
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) CA WPIDS MEDLINE: Combinatorial protein/peptide/polypeptide; gene/DNA shuffling; domain swapping; vaccine; synthetic protein/peptide polypeptide		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 00/18906 A. MAXYGEN INC. 6/4/00	All
X	WO 99/41402 A. MAXYGEN INC. 19/8/99	All
X	WO 99/41369 A. MAXYGEN INC. 19/8/99	All
X	WO 99/41368 A. MAXYGEN INC. 19/8/99	All
X	Ryu DDY and Nam D-H. Recent progress in biotechnological engineering. Biotechnol Prog. Jan-Feb 2000. 16: 2-16.	All
X	Punnonen J. Molecular breeding of allergy vaccines and antiallergic cytokines. Int Arch Allergy Immunol. March 2000. 121: 173-182	All
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C <input checked="" type="checkbox"/> See patent family annex		
* "A" "E" "L" "O" "P"	"T" "X" "Y" "&"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art document member of the same patent family
Date of the actual completion of the international search 1/8/01		Date of mailing of the international search report 7 August 2001
Name and mailing address of the ISA/AU AUSTRALIAN PATENT OFFICE PO BOX 200, WODEN ACT 2606, AUSTRALIA E-mail address: pct@ipaustalia.gov.au Facsimile No. (02) 6285 3929		Authorized officer Gillian Allen Telephone No : (02) 6283 2266

INTERNATIONAL SEARCH REPORT

International application No.

PCT/AU01/00622

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Coward E. Shufflet: shuffling sequences while conserving the k-let counts. Bioinformatics. 1999. 15(12): 1058-59.	60-77
X	Crameri A et al. DNA shuffling of a family of genes from diverse species accelerates directed evolution. Nature. 1998. 391: 288-291.	1,3,4-14, 30-33,47
X	Giver L and Arnold H. Combinatorial protein design by <i>in vitro</i> recombination. Curr Opin Chem Biol. 1998. 2: 335-338	1,3,4-14, 30-33, 47
X	Zhao H et al. Molecular evolution by staggered extension process (StEP) <i>in vitro</i> recombination. Nature Biotech. 1998. 16: 258-61.	
X	Patten P et al. Applications of DNA shuffling to pharmaceuticals and vaccines. Curr Opin Biotech. 1997. 8: 724-33	1, 3, 4-14, 19-33, 47
X	Fisch I et al. A strategy of exon shuffling for making large peptide repertoires displayed on filamentous bacteriophage. Proc Nat Acad Sci USA. 1996. 93: 7761-66	1, 2, 4-14, 30-33, 47
X	Stemmer WPC. DNA shuffling by random fragmentation and reassembly: <i>in vitro</i> recombination for molecular evolution. Proc Nat Acad Sci USA. 1994. 91: 10747-751.	1-18, 30-33, 47
X	Stemmer WPC. Rapid evolution of a protein <i>in vitro</i> by DNA shuffling. Nature. 1994. 370: 389-391.	1, 2, 4-14, 30-33

INTERNATIONAL SEARCH REPORT
Information on patent family members

International application No.
PCT/AU01/00622

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report		Patent Family Member	
WO 00/18906 A.	AU 11990/00	WO 99/41369 A.	AU 26741/99
	EP 1117777		AU 26742/99
WO 99/41402 A.			AU32891/ 99
			AU 32910/99
	AU 26742/99		EP 1053312
	AU 32891/99		EP 1053343
	AU 32910/99		EP 1054973
	EP 1053312		EP 1056842
	EP 1053343		
	EP 1054973	WO 99/41368 A	AU 26741/99
			AU26742/99
			AU 32891/99
			EP 1053312
			EP 1053343
			EP 1056842
END OF ANNEX			